A1927187 wo88c02.x1 NCI\_CGAP A143316 ti32a11.x1 NCI\_CGAP A143314 ti32a11.x1 NCI\_CGAP A0016729 MOUSE two-A0016729 MOUSE two-A1434956 ti46f04.x1 NCI\_CGAP B0C58804 naf1009.x1 Saares\_ BG540633 602570520F1 NHLMGC\_ CG6748 C86748 MOUSE fertiliz I AL265022 Terradoon nigrovir C66749 C86879 MOUSE fertiliz BF682484 wb05201.x1 NCI\_CGAP A1654506 wb65404.x1 NCI\_CGAP A1654506 wb65404.x1 NCI\_CGAP A1654506 wb65404.x1 NCI\_CGAP A1304490 qo54e06.x1 NCI\_CGAP A130490 AL530080 LTI\_NFL001 AM600940 RCI-BN0014-210100-0 AA021815 mh88d06.r1 Soares mou C87366 C87366 MOUSE fertiliz BG058796 naf10f12.x1 Soares A1157673 ue48910.r2 Soares m A1534937 tz74f09.x1 NCI\_CGAP AA016439 MOUSE two-A016439 MOUSE two-A016439 MOUSE two-ANGO1643 MOUSE two-ANGO16439 MOUSE TWO-ANGO16430 MOUSE TWO-ANGO16430 MOUSE TWO-ANGO16430 MOUSE TWO-ANGO16430 MOUSE TWO-ANGO16430 MOUSE TWO-ANGO1643

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uq46g03.yl NCI_CGAP_Mam5 Mus musculus cDNA clone IMAGE:2812468 5' similar to gb:M32745 mouse transforming growth factor beta-3 mRNA, Complete (MOUSE); mRNA, sequence.
755.93
729.91
703.78
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688.68
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Mus musculus
                       gb_est20:A1430179
gb_est20:A1433146
gb_est20:A1433146
gb_est20:A14529
gb_est20:A1434956
gb_est20:A1434956
gb_est20:BC58804
gb_gss4:CNS03XHH
gb_gss4:CNS03XHH
gb_est103:C86748
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9b_est18.A1273619

9b_est18.A1272440

9b_est17.A1192407

9b_est27.AA192407

9b_est27.AA600938

9b_est29.AA600938

9b_est49.AW600938

9b_est113.AW600938

9b_est16.AA604038

9b_est111.W98872

9b_est111.W98872

9b_est111.W98872

9b_est111.W98873

9b_est111.W98873

9b_est111.A44037673

9b_est27.A164914

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9b_est19.AA1604914
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gb_est1.AA016946
gb_est26.AI91883
gb_est49.AW600960
gb_est40.AI41206
gb_est20.AI414206
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gb_est30:AU050770
gb_est49:AW600942
gb_est106:N36741
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gb_est8:AA533093
gb_est78:BE737006
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gb_est23:AI654506
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gb_est91:BF723491
                                                                                                                                                                                                                                                                          gb_est91:BF682484
gb_est25:AI824845
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gb_est28:AL362754
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gb_est94:BF901708
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DEFINITION
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BG175423 60233778F1 NCI_CGAP_M
AL52438 AL53438 LTI_NEL001_NF
BF542567 U1-R-C3-sm-a-12-0-U1.r
I BF101203 601754782F1 NCI_CGAP_
AW670561 114647 MARC IPIG SUS S
BF042849 BP250019B10B3 Soares F
BF044812 BP250019B10B3 Soares F
BF044612 BP250019B10B3 Soares F
BG067564 H3055007-3 NIA Mouse I
AL323791 mm4760B.x1 Stratagene
BG575698 dc62d10.x1 NICHD XGC F
AM600944 RCI-BN0014-210100-012-
AA915041 vz01907.r1 Soares mous
BG244370 602356090F1 NCI_CGAP_M
AM919738 EST351042 Rat gene ind
A1323392 mj35f01.x1 Soares mous
BG518882 60276182F1 NCI_CGAP_M
AM958056 EST370126 MAGE reseque
BE464608 hx84h02.x1 NCI_CGAP_FI
AM958056 EST370126 MAGE reseque
BE464608 hx84h02.x1 NCI_CGAP_FI
A1323392 mj35f01.x1 Soares mous
BC518882 6027618271 NCI_CGAP_FI
AM958056 EST370126 MAGE reseque
BE464608 hx84h02.x1 NCI_CGAP_FI
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                                                                                                                                                                 Command line parameters:
-MODEL-frame+_p2n.model -DEV-x1h
-Q-CGGD_LTG2247_25239/app_query.fasta_1.159
-Q-CGGD_LTGSPTQ_spool/DUEFY097/xunat_29102001_162247_25239/app_query.fasta_1.159
-DB-EST -QFWT=fastap -SUFFIX=rst -GAPOP=12.000 -GAPEXT=4.000
-MINMARCH=0.100 -LOOPEXT=0.000 -CGAPOP=4.500
-GGAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500 -FGAPOP=6.000
-GGAPEXT=7.000 -YGAPOP=10.000 -XGAPEXT=0.500 -FGAPOP=6.000
-FGAPEXT=7.000 -YGAPOP=11.000 -YGAPEXT=0.500 -FGAPOP=6.000
-FGAPEXT=7.000 -GAPOP=11 -MATRIX-blosun62 -TRANS-human40.cdi
-LIST=100 -DOCALIGN=200 -THR_XSCORE=PCT -THR_MAX-100 -THR_MIN=0
-ALIGN=100 -MODE=LOCAL -OUTFWT=P1S -NORM=6Xt -MINLEN=0
-AALIGN=100 -WODE=LOCAL -OUTFWT=P1S -NORM=6XT -MAIT
-LOOPE -LOO
                                                                                              About: Results were produced by the GenCore software, version 4.5, Copyright (c) 1993-2000 Compugen Ltd.
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  out_format : pfs
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Query: TGFB3P
Query length: 113
Database: EST:*
Database sequences: 10228115
Database length: 431459454
Search time (sec): 1008.120000
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  OM Of: TGFB3P to: EST:*
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gb_est46:AM412139

gb_est46:AM412139

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gb_est89:BF542567

gb_est89:BF542567

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gb_est49:AW600952
gb_est42.AW073988
gb_est16:A1089904
gb_est16:A118173
gb_est16:A1148173
gb_est16:A1148173
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gb_est97:BG180040
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gb_est24:AI760533
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A1362754 AL362754 ICREP 522
A1452754 2155a05.x1 Soares\_N
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N55274 yv46d05.s1 Soares fet
A1610679 tp17q12.x1 NCI\_CGAP
BF723491 mab32f06.y1 Soares\_ BG247154 602561136F1 NCI\_CGAP
R36467 yh88d11.s1 Soares\_Pla

tgfb3p.rst

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Email: cgapbs-rémail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: The I.M.A.G.E. Consortium (CLNL)
Conne distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Organ: mammary; Vector: pCNV-SPORT6; Site_1: Sall; Site_2: Not1; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigators providing samples: Lothar Hennighausen/Robin Humphreys,
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                       1 (bases 1 to 645)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps: 0
Percent Identity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone_lib-"NCI_CGAP_Mam5"
/tissue_type="tumor, gross tissue"
/dev_stage="7 months"
/lab_host="DHIOB"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Align seg 1/1 to: AW412139 from: 1 to: 645
                                                                                                           Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1. .645
/organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                     High quality sequence stop: 446.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /strain="C57/B6"
/db_xref="taxon:10090"
/clone="IMAGE:2812468"
                                                                                                                                                                                                                                                                                                                                                                                                             primer: -40RP from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    175 g
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Percent Similarity: 100.000
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Ratio:
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TGFB3P x AW412139
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                                            REFERENCE
                                                                                                                                     JOURNAL
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                                                                                        TITLE
                                                                                                                                                          COMMENT
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BG175423 812 bp mRNA EST 06-FEB-2001
602337778F1 NCI_CGAP_Mam1 Mus musculus CDNA clone IMAGE:4460706 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: SalI; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigator providing samples: Gilbert Smith, NIH"

210 c 245 g 160 t
                                                                                                                                                                                                                                                                                                                                                    Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Confect: Robert Strausberg, Ph.D.

Email: Ggapbs-r@mail.nih.gov
    Tissue Procurement: Gilbert Smith, Ph.D.
    CDNA Library Preparation: Life Technologies, Inc.
    CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
    DNA Sequencing by: Incyte Genomics, Inc.
    Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
    http://inage.llnl.gov
    High quality sequence stop: 735.
    High quality sequence stop: 735.
                                                                                                                                                                                                                                                                                                                                                                                                                       1 (bases 1 to 812)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            159 ACGAACCTAAGGGTTACTATGCCAACTTCTGCTCAGGCCCTTGCCCATAC 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Mus musculus"
/strain="FVB\N"
/db_xref="taxon:10090"
/clone="IMAGE:4460706"
/clone_lib="NCI_CGAP_Mam1"
/tissue_type="tumor, blopsy sample"
/dev_stage="3 months, virgin"
/lab_host="bHl08"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length: 112
Gaps: 0
Percent Identity: 100.000
101 LeuSerAsnMetValValLysSerCysLysCysSer 112
                                                409 CTGTCCAACATGGTGGTGAAGTCGTGAAGTGCAGC 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Align seg 1/1 to: BG175423 from: 1 to: 812
                                                                                                                                                                                                                                                                          BG175423.1 GI:12682126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ratio: 5.652
Percent Similarity: 100.000
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                                                                                              seq_name: gb_est97:BG175423
                                                                                                                                                                                                                            mRNA sequence.
BG175423
                                                                                                                                                 seq_documentation_block:
                                                                                                                                                                                                                                                                                                                             house mouse
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TGFB3P x BG175423
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                                                                                                                                                                                                  DEFINITION
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COMMENT
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TITLE
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                                                                                                                                                                                                                                                                          VERSION
KEYWORDS
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84

3

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University of Iowa 451 Eckstein Medical Research Building Iowa City, IA 52242, USA 7e1: 319 335 826
Fax: 319 335 826
Email: msoares@blue.weeg.uiowa.edu
cDNA Library Preparation: M.B. Soares Lab Clone distribution:
clones will be available through Research Genetics (www.resgen.com)
This clone is also available through the I.M.A.G.E. Consortium at
LLNL (info@lmage.llnl.gov). IMAGE ID= 1768868
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        //dev_stage="adult"
//dev_stage="adult"
//lab_host="nbH10B (Life Technologies)"
//note="Vector: pT7730-pec (Pharmacia) with a modified
//note="Vector: pT7730-pec (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-C3
library is a subtracted library of a series, ultimately
derived from a mixture of individually tagged normalized
libraries from rat placenta, adult lung, brain, liver,
kidney, heart, spleen, ovary, muscle, and 8, 12 and 18-day
embryos, after a series of subtractions to reduce the
representation of cDNAs from which ESTs had already been
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ( ) (bases 1 to 503)

Bonaldo,M.F., Lennon,G. and Soares,M.B.

Normalization and subtraction: two approaches to facilitate gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BF542567 503 bp mRNA EST 11-DEC-2000 UI-R-C3-sm-a-12-0-UI.rl UI-R-C3 Rattus norvegicus cDNA clone UI-R-C3-sm-a-12-0-UI 5', mRNA sequence.
                                                                                                         84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                          561 AGCCCCTGACCATCCTGTACTATGTTGGGAGGACCCCCAAAGTGGAGCAG 610
                                                      361 GCGCCCCCTCTACATTGACTTCCGACAGGATCTGGGCTGGAAGTGGGTCC 410
        17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
                                                                                                                                                                                                                   LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh
                                                                                                                                                                                                                                                                                                                          rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Soares, MB Program for Rat Gene Discovery and Mapping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone="UI-R-C3-sm-a-12-0-UI"
/clone_lib="UI-R-C3"

    .503
    /organism="Rattus norvegicus"

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/db_xref="taxon:10116"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq_name: gb_est89:BF542567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Norway rat.
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TITLE
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MEDLINE
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KEYWORDS
SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 964)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
Contact: Genoscope
                                                                                                                                                                                                                                                                                                                                                                                                                                    AL532438 964 bp mRNA EST 13-FEB-2001
AL532438 LTI_NFL001_NBC4 Homo sapiens cDNA clone CS0DM014YD15 5
Prime, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              209 CTCCGCAGCGCAGACACCATAGCACGTGCTTGGACTATACAACAC 258
                                                                                                         84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
                                                                                                                                                                                                              67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG
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Percent Identity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="neuroblastoma cells"
                                                                                                                                                                                                                                                                                          101 LeuSerAsnMetValValLysSerCysLysCysSer 112
                                                                                                                                                                                                                                                                                                                       359 CTGTCCAACATGGTGTGAAGTCGTGTAAGTGCAGC 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone="CS0DM014YD15"
/clone_lib="LTI_NFL001_NBC4"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AL532438.1 GI:12795931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Quality: 633.00
Ratio: 5.652
Percent Similarity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                 seq_name: gb_est29:AL532438
                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
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TGFB3P x AL532438
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source

FEATURES

human.

ORGANISM

TITLE

COMMENT

REFERENCE AUTHORS

EST.

KEYWORDS SOURCE

DEFINITION

ACCESSION

VERSION

alignment\_scores:

BASE COUNT

ORIGIN

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seg_documentation_block:
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                                              TITLE
JOURNAL
               AUTHORS
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                                                                                                                            COMMENT
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generated. The following serially subtracted libraries were generated in this process: UI-R-C3, UI-R-C2p, UI-R-C1, UI-R-C0, UI-R-C2, UI-R-C2, UI-R-C1, UI-R-C1, UI-R-C3, UI-R-
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LOCUS BF101203 1820 bp mRNA EST 19-OCT-2000
DEFINITION 601754782F1 NCI_CGAP_Mam1 Mus musculus cDNA clone IMAGE:3983588 5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus
Sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia: Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases"1 to 1820)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          87 hrIleLeuTyrTyrValGlyArgThrProLysValGluGlnLeuSerAsn 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      312 CCATCTTGTACTATGTTGGCAGAACCCCCAAGGTGGAGCAGCTGTCCAAC 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 ThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysValArgProLe 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20 uTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValHisGluProL 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyrLeuArgSer 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      oGluAlaSerAlaSerProCysCysValProGlnAspLeuGluProLeuT 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Identity: 98,165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     to: 503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MetValValLysSerCysLysCysSer 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                362 ATGGTGGTGAAGTCGTGTAAGTGCAGC 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BF101203.1 GI:10883729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ratio: 5.606
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Align seg 1/1 to: BF542567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                611.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq_name: gb_est83:BF101203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mRNA sequence.
BF101203
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             106
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KEYWORDS
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/note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: Sall; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigator providing samples: Gilbert Smith, NIH"
533 c 590 g 184 t
                                                                      Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.

Tissue Procurement: Gilbert Smith, Ph.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Right row; d column: 21

High quality sequence stop: 601.
                                                                                                                                                                                                                                            þę
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    216 ACGCCCCTTTATATTGACTTCCGGCAGGATCTAGGCTGGAAATGGGTCC 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           166 GCCCTGGACACCAATTACTGCTTCCGCAACCTGGAGAACTGCTGTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue_type="tumor, biopsy sample"
/dev_stage="3 months, virgin"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps: 0
Percent Identity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1. .1820
/organism="Mus musculus"
/strain="reyb.N"
/db_xref="taxon:10090"
/clone="IMAGE:3983588"
/clone_lib="NCI_CGAP_Mam1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         465 CTGTCCAACATGGTGGAAGTCGTGTAAGTGCAGC 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              101 LeuSerAsnMetValValLysSerCysLysCysSer 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Align seg 1/1 to: BF101203 from: 1 to: 1820
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Percent Similarity: 100.000
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Ratio:
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TGFB3P x BF101203
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1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17
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                                                                                                                                                        DEFINITION
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JOURNAL
COMMENT
                                                                                                                                                                                          ACCESSION
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KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                 REFERENCE
                                                                                                                                                                                                                                                                                                                                                   AUTHORS
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                                                                                                                                                                                                                                                                                        DSDA, ASS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Fax: 402 762 4390
Fax: 402 762 4390
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
PCR PRIMERS
FORWARD: AGGAAACAGCTATGACCAT
                                                                                   pig.
Sus scrofa
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
1 (bases 1 to 477)
Fahrenkrug, S.C., Freking, B.A., Rohrer, G.A., Smith, T.P.L., Casas, E., Stone, R.T., Heaton, M.P., Grosse, W.M., Bennett, G.A., Laegreid, W.W. and Keele, J.W.
                                                                                                                                                                                                                   Design and use of two pooled tissue normalized cDNA libraries for EST discovery in swine Unpublished (2000)
Contact: Smith TPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI; Library made from pooled tissue from day 11, 13, 15, 20, and 30 embryos."
 09-JUL-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AW670561 477 bp mRNA 5', mRNA sequence.
114647 MARC 1PIG Sus scrofa cDNA 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps: 0
Percent Identity: 98.936
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Sus scrofa"
/db_xref="taxon:9823"
/clone_lib="MARC 1PIG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BACKWARD: GTTTCCCAGTCACGAG
Plate: 43 row: B column: 5
Seg primer: ATTTAGGTGACACTATAG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue_type="pooled"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            135 g
                                                 AW670561.1 GI:7527075
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                               AW670561
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TGFB3P x AW670561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alignment_scores:
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               DEFINITION
ACCESSION
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ORGANISM
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AUTHORS
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KEYWORDS
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Fax: 217 344 5617

Bmail: h-lewin6uiuc.edu

Faxearch Initiative, Animal Genome Resource Grant AG 99-3205-8534

To H. A. Lewin and J. E. Womack. Base Calling/Quality Scores: PHRED from Washington University Genome Center. Vector Trimmi g:

Cross_match from Washington University Genome Center PHRAP suite.

This sequence is vector free and at least 200 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 515)
Lewin,H.A., Soares,M.B., Rebeiz,M., Pardinas,J., Liu,L. and Larson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Organ: placenta; Vector: pT7T3Pac; Site_1: EcoRI; Site_2: NotI; The cDNA library was contributed by the Soares laboratory and it was constructed and normalized as described by Bonaldo, M.F., Lennon, G. and Soares, M.B. (1996), Genome Research 6(9): 791-806. "
113 c 111 g 165 t
                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (2000)
Contact: Lewin, H. A.
W. M. Keck Center for Comparative and Functional Genomics
University of Illinois at Urbana-Champaign
340 Edward R. Madigan Laboratory, 1201 W. Gregory Dr., Urbana, IL
                                                                                                                                                                                     BF042894 515 bp mRNA EST 10-OCT-2000 BP250019B10B3 Soares normalized bovine placenta Bos taurus CDNA clone BP250019B10B3 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1. 515
//organism="Bos taurus"
//do_xref="taxon:9913"
//clone="BP250019B10B3"
//clone=lbb="Soares normalized bovine placenta"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   to: 515
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FORMARD: TATACGACTCACTATAGGG
BACKWARD: ATTAACCCTCACTAAAG
Insert Length: 515 Std Error: 0.00
Plate: BP250019B10 row: B column: 3
Seq primer: AGCGGATAACAATTCACAGGA
High quality sequence stop: 515.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   from: 1
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to reverse of: BF042894
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /sex="female"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                     BF042894.1 GI:10759949
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5.095
93.750
                                                                                                        seq_name: gb_est82:BF042894
                                                                                                                                                               seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bovine ESTs
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TGFB3P x BF042894/rev
                                                                                                                                                                                                                                                                                                                                                                                Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61801, USA
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TGFB3P x BF543086/rev
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CDNA Library Preparation: M.B. Soares Lab Clone distribution:

clones will be available through Research Genetics (www.resgen.com)

This clone is also available through the I.M.A.G.E. Consortium at

LLNL (info@image.llnl.gov). IMAGE ID= 1790668

Seq primer: MI3 Forward.
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/lab_host="DH10B (Life Technologies)"
/note="Vector: pT7T3D-Fac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-AF1
library is a normalized library constructed from 15 dpc
rat atriaventricular (AV) canal. The tag is a string of
hucleotides present between the Not I site and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Métazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bonaldo,M.F., Lennon,G. and Soares,M.B. Normalization and subtraction: two approaches to facilitate gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BF543086 471 bp mRNA EST 11-DEC-2000 UI-R-AFI-aaq-f-07-0-UI.rl UI-R-AFI Rattus norvegicus cDNA clone UI-R-AFI-aaq-f-07-0-UI 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
451 Ecstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 9256
Fax: 319 335 9565
374 ATGAGCCTAAAGGGTACAATGCCAACTTCTGTGCTGGAGCATGCCCATAT 325
                                                                                                                                                                                                                                                                                                                                                                              84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
                                                                                                                                      17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
                                                                                                                                                                                                                                                                                                   84
                                                                                                                                                                                                                                                                                                 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone="UT-R-AR1-aaq-f-07-0-UI"
/clone_lib="UT-R-AR1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Rattus norvegicus"
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Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq_name: gb_est89:BF543086
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JS BF543086
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SOURCE

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oligo-dr track. The library was constructed as described by Bonaldo, Lennon and Soares, Genome Research 6: 791-806 , 1996. Tissue provided by Jim Lin, Department of Biology, University of Lowa." 1 others
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Lewin, H.A., Soares, M.B., Rebeiz, M., Pardinas, J., Liu, L. and Larson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  W. M. Keck Center for Comparative and Functional Genomics
University of Illinois at Urbana-Champaign
340 Edward R. Madigan Laboratory, 1201 W. Gregory Dr., Urbana, IL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          normalized bovine placenta Bos taurus cDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    364 ATGAACCCAAAGGATACAATGCTAACTTCTGTGCTGGGGCATGCCCTTAT 315
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571
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Percent Identity: 78.
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Fax: 217 244 5617
Email: h-lewin@uiuc.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq_documentation_block:
LOCUS BF044612 514 bp
DEFINITION BP250020A20D5 Soares
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Unpublished (2000)
                                                                                                                                                                                        530.00
5.048
93.750
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H3055G07 3', mRNA sequence.
BG067564
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AUTHORS
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KEYWORDS
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  Funding for cattle EST sequencing was provided by the USDA National Research Initiative, Animal Genome Resource Grant AG 99-3205-8534 to H. A. Lewin and J. E. Womack. Base Calling/Quality Scores: PHRED from Washington University Genome Center. Vector Trimmi g: Cross_match from Washington University Genome Center PHRAP suite. This sequence is vector free and at least 200 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Organ: placenta; Vector: pT7T3Pac; Site_1: EcoRI; Site_2: Not1; The cDNA library was contributed by the Soares laboratory and it was constructed and normalized as described by Bonaldo, M.F., Iennon, G. and Soares, M.B. (1996), Genome Research 6(9): 791-806. " Soares, as 113 c 110 g 163 t 2 others
                                                                                                                                                                                                                                                                                                                                         /organism="Bos taurus"
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/clone="BP250020A20D5"
/clone_lib="Soares normalized bovine placenta"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
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Percent Identity: 78.571
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BACKWARD: ATTAACCCTCACTAAAG
Insert Length: 514 Std Error: 0.00
Plate: BP250020A20 row: D column: 5
                                                                                                                                                                                                                                                 Seq primer: AGGGGATAACAATTTCACAGGAHigh quality sequence stop: 514.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                     /sex="female"
/lab_host="DH10B"
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92.857
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TGFB3P x BF044612/rev
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LOCUS BG067564 608 bp mRNA EST 26-JAN-2001 DEFINITION H3055G07-3 NIA Mouse 15K CDNA Clone Set Mus musculus CDNA clone

seq\_documentation\_block:

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Industrial phose "Industrial Protectors of the post of 15,247 clones from 11 clone is among a rearrayed set of 15,247 clones from 11 clone is among a rearrayed set of 15,247 clones from 11 clone is among a rearrayed set of 15,247 clones from 11 clone or 15 clones from 12 clones from unfertilized egg to blastocyst, embryonic part of E7.5 cembryos, extraembryonic part of E7.5 cembryos, and E12.5 female mesonephros/gonad) and one newborn ovary cDNA library. Average insert size 1.5 kb. All source libraries are cloned unidirectionally with Oligo(dr )-Not primers. References include: (1) Genome-wide expression profiling of mid-gestation placenta and embryo using a 15,000 mouse developmental cDNA microcarray, 2000, Proc. Natl. Acad. Sci. U S A, 97: 9127-9132; (2) Large-scale cDNA analysis reveals phased gene expression patterns during prelimplantation mouse development, 2000, Development, 127: 173-1749; (3) Genome-wide mapping of unselected transcripts from extraembryonic tissue of 7: 5-day mouse embryos reveals enrichment in the t-complex and under-representation on the X chromosome, 1998, Hum Mol Genet 7: 1967-1978."
                                                                                                                                                                                                                                                                                                                                                                                                                                                     National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
Bemail: cdnedgrun.grc.nia.nih.gov
This clone set has been freely distributed to the community. Please
visit http://lgsun.grc.nia.nih.gov/cDNA/15k.html for details.
Flate: H3055 row: G column: 07
Seg primer: -21M13 Forward
High quality sequence stop: 608
                                                                                                                                                                                          1 (bases 1 to 608)

Kargul,G.J., Dudekula,D.B., Qian,Y., Lim,M.K., Jaradat,S.A., Tanaka, T.S., Carter,M.G. and Ko,M.S.H.

Verification and initial annotation of NIA mouse 15K cDNA clone set
                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone_lib="NIA Mouse 15K cDNA Clone Set"
/sex="Clones arrayed from a variety of cDNA libraries"
/dev_stage="Clones arrayed from a variety of cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Align seg 1/1 to reverse of: BG067564 from: 1 to: 608
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137 c 145 g 1
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/db_xref="taxon:10090"
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                                                                                                                                                                                                                                                                                                                                                                                                  Contact: George J. Kargul
Laboratory of Genetics
BG067564.1 GI:12550133
                                                                                                                                                                                                                                                                                                                                  Unpublished (2001)
Other_ESTs: H3055G07-5
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163
3' ~3' adaptor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Xenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  African clawed frog.
                                                                                                                       530.00
5.048
93.750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq_name: gb_est76:BE575698
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seq_documentation_block:
                                                                                                                                                                                                           alignment_block:
TGFB3P x AI323791/rev
                     164 a
                                                                                                                                                                  Percent Similarity:
                                                                                                        alignment_scores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCUS
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                       BASE COUNT
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AUTHORS
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /dev_stage="M2 cells"
/lab_host="SOLR (kanamycin resistant)"
/note="Organ: Skin; Vector: pBluescript SK-; Site_1: ECORI
; Site_2: XhoI; Cloned unidirectionally. Primer: Oligo
dT. From M2 cells, a highly metastatic derivative of the
K-1735 (wouse) melanoma. Average insert size: 1.0 kb;
Uni-ZAP XR Vector; -5' adaptor sequence: 5' GAATTCGGCACGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 (bases 1 to 681)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schallenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This clone was previously sequenced on the 5' end only, this new data is from the 3' end
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="taxon:10090"
/clone="liMAGE:524678"
/clone=lib="&tratagene mouse melanoma (#937312)"
/tissue_type="melanoma"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                        84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
                                                                                                                                                                                                                                                                                                                                                          102 TCGCCCTCTTTACATTTTAAGAGGGATCTTGGATGGAAATGGATCC 353
  51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
                                                                                                                                                                                                                                                 67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
                                                                                   isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr
                                                                                                                                                                                                                                                                                                                                                                                                                    101 LeuSerAsnMetValValLysSerCysLysCysSer 112
                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The WashU-HHMI Mouse EST Project Unpublished (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    High quality sequence stop: 366.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AI323791.1 GI:4058220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq_name: gb_est18:AI323791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Waterston, R.
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AUTHORS
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JOURNAL
COMMENT
                                                                                   34
                                                                                                                                                                                                                                                                                            252
                                                                                                                                                                                                                                                                                                                                                                           202
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KEYWORDS
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Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Email: capabbs-remail.nih.gov
Tissue Procurement: Martha Rebbert, Steven L. Klein, Ph.D.
CONA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: Xenopus clones from this library are available through the I.M.A.G.E. Consortium/LLNL at: info@image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BES75698 445 bp mRNA EST 15-AUG-2000 dc62d10.x1 NICHD XGC Emb1 Xenopus laevis cDNA clone IMAGE:3401683 3' similar to gb:Y00083 TRANSFORMING GROWTH FACTOR BETA 2 PRECURSOR (HUMAN); gb:X57413 Mouse mRNA for transforming growth factor-beta 2 BE575698
sequence: 5' CTCGAGTTTTTTTTTTTTTTTTT 3'"
3 q 200 t 3 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 (bases 1 to 445)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleost
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
                                                                                                                                                                                                                                                                                                                                                                                                      1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG
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Percent Identity: 78.571
                                                                                                                                                                                                                                                                                                                                                     ..
2
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seq_name: gb_est13:AA915041
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Quality:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            alignment_block:
TGFB3P x AW600944
                                            Brazil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             alignment_scores:
                                                                                                                                                                                                                                                                                source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BASE COUNT
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                                                                                                                                                                                                                                                          FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORIGIN
                                                                                          /clone="IMAGE:3401683"
/clone_lib="NICHD XGC Emb1"
/clone_lib="NICHD XGC Emb1"
/lab_host="embryo (stage 10)"
/lab_host="Publib (phage-resistant)"
/note="Vector: pCMV-SPORT6; Site_1: Not1; Site_2: Sal1;
/cloned unidirectionally. Primer: Oligo dT. Average insert size 1.55 kb. Constructed by Life Technologies. Note: This is a Xenopus Gene Collection (XGC) library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AW600944 336 bp mRNA EST 23-MAR-2000
RC1-BN0014-210100-012-e01 BN0014 Homo sapiens cDNA, mRNA sequence.
AW600944 GI:7305683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I (bases 1 to 336) HCPP http://www.ludwig.org.br/ORRESTES. The FAPESP/LICR Human Cancer Genome Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              173 CATTAATCCGGAAGCATCTGCCTCCCCGTGTTGTGTATATCTAAGATTTAG 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       323 ACGICCCITATACATIGACITIAAAAGAGACCITGGIIGGAAGIGGAIAC 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              273 ATGAACCCAAAGGTTACAACGCAAATTTTTGTGCCGGAGCTTGTCCATAT 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG
                                                                                                                                                                                                                                                                                                                                                     Length: 112
Gaps: 0
Percent Identity: 77.679
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Xenopus laevis"
/db_xref="taxon:8355"
High quality sequence stop: 417.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (1999)
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Align seg 1/1 to reverse of: BE575698
                                                                                                                                                                                                                                                                                                                                                     522.00
5.068
91.964
                                      1. .445
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LOCUS AW600944
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                                                                                                                                                                                                                                                                                                                                                     Quality:
                                                                                                                                                                                                                                                                                                                                                                                           Percent Similarity:
                                                                                                                                                                                                                                                          116
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VERSION
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AUTHORS
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JOURNAL
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SOURCE
                  FEATURES
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/note="Organ: breast_normal; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions.
                                                                                                                           Email: asimpsoneludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RCl&t2=RCl-BN0014-
210100-012-e01&t3=2000-01-21&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 20
High quality sequence start: 20
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCUS AA915041 560 bp mRNA EST 14-APR-1998
DEFINITION v201g07.rl Soares_mammary_gland_NbMMG Mus musculus cDNA clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            88 leLeuTyrTyrValGlyArgThrProLysValGluGlnLeuSerAsnMet 104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     38 lyTyrTyrAlaAsnPheCysSerGlyProCysProTyrLeuArgSerAla 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           71 uAlaSerAlaSerProCysCysValProGlnAspLeuGluProLeuThrI 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5 AsnTyrCysPheArgAsnLeuGluGluAsnCysCysValArgProLeuTy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   55 AspThrThrHisSerThrValLeuGlyLeuTyrAsnThrLeuAsnProGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps: 0
Percent Identity: 78.704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length:
                                                                                                                                                                                                                                                                                                                                                                                1. .336
/organism="Homo sapiens"
/db_xref="taxon:9606"
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/dev_stage="Adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Align seg 1/1 to: AW600944 from: 1 to: 336
                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
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                                                                           Tel: +55-11-2704922
Fax: +55-11-2707001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   519.00
5.088
94.444
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T 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into He Not I and Eco RI sites of the modified pr773 vector. RNA provided by Dr. Minoru Ko, Wayne State Univ. Library constructed and normalized by Bento Soares and M.Fatima
                                                                                                                                                                                                          Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (Dases I to 560)
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Steptce, M., Tan, F., Underwood, K., Moore, B.,
Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
Waterston, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Organ: mammary gland; Vector: pT7T3D-Pac (Pharmacia ) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
IMAGE:1314492 5' similar to gb:M32745 mouse transforming growth factor beta-3 mRNA, complete (MOUSE);, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone_lib="Soares_manmary_gland_NDMMG"
/sex="male"
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Gaps: 0
Percent Identity: 99.000
                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashD-HHMI Mouse EST Project
Washington University School of MedicineP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Seq primer: -28ml3 rev2 ET from Amersham High quality sequence stop: 473. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tissue_type="mammary gland"
/dev_stage="4 weeks"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1. .560
/organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                              The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:10090"
/clone="IMAGE:1314492"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               142 g
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                                                                              AA915041.1 GI:3054433
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Percent Similarity: 100.000
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                                                                                                                                 house mouse.
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TGFB3P x AA915041
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                                                   ACCESSION
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                                                                                                         KEYWORDS
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                                                                              VERSION
                                                                                                                                 SOURCE
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BG244370 966 bp mRNA EST 13-FEB-2001 602356090F1 NCI_CGAP_Mam1 Mus musculus cDNA clone IMAGE:4484686 5',
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. I. (bases 1 to 966)
NIH-MGC http://mgc.ncl.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: cgapDs-remail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov. c column: 23
84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
                                                                                     67
                                                                                                                                                                       84
                                                                                                                                                                                             LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh
                                                                                                                                                                     67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Mus musculus"
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/clone_lib="NCI_CGAP_Mam1"
/fissue_type="tumor, blopsy sammage"
/dev_stage="3 months, virgin"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Align seg 1/1 to reverse of: BG244370 from: 1
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93.750
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BG244370
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KEYWORDS
SOURCE
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                                                                                  51
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5 AsnTyrCysPheArgAsnLeuGluGluAsnCysCysValArg.ProLeuT 21

Align seg 1/1 to: AA915041 from: 1 to: 560

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Quality:
Ratio:
                                                                         alignment_block
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LOCUS AM919738 510 bp mRNA EST 25-MAY-2000
DEFINITION EST351042 Rat gene index, normalized rat, norvegicus, Bento Soares
ACCESSION AW919738
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Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lee, N.H., Glodek, A., Chandra, I., Mason, T.M., Quackenbush, J.,
Kerlavage, A.R. and Adams, M.D.
Rat Genome Project: Generation of a Rat EST (REST) Catalog & Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone_lib="Rat gene index, normalized rat, norvegicus,
Bento Soares"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Lee, NH
The Institute for Genomic Research
The Institute for Genomic Research
The Institute for Genomic Research
Toll -838-3529
Fax: (301)-888-3529
Fax: (301)-888-0208
Fax: (303)-888-0208
Final: inhlee@tigr.org
This clone is available through the ATCC, contact the ATCC tel#703-365-2700 for further information
Seq primer: MI3 Reverse.
87 ThrIleLeuTyrTyrValGlyArgThrProLysValGluGlnLeuSerAs 103
                                                                                                                                                                                                                                                                                                                                                                   54 laAspThr.ThrHisSerThrValLeuGlyLeuTyrAsnThrLeuAsnPr 70
                                                    21 yrIleAspPheArgGlnAspLeuGlyTrpLysTrpValHisGluProLys
                                                                                                                          38 GlyTyr.TyrAlaAsnPheCysSerGlyProCysProTyrLeuArgSerA
                                                                                                                                                                                                                                                                          70 oGluAlaSerAlaSer.ProCysCysValProGlnAspLeuGluProLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Rattus norvegicus"
/db_xref="taxon:10116"
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                                                                                                                                                                                                                                                                                                                                                                                                                                             182 CATGGTGTGAAGTCGTGTAAGTGCAGC 355
                                                                                                                                                                                                                                                                                                                                                                                                                        103 nMetValValLysSerCysLysCysSer 112
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Rattus norvegicus
Eukaryota; Metazoa; C
Mammalia; Eutheria; R
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                seq_name: gb_est53:AW919738
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SOURCE
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alignment\_scores

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seq_documentation_block:
LOCUS A1599959 529 bp mRNA EST 21-APR-1999
DEFINITION EST251662 Normalized rat embryo, Bento Soares Rattus sp. cDNA clone
REMERS13' end, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rattus sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             & Rat
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/db_xref="taxon:10118"
/clone="REMEK51"
/clone_lib="Normalized rat embryo, Bento Soares"
/dev_stage="embryo 8, 12, 18 dpc"
/note="Vector: pT7T3Pac; Site_1: EcoRI; Site_2: NotI"
142 c 194 g 105 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 (bases 1 to 529)
Lee,N.H., Glodek,A., Chandra,I., Mason,T.M., Quackenbush,J.
Kerlavage,A.R. and Adams,M.D.
Rat Genome Project: Generation of a Rat EST (REST) Catalog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The Institute for Genomic Research
9712, Medical Center Drive, Rockville, MD 20850, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                    257 ACGAGCCCAAGGCTACCATGCCAACTTCTGTCTGGGGCCCTGCCCTAC 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
                                                                                                                                                                                                                                                                                                                                                        20
                                                                                                                                                                                                                                                                       17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
                                                                                                                                                                                                                                                                                                                                                     34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG
Length: 112
Gaps: 0
Percent Identity: 77.679
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AI599959.1 GI:4609007
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Email: nhlee@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tel: (301)-838-3529
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (1998)
  503.00
5.133
87.500
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                                          Percent Similarity:
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                                                                                                     TGFB3P x AW919738
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end only, this new
                                                                                                                                   /db_xref="taxon:10090"
/clone="IMAGE:478105"
/clone_lib="Soares mouse embryo NbME13.5 14.5"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG
This clone was previously sequenced on the 5' data is from the 3' end High quality sequence stop: 454.

Location/Qualifiers
                                                                                                                                                                                             /sex="unknown"
/tissuc_type="embryo"
/dev_stage="13.5-14.5dpc total fetus"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length: 112
Gaps: 0
Percent Identity: 77.679
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          179 TIGICCAACATGATTGTGCGCTCCTGCAAGTGCAGC
                                                                                                 /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mRNA
                                                                                                                     /strain="C57BL/6J
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TGFB3P x AI323392/rev
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Ratio:
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                                                             FEATURES
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LOCUS A132339 573 bp mRNA EST 23-DEC-1998

DEFINITION mj35f01.x1 Soares mouse embryo NbME13.5 14.5 Mus musculus cDNA clone IMAGE:478105 3' similar to 9b:X02812_cds1 TRANSFORMING GROWTH FACTOR BETA 1 PRECURSOR (HDMAN); 9b:M32745 mouse transforming growth factor beta-3 mRNA, complete (MOUSE);, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylle,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 573)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This clone is available royalty-free through LLNL ; contact the IMAGE Cdnsortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The WashU-HHMI Mouse EST Project
Unpublished (1996)
Contact: Marra MyMouse EST Project
WashU-HHMI Mouse EST Project
WashIngton University School of Medicinep
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Faz: 314 286 1810
Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                           277 ACACAACCGGGTGCTTCCGCATCACCGTGCTGCGTGCCGCAGGCTTTGG 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               227 AGCCACTGCCCATGGTCTACTACGTGGGTCGCAAGCCCAAGGTGGAGCAG 178
                                                                                                                                                                                                                                                                                                                                                                                         1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG
                                                           112
                                                                                                 Percent Identity: 77.679
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                                                           Length:
                                                                               Gaps:
                                                                                                                                                                                             Align seg 1/1 to reverse of: AI599959
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                                                                             5.133
87.500
                                                           503.00
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TGFB3P x AI599959/rev
                                     alignment_scores:
Quality:
                                                                                               Percent Similarity:
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602578182F1 NCI_CGAP_Mam5 Mus musculus cDNA clone IMAGE:3481700 5',
                                                                                                                                                                                                                                                 Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov.
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov.
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys cDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.llnl.gov
Plate: LLAM8510 row: d column: 21
High quality sequence stop: 640.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: Sall; Stle_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigators providing samples: Lothar Hennighausen/Robin Humphreys,
                                                                                                                                             Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 721)
                                                                                                                                                                                                            NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /strain="C57/B6"
/db_xref="kaxon:10090"
/clone="IMAGE:3481700"
/clone_lib="NCI_CGAP_Mam5"
/tissue_type="tumor, gross tissue"
/dev_stage="7 months"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Identity: 77.679
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1. .721
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                                                               BG518882.1 GI:13514180
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87.500
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                     mRNA sequence.
                                                                                                        house mouse.
Mus musculus
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                                             BG518882
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TGFB3P x BG518882
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JOURNAL
                                         ACCESSION
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                                                                                                        SOURCE
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Hegde,P., Qi,R., Abernathy,K., Dharap,S., Gaspard,R., Gay,C., Holt
,I.E., Saeed,A.I., Sharov,V., Lee,N.H., Yeatman,T.J. and
Quackenbush,J.
                                                                                                                                                                                   seq_documentation_block:
LOCUS AW958056 505 bp mRNA EST 01-JUN-2000
DEFINITION EST370126 MAGE resequences, MAGE Homo sapiens cDNA, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Assessment of gene expression patterns in a model of colon tumor metastasis using a 19,200 element cDNA microarray motbulished (2000)
Contact: John Quackenbush
The Institute for Genomic Research
712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 3528
Fax: 301 838 0208
84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     109 ACGAGCCCAAGGCTACCATGCCAACTTCTGCCTCGGGCCCTGCCCTAC 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                159 ATTTGGAGCCTGGACACGCAGTACAAGGTCCTGGCCCTGTACAACCA 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         59 GCGCCAGCTGTACATTGACTTCCGCAAGGACCTCGGCTGGAAGTGGATCC 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Align seg 1/1 to: AW958056 from: 1 to: 505
                                                                           101 LeuSerAsnMetValValLysSerCysLysCysSer
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1. 505
/organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                   AW958056
AW958056.1 GI:8147739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: johnq@tigr.org
Plate: 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Seg primer: Reverse.
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Source
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: cgapbs-remail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL, send email to: info@image.llnl.gov
Seq primer: -400P from Gibco
High quality sequence stop: 395.
Location/Qualifiers
I. 568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               //note="Organ: Kidney; Vector: pT773D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Plasmid DNA from the normalized library NCI_CGAP_Kid3 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hypridization reaction. The driver was PCK-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1322376-1323911, 1456007-1456775, and 1500552-15002855). Subtraction by Bento Soares and M. Fatima Bonaldo.
                                                                                                                                                                                                                                                                                            seq_documentation_block:
LOCUS BE464068 568 bp mRNA EST 27-JUL-2000
DEFINITION hx84h02.x1 NI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3194547 3'
similar to gb:X02812_cds1 TRANSFORMING GROWTH FACTOR BETA 1
PRECURSOR (HUMAN); contains element TAR1 TAR1 repetitive element;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 (bases 1 to 568)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                  84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
                                                                             209 GCATAACCCGGGCGCCTCGGCGGCGCGTGCTGCTGCCGCGCAGGCGCTGG
                                                                                                                                                  101 LeuSerAsnMetValValLysSerCysLysCysSer 112
                                                                                                                                                                                    309 CTGTCCAACATGATCGTGCGCTCCTGCAAGTGCAGC 344
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
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159 c 20
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                                                                                                                                                                                                                                                       seq_name: gb_est75:BE464068
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BE464068
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to: 568

to reverse of BE464068 from: 1

TGFB3P x BE464068/rev

Align seg 1/1

alignment\_block

Length: 112 Gaps: 0 Percent Identity: 76.786

500.00 5.102 87.500

Percent Similarity:

Quality: Ratio:

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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Chris Moskluk, M.D., Ph.D., Michael R.
Tissue Procurement: Chris Moskluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., CDNA Library Preparation: Life Technologies,
Inc. cDNA Library Arrayed by: Christa Prange, The I.M.A.G.E.
Consortium DNA Sequencing by: Washington University Genome
Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llni.gov/bbrpy/mage/image.html
Seq primer: -40UP from Gibco.
High quality sequence stops 425.
High quality sequence stops 425.
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/note="Organ: brain, Vector: pCMV-SPORT6; Site_1: SalI;
Library constructed by Life Technologies."
a 173 c 222 g 107 t lothers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 598)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NAIONAI Cancer Institute, Cancer Genome Anatomy Project (CGAP), Unpublished (1997)
279 GCATAACCCGGGGCGCCTCGGCGGCGCCGTGCTGCGTGCCGCGCGCGCGCGTGG 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                379 AcGAGCCCAAGGCTACCATGCCAACTTTTGCCTCGGGCCCTGCCCTAC 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
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                                                                                                                                                                                                                                              34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr
                                                                                                                          17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH
                                                                                                                                                                                                                                                                                                                                                                  LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG
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LOCUS A1951831
DEFINITION wx38b08.x1 NC:
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LOCUS AI131171
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KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
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BY"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
I bases 1 to 600)
Wistow,G.J., Bernstein,S., Behal,A. and Smith,D.
NEIBANK: EST analysis and bioinformatics for ocular genomics Invest. Ophthalmol. Vis. Sci. 41 (2000) In press
Contact: Wistow G. Section on Molecular Structure and Function
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BF726995 600 bp mRNA EST 05-JAN-2001 by15c03.yl Human Lens cDNA (Un-normalized, unamplified): BY Homo sapiens cDNA clone by15c03 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 326 ATTIGGAGCCTGGACACGCAGTACAGCAAGGTCCTGGCCCTGTACAACCA 277
                                                                                                                                                                                                                                 17 largProLeuTyrILeAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
                                                                                                                                                                                                                                                                                                    34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
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                                                                                                                                                                  1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17
                                                                                                                                                                                                                                                                                                                                                                     LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
                                                                                                                                                                                                                                                                                                                                                                                                                                    67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG
                                                                                                                                   to: 598
               Length: 112
Gaps: 0
Percent Identity: 76.786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6/331, NIH, Bethesda, MD 20892-2740, USA
Tel: 301 402 3452
Fax: 301 496 0078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: graeme@helix.nih.gov
Plate: 15 row: c column: 03
Seq primer: M13RP1 reverse primer (ABI).
Location/Qualifiers
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                                                                                                                                 to reverse of: A1951831
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                              5.102
87.500
               500.00
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LOCUS
BF726995
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                 Quality:
                                              Percent Similarity:
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alignment_scores:
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VERSION

SOURCE

FEATURES

COMMENT

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/note="Organization of the provided of the proposition of the provided of the 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 others
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//de.204ge="Daylor Ampicillin resistant)"
//de.204ge="Daylor Ampicillin resistant)"
//de.204ge="Daylor Ampicillin resistant)"
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 727)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
                                                                                                                                                                                                                                                 Contact: Robert Strausberg, Ph.D.
Email: cgapbs.remail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (life@image.llnl.gov) for further information.
Insert Length: 782 Std Error: 0.00
Seq primer: -40ml3 fwd. Er from Amersham
High quality sequence stop: 390.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             433 GCGCCAGCTGTACATTGACTTCCGCAAGGACCTCGGCTGGAAGTGGATCC 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         233 AGCCGCTGCCCATCGTGTACTACGTGGCCGCAAGCCCAAGGTGGAGCAG 184
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="IMAGE:1709664"
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Gaps: 0
Percent Identity: 76.786
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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A1323037 477 bp mRNA EST 23-DEC-1998 mj35f01.y1 Scares mouse embryo NDWE13.5 14.5 Mus musculus cDNA clone IMAGE-478105 5' similar to qb:XO2812_cds1 TRANSFORMING GROWTH FRACTOR BETA 1 PRECURSOR (HUMAN); qb:M32745 mouse transforming growth factor beta-3 mRNA, complete (MOUSE);, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            T 3'], on equal amounts of mRNA from 2 13.5dpc and 2
14.5dpc embryos [total RNA provided by Minoru Ko, Wayne
State Univ., from 2 ]; double-stranded cDNA was ligated to
Eco RI adaptors (Pharmacia), digested with Not I and
cloned into the Not I and Eco RI sites of the modified
pT7T3 vector. Library went through one round of
normalization, and was constructed by Bento Soares and
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Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This read is a RESEQUENCE of a previously sequenced mouse clone This read has been verified (found to hit its original self in the correct orientation)
Seq primer: -40RP from Gibco
High quality sequence stop: 415.
                                                                                                                                                                                                                                                                                                                                                                              This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                               Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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/tissue_type="embryo"
/dev_stage="13.5-14.5dpc total fetus"
/lab_nost="DH10B"
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Gaps: 0
Percent Identity: 76.786
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Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
WashIngton University School of MedicineP
183 CTGTCCAACATGATCGTGCGCTCCTGCAAGTGCAGC 148
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: mouseest@watson.wustl.edu
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/clone="IMAGE:478105"
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M.Fatima Bonaldo.
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                                                                         seq_name: gb_est18:AI323037
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                                                                                                                                                                                                                                                                                                                                                           SOURCE
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Email: asimpsongludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC1&t2=RC1-BN0014210100-012-fl1&t3=2000-01-21&t4=1)
Seq primer: puc 18 forward AW600<u>9</u>52 325 bp mRNA EST 23-MAR-2000 RC1-BN0014-210100-012-f11 BN0014 Homo sapiens CDNA, mRNA sequence. AW600952 Eukaryotania, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

1 (bases 1 to 325)

HCGP http://www.ludwig.org.br/ORESTES.

The FAPESP/LICH Human Cancer Genome Project
Unpublished (1999) Paulo-SP Contact: Simpson A.J.G. Laboratory of Cancer Genetics Ludwig Institute for Cancer Research Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100 1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17 51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67 191 GCGCCAGCTGTACATTGACTTTAGGAAGGACCTGGGTTGGAAGTGGATCC 34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 101 LeuSerAsnMetValValLysSerCysLysCysSer 112 High quality sequence start: 10 High quality sequence stop: 325. AW600952.1 GI:7305691 Tel: +55-11-2704922 Fax: +55-11-2707001 Align seg 1/1 to: AI323037 seq\_name: gb\_est49:AW600952 seq\_documentation\_block: LOCUS AW600952 Homo sapiens TGFB3P x AI323037 human. Brazil aliqnment\_block DEFINITION ORGANISM TITLE JOURNAL COMMENT ACCESSION VERSION KEYWORDS SOURCE AUTHORS REFERENCE 84

/note="Organ: breast\_normal; Vector: pucl8; Site\_1: Smal; Site\_2: Smal; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application

/organism="Homo sapiens" /db\_xref="taxon:9606" /clone\_lib="BN0014"

/dev\_stage="Adult"

Location/Qualifiers

source

FEATURES

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No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions.
76 c 63 g 88 t
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Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 572)
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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Unpublished (1997)

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Chris Moskaluk, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: Life

Technologies, Inc. cDNA Library Arrayed by: Christa Prange, The I.M.A.G.E. Consortium DNA Sequencing by: Washington University Genome Sequencing Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      93 lyArgThrProLysValGluGlnLeuSerAsnMetValValLysSerCys 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10 AATGTGCAGGATAATTGCTGCCTACGTCCACTTTACATTGATTTCAAGAG 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60 ThrValLeuGlyLeuTyrAsnThrLeuAsnProGluAlaSerAlaSerPr 76
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 160 AGGGTCCTGAGCTTATATACATACCATAAACCCAGAAGCATCTGCTTCTCC
                                                                                                                                                                                                                                                                                                                                                                                                                            10 AsnLeuGluGluAsnCysCysValArgProLeuTyrIleAspPheArgGl
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                                                                                                                                                                                                               Length: 103
Gaps: 0
Percent Identity: 79.612
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source

FEATURES

BASE COUNT

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1. .480
/organism="Homo sapiens"
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5.125
87.273
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Clone distribution: NCI-CGAP clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: -400P from Gibco
High quality sequence stop: 396.
Location/Qualifiers
                                                                                                                                                                                                                                                                                               /note="Organ: genitourinary tract; Vector: pCMV-SPORT6; Site_1: Sal1; Site_2: Not1; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life
                                                                                                                                                          /db_xref="taxon:9606"
/clone="IMAGE:2575474"
/clone_lib="NCI_CGAP_GUI"
/tissue_type="2 pooled high-grade transitional cell
tumors"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            338 ATTTGGAGCCTGGACACGCAGTACAGCAAGGTCCTGGCCCTGTACAACCA 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 438 GCGGCAGCTGTACATTGACTTCCGCAAGGACCTCGGCTGGAAGTGGATCC 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               388 ACGAGCCCAAGGGCTACCATGCCAACTTTTGCCTCGGGCCCTGCCCCTAC 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17 largProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      isGluProLysClyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Identity: 75.893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       188 CTGTCCAACATGATCGTGCGCTCCTGCAAGTGCAGC 153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps:
                                                                                                                              1. .572
/organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           to reverse of: AW073988
                                                                                                                                                                                                                                                                            /lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                   rechnologies.
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5.041
87.500
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LOCUS A1089904
DEFINITION qa16a08.x1 NC
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Ratio:
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ORGANISM

SOURCE

ACCESSION VERSION KEYWORDS

Donaldo, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NGI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

www.bio.llnl.gov/brp/image/finage.html

Insert Length: 8955 std Error: 0.00

Seq primer: -40ml3 fwd. ET from Amersham

High quality sequence stop: 414. Email: cgapbs-r@mail.nih.gov Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D., Chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Hominidae; Homo. Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 480)
NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BTGAP), Tumor Gene Index
Unpublished (1998)
Contact: Robert Strausberg, Ph.D. cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima 3 AspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysValArgPr 19 19 oLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValHisGluP 36 36 roLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyrLeuArg 52 53 SerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnThrLeuAs 69 nProGluAlaSerAlaSerProCysCysValProGlnAspLeuGluProL 86 /db\_xref="taxon:9606"
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DEFINITION

SOURCE

ACCESSION

VERSION

REFERENCE AUTHORS

TITLE

JOURNAL

COMMENT

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qb56001.x1 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:1704097 3' similar to gb:X02812_cds1 TRANSFORMING GROWTH FACTOR BETA 1 PRECURSOR (HUMAN);contains PTR5.b3 TAR1 repetitive element ;, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I Chases 1 to 785)
NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BRGAP), Tumor Gen Index
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNT Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Seq
Clone distribution: NCI-CGAP clone distribution inf
found through the I.M.A.G.E. Consortium/LINL at:
www-bio.linl.gov/Dbrp/image/image.html
Insert Length: 953 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 356.

Location/Qualifiers
ce
  393 AGCCCAAGGCTACCATGCCAACTTTTGCCTCGGGCCCTGCCCTACATT 344
                                                                                                                                                                                                                                                               85 roLeuThrileLeuTyrTyrValGlyArgThrProLysValGluGlnLeu 101
                                                                                                                                                                                                                                                                                         293 TAACCCGGCCCTCGCCGCCCCGTGTTGCGTGCCCCAGGCGCTGGAAC
                                                                        52 ArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnThrLe
                                                                                                                                                                  68 uAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuGluP
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                                                                                                                                                                                                                                                                                                                                                                                      193 TCCAACATGATTGTGCGCTCCTGCAAGTGC 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mRNA
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AI148173.1 GI:3675855
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_name: gb_est16:A1148173
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LOCUS A1148173
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AUTHORS
TITLE
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COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACCESSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequencing Center
information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Organ: lymph node; Vector: pCMV-SPORT6; Site_1:
Sall; Site_2: Not1; Cloned unidirectionally. Primer:
Oligo dT: Average insert size 1.25 kb. Life Technologies
catalog #: 11547-015
                                                                                                                                                                                                                                                            AW512491 646 bp mRNA EST 03-MAR-2000 XX5402.x1 NCI_CGAP_LYM12 Homo sapiens cDNA clone INAGE:2849475 3' similar to gb:X02812_cds1 TRANSFORMING GROWTH FACTOR BETA 1 PRECURSOR (HUMAN); contains element TAR1 repetitive element; mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
I (bases I to 646)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone="IMAGE:2849475"
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86 euThrIleLeuTyrTyrValGlyArgThrProLysValGluGlnLeuSer 102
                        121 TGCCCATGGTGTACTACGTGGGCCGCAAGGTCCAAGGTGGAGCAGCTGTCC 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 LeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysValAr 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    35 luProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyrLeu 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Life Technologies catalog #: 11547-015
DNA Sequencing by: Washington University Genome
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image.llnl.gov/image/hrnl/iresources.shtml
Seq primer: -400p from Gibco
High quality sequence stop: 396.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rêmail.nih.gov
                                                                                            103 AsnMetValValLysSerCysLysCysSer 112
                                                                                                                    Align seg 1/1 to reverse of: AW512491
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                                                                                                                                                                                                                                                                                                                                                                              AW512491
AW512491.1 GI:7150569
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87.273
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FEATURES

26-OCT-1998

Sequencing Center information can be

BASE COUNT

ORIGIN

Tue

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Contact: Marra M/Mouse EST Project
                                                                                                                                                                                       Ratio:
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 (bases 1 to 529)
Malek, R.L., Cho, J., Lee, Y., Karamycheva, S., Parvizi, B., Pertea, G., Sultana, R., Tsai, J., White, J., Quackenbush, J. and Lee, N.H. Generation of ESTs from Normalized Rat Embryo, Bento Soares
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Norway rat.
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_documentation_block: 529 bp mRNA EST 28-NOV-2000 LOCUS BF287476 Sat Gene Index, normalized rat, Rattus norvegicus cDNA clone RGIGG52 3' sequence, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              contact the ATCC
                                                                                                                                                                                                                                                                                                                              248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 497 GCCCTGGACACCCAAATATTGCTTCAGCTCCACGGAGAAGAACTGCTGCGT 448
                                                                                                                                                                                                                                                           34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
                                                                                                                                                                       1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17
                                                                                                                                                                                                                                         17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
                                                                                                                                                                                                                                                                                                                                                                               51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                 67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20850,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Lee, NH
The Institute for Genomic Research
9712, Medical Center Drive, Rockville, MD 206
Tel: (301) 838-3529
Fax: (301) 838-0208
Email: nhlee@tigr.org
This clone is available through the ATCC, cortel#703-365-2700 for futher information.
              Length: 112
Gaps: 0
Percent Identity: 75.000
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                                                                                                                                   Align seg 1/1 to reverse of: AI148173
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BF287476.1 GI:11218546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (2000)
Other_ESTs: EST351042
            491.00
5.010
87.500
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                                                                                                  TGFB3P x AI148173/rev
                 Quality:
                                            Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rattus.
alignment_scores:
                                                                                 alignment_block
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      source
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COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KEYWORDS
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seq_documentation_block:
LOCUS AA000733 431 bp mRNA EST 18-JUL-1996
LOCUS AA000733 431 bp mRNA
DEFINITION mg35b06.rl Soares mouse embryo NbME13.5 14.5 Mus musculus cDNA
clone IMAGE:425747 5' similar to gb:X02812_cds1 TRANSFORMING GROWTH
FACTOR BETA 1 PRECURSOR (HUMAN); gb:M32745 mouse transforming
growth factor beta-3 mRNA, complete (MOUSE);, mRNA sequence.
                                                                                                                      RSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 431)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                             Site_2: Not1;
RLU, REM, RMU,
  Rattus
normalized rat,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           327 ATTTGGAGCCTGGACACACAGTACAGCAAGGTCCTTGCCTTTACAACCA 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
                                          /tissue_type="mixed tissue"
/lab_host="DH5-alpha"
/note="Vector: pr377Pac; Site_1: EcoR1;
Combination of ROV, RBR, RKI, RLI, RPL,
RHE, RPC, RPN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               477 GCCCTGGATACCAATTACTGCTTCAGCTCCACAGAGAAGTGCTGTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG
                                                                                                                                                                                                                                                                                           Length: 112
Gaps: 0
Percent Identity: 76.786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      to:
/clone_lib="Rat Gene Index,
norvegicus cDNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Align seg 1/1 to reverse of: BF287476 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LeuSerAsnMetValValLysSerCysLysCysSer 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          177 TTGTCCAACATGATCGTGCGCTCCTGCAAGTGCAGC 142
                                                                                                                                                                      107 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The WashU-HHMI Mouse EST Project Unpublished (1996)
                                                                                                                                                                    190 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AA000733.1 GI:1436599
                                                                                                                                                                    141 c
                                                                                                                                                                                                                                                                                                                    5.052
86.607
                                                                                                                                                                                                                                                                                             490.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seq_name: gb_est1:AA000733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    house mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                    TGFB3P x BF287476/rev
                                                                                                                                                                                                                                                                                                  Quality:
                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
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ORGANISM
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                                                                                                                                                                                     ACCESSION
VERSION
                                                                                                                                                                                                                                                                                  REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                         JOURNAL
                                                                                                                                                                                                                KEYWORDS
SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BASE
                                                                                                                                                                                                                                                                                                                                    WashIngton University School of MedicineP
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
441 286 1800
Fat: 314 286 1810
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the IMAGE_Consortium (info@lmage.llnl.gov) for further information.
                                                                                                                                                                                                                                      /db_xref="taxon:10090"
/clone="IMAGE:425747"
/clone_lib="Soares mouse embryo NbME13.5 14.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               143 GCGCCAGTGATACATTGACTTTAGGAAGGACCTGGGTTGGAAGTGGAAGTC 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    243 ATTTGGAGCCTGGACACACAGTACAGCAAGGTCCTTGCCCTCTACAACCA 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
                                                                                                                                                                                                                                                                                  /sex="unknown"
/tissuc_type="embryo"
/dev_stage="13.5-14.5dpc total fetus"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length: 112
Gaps: 0
Percent Identity: 75.000
                                                                                                         MGI:260299
Putative full length read
Vector to vector length is 661
Seq primer: ETPrimer
High quality sequence stop: 321.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Align seg 1/1 to: AA000733 from: 1 to: 431
                                                                                                                                                                                                              /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             113 g
                                                                                                                                                                                                                             /strain="C57BL/6J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            M.Fatima Bonaldo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              488.00
5.031
86.607
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Ratio:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGFB3P x AA000733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alignment_block
                                                                                                                                                                                                    Source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BASE COUNT
ORIGIN
                                                                                                                                                                                    FEATURES
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/nea_most=_unstructure
/note="Organ: pooled; Vector: pT773D-Pac (Pharmacia) with
a modified polylinker; Site_1: Not I; Site_2: Eco RI;
Equal amounts of plasmid DNA from five normalized
libraries were mixed, and ss circles were made in vitro.
Following HAP purification, this DNA was used as tracer in
a subtractive hybridization reaction. The driver was
PCR-amplified cDNAs from pools of 5,000 clones made from
the same 5 libraries. The pools consisted of the following
libraries and cloneIDs: Soares NbHSF pool 1:
145032-147335, 14770-148103, 148872-149255, 15002 -
150407, 151176-15237 Soares NbHFR-9W pool 1:
758280-760583, 772104-774407 Soares NbHPA pool 1:
758280-760583, 772104-774407 Soares NbHPA pool 1:
723720-726407, 739080-740999 Subtraction by Bento
Soares and M. Fatima Boraldo."
                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 778)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                        A1743724 778 bp mRNA EST 19-DEC-1999 wg53b06.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2368787 3' similar to gb:x02812_cds1 TRANSFORMING GROWTH FACTOR BETA 1 PRECURSOR (HUMAN);contains element MSR1 repetitive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: cgapbs-remail.nih.gov
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 863 Exror: 0.00
Seq primer: -400P from Gibco
High quality sequence stop: 449.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Align seg 1/1 to reverse of: AI743724 from: 1 to: 778
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Identity: 76.106
101 LeuSerAsnMetValValLysSerCysLysCysSer 112
                              Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       269 g
                                                                                                                                                                                                                                                                                                      element;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                               AI743724
AI743724.1 GI:5112012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       223 c
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4.969
86.726
                                                                                                             seq_name: gb_est24:AI743724
                                                                                                                                                                  seq_documentation_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                      human.
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34

51

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                                                                                                                                                  Percent Similarity:
                                                                                                                                Ratio:
  75
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                                                                                        alignment_scores:
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BASE COUNT
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KEYWORDS
SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Organ: prostate; Vector: pr773D-Pac (Pharmacia)
with a modified polylinker; Plasmid DNA from the
normalized library NCL_GGAP_Pr22 was prepared, and ss
circles were made in vitro. Following HAP purification,
this DNA was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from a pool
of 5,000 clones made from the same library (cloneIDs
985608-986759, 1101192-1101959, and 1217928-1220615).
Subtraction by Bento Soares and M. Fatima Bonaldo."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL, send email to:
info@image.llnl.gov from Gibco.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ď
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael
Emmert-Buck, M.D., Ph.D.
                                                                                                        84 lu. ProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGl 100
                                                                                                                                                                                                                                                                                                                                                                   GCGGCAGCTGTACATTGACTTCCGCAAGGACCTCGGCTGGAAGTGGATCC 385
                                                                                                                                                                    LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
                                                                                                                                                                                                                                                          84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 (bases I to 474)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy
isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr
||||||||||||||||||||
                                                                                                                                                                                                                                                        67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG
                                                                                                                                                                                                                                                                                                                                                                                                                                                       nLeuSerAsnMetValValLysSerCysLysCysSer 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="NCI_CGAP_Pr28"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone="IMAGE:3288259"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /dev_stage="adult"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BE645704
BE645704.1 GI:9970015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seq_name: gb_est77:BE645704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            human.
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AUTHORS TITLE

JOURNAL

COMMENT

FEATURES

REFERENCE

ACCESSION VERSION KEYWORDS

SOURCE

100

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 589)
10.1-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (GGAP), Tumor Gene Index
Onpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A199139 27-OCT-1999
W138903.x1 Soares_Dieckgraefe_colon_NHCD Homo sapiens cDNA clone
IMAGE:2522356 3' similar to gb:x02812_cds1 TRANSFORMING GROWTH
FACTOR BETA 1 PRECURSOR (HUMAN); contains element TAR1 TAR1
repetitive element ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: cgapbs-remail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40UP from Gibco
High quality sequence stop: 459.
                                                                                                                                                                                                                                                                                                                                                                                                            87 hrIleLeuTyrTyrValGlyArgThrProLysValGluGlnLeuSerAsn 103
                                                                                                                                                                                                                                                                                                                                                323 CTGGACACGCAGTACAGCAAGGTCCTGGCCCTGTACAACCAGCATAACCC 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     373 AGGGCTACCATGCCAACTTTTGCCTCGGGCCCTGCCCCTACATTTGGAGC 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 ThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysValArgProLe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                54 AlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnThrLeuAsnPr
                                                                                                          Length: 109
Gaps: 0
Percent Identity: 76.147
                                                                                                                                                                                                                                                                         Align seg 1/1 to reverse of: BE645704 from: 1
85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2522356"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         173 ATGATCGTGCGCTCCTGCAAGTGCAGC 147
    Б
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                                                                                                             486.00
5.116
87.156
138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seq_documentation_block:
LOCUS AI991139
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MGI:1058490
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Ratio:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         134
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                  REFERENCE
                                  AUTHORS
                                                                                   JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         34
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                                                                                                                                                                                                                                                                                                                                       FEATURES
                                                   TITLE
                                                                                                 COMMENT
                                                             /clone_lib="Soares_Dieckgraefe_colon_NHCD"
.tissue_type="colonic mucosa from 3 patients with Crohn's
                                                                                                                                                                                               provided by Dr. Brian Dieckgraefe (Washington University, dieck@im.wustl.edu); colonic mucosa represents a range of disease involvement from moderate to severe Crohn's disease; samples include both perforating (fistulas) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ur71c12.yl NCI_CGAP_Mam3 Mus musculus cDNA clone IMAGE:3155734 5' similar to gb:M32745 mouse transforming growth factor beta-3 mRNA, complete (MOUSE);, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                 non-perforating samples. Library constructed by Bento
Soares and M. Fatima Bonaldo. " 5 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   84 GluProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGl 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       226 GAGCCGCTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCA 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsn.T 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      67 hrLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeu 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Align seg 1/1 to reverse of: AI991139 from: 1 to: 589
                                               /lab_host="DH10B (phage-resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                      Gaps: 1
Percent Identity: 75.221
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4.899
87.611
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TGFB3P x A1991139/rev
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VERSION
KEYWORDS
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Chu-Xia Deng Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.B. Consortium (LINL)
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
image.llnl.gov/image/html/iresources.shtml
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: Sall; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigators providing samples: Lothar Hennighausen/Chu-Xia Deng, NIH Reference for transgenic model: Xu et al., Nature Genetics 22, 37-43 (1999)."
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus I bases 1 to 509)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               277
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             278 ACGCCCCTTTATATTGACTTCCGGCAGGATCTAGGCTGGAAATGGGTCC 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               427
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     228 GCCCTGGACACCAATTACTGCTTCCGCAACCTGGAGGAGAACTGCTGTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr
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Gaps: 0
Percent Identity: 94.681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone_lib="NCI_CGAP_Mam3"
/tissue_Yppe="tumor, gross tissue"
/dev_stage="10 months"
/lab_host="PH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         to: 509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Mus musculus"
/strain="129 - C57/B6 - F
/db_xref="taxon:10090"
/clone="IMAGE:3155734"
                                                                                                           Tumor Gene Index
Oppublished (1997)
Other ESTs: ur71c12.x1
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                477 AGCCCCTGACCATCTTGTACTATGTGGCCAGA 508
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Seq primer: -40RP from Gibco
High quality sequence stop: 418.
Location/Qualifiers
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5.228
97.872
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LOCUS W45844 478 bp mRNA EST 23-MAY-1996
DEFINITION mc77e02.rl Scares mouse embryo NbME13.5 14.5 Mus musculus cDNA
clone IMAGE:354554 5, similar to qb:X02812_cds1 TRANSFORMING GROWTH
FACTOR BETA 1 PRECURSOR (HUMAN); qb:W32745 mouse transforming
growth factor beta-3 mRNA, complete (MOUSE);, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Gelsel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptce, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                         264 CGCCTCGGCGCGCCCTGCTGCTGCTGCCCCTGGAGCCGCTGCCCCA 215
                                                                                                                                    364 GCTACCATGCCAACTTCTGCCTCGGCCCTGCCCCTACATTTGGAGCCTG 315
                                                                                                                                                                                                                                                                                                                             88 leLeuTyrTyrValGlyArgThrProLysValGluGlnLeuSerAsnMet 104
38 lyTyrTyrAlaAsnPheCysSerGlyProCysProTyrLeuArgSerAla 54
                                                                                                                                                                                                                  71 uAlaSerAlaSerProCysCysValProGlnAspLeuGluProLeuThrI
                                                                                                          AspThrThrHisSerThrValLeuGlyLeuTyrAsnThrLeuAsnProGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Waterston, R.
The WashU-HHMI Mouse EST Project
Unpublished (1996)
Contact: Marra M/Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                     105 ValValLysSerCysLysCysSer 112
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EST.
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JOURNAL
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KEYWORDS
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                                                                                                       52
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tissue Procurement: Ash Alizadeh, John Byrd, M.D., Mike Grever, M.D., Louis M. Staudf, M.D., Ph.D. CDNA Library Preparation: M. Bento Soares, Ph.D. CDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-GGAP clone distribution in A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and cloned into
                                                                      seq_documentation_block:

LOCUS A1760533 546 bp mRNA EST 20-DEC-1999

DEFINITION Wh88D99.x1 NCI_CGAP_CLL1 Homo sapiens CDNA clone IMAGE:2387801 3'

Similar to 9b:x02812_c631 TRANSFORMING GROWTH FACTOR BETA 1

PRECURSOR (HUMAN);contains element TAR1 repetitive element ;, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        T 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into Library is normalized, and was constructed by Bento Soares and M.Fatima Bonaldo."
                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 546)
                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCI-CGAP http://www.ncbi.nlm.nih.gov/nciogap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone="IMAGE:2387801"
/clone_lib="NOT_CGAP_CLL1"
/tissue_type="B-cell, chronic lymphotic leukemia"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 714 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 465.
Location/Qualifiers
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/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
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                                                                                                                                                                                                                                                                  AI760533.1 GI:5176200
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Unpublished (1997)
                      seq_name: gb_est24:AI760533
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                                                                                                                                                                                                                                                                                                                       SOURCE
ORGANISM
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VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                            AUTHORS
TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JOURNAL
                                                                                                                                                                                                                                                                                              KEYWORDS
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5 AsnTyrCysPheArgAsnLeuGluGluAsnCysCysValArgProLeuTy 21

to reverse of: AI760533 from: 1 to: 546

TGFB3P x AI760533/rev

Align seg 1/1

alignment\_block:

Length: 108 Gaps: 0 Percent Identity: 75.926

481.00 5.117 87.037

Percent Similarity:

Quality: Ratio:

alignment\_scores

21 rIleAspPheArgGlnAspLeuGlyTrpLysTrpValHisGluProLysG 38

Eco RI adaptors (Pharmacia), digested with Not I and

seq\_documentation\_block:
LOCUS AW627667 466 bp mRNA EST 31-MAR-2000
DEFINITION hh89h10.x1 NCI\_CGAP\_GU1 Homo sapiens cDNA clone IMAGE:2970019 3'
Similar to gb:X02812\_cda1 TRANSFORMING GROWTH FACTOR BETA 1
PRECURSOR (HUMAN); contains element TAR1 repetitive element ; , mRNA Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

I (bases 1 to 466)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

Unpublished (1997) cloned into the Not I and Eco RI sites of the modified pTTT3 vector. Library went through one round of normalization, and was constructed by Bento Soares and M.Fatima Bonaldo. Email: ggapbs-r@mail.nih.gov
Tissue Procurement: Chris Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D., CDNA Library Preparation: Life
Fechnologies, Inc. CDNA Library Arrayed by: Christa Prance, The
I.M.A.G.E. Consortium DNA Sequencing by: Washington University 240 ACGAGCCCAAGGGCTACCATGCCAACTTCTGTCTGGGACCCTGCCCCTAT 289 34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50 84 17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67 1 others 1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17 67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 340 ACACAACCCGGGCGCTTCGGCGTCACCGTGCTGCGTGCCGCAGTTNATGG Length: 112 Gaps: 0 Percent Identity: 76.786 90 t Contact: Robert Strausberg, Ph.D. Align seg 1/1 to: W45844 from: 1 to: 478 126 g AW627667 AW627667.1 GI:7374457 155 c 4.898 480.00 seq\_name: gb\_est49:AW627667 Homo sapiens ø Ratio: Percent Similarity: Quality: 106 human. alignment\_scores: alignment\_block: TGFB3P x W45844 BASE COUNT ORIGIN ORGANISM ACCESSION VERSION KEYWORDS SOURCE REFERENCE AUTHORS JOURNAL 51 TITLE COMMENT

þe Clone distribution: NCI-CGAP clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov/thage/html/iresources.shtml
Seg primer: -400P from Gibco
High quality sequence stop: 378. Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; /lab\_host="DH10B"
//note="Organ: genitourinary tract; Vector: pCMV-SPORT6; Site\_1: Sall; Site\_2: NotI; Cloned unidirectionally.
Primer: Oligo dT. Library constructed by Life
Technologies." EST 06-FEB-2001 (6023290) HOMO sapiens CDNA clone IMAGE:4431214 /clone="IMAGE:2970019"
/clone="IMAGE:2970019"
/clone=lib="NOI\_CGAP\_GU1"
/tissue\_type="2 pooled high-grade transitional cell tumors" 89 euTyrTyrValGlyArgThrProLysValGluGlnLeuSerAsnMetVal 105 216 TGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAGCTGTCCAACATGATC 167 22 22 eAspPheArgGlnAspLeuGlyTrpLysTrpValHisGluProLysGlyT 39 39 yrTyrAlaAsnPheCysSerGlyProCysProTyrLeuArgSerAlaAsp 55 56 ThrThrHisSerThrValLeuGlyLeuTyrAsnThrLeuAsnProGluAl 72 72 aSerAlaSerProCysCysValProGlnAspLeuGluProLeuThrIleL 89 416 TGACTTCCGCAAGGACTTCGGTTGGAAGTGGATCCACGAGCCCAAGGGCT 6 TyrCysPheArgAsnLeuGluGluAsnCysCysValArgProLeuTyrIl Percent Identity: 74.766 from: 1 Gaps: Length: 86 1. .466 /organism="Homo sapiens" /db\_xref="taxon:9606 Location/Qualifiers 167 g Align seg 1/1 to reverse of: AW627667 Genome Sequencing Center BG180040.1 GI:12586743 106 ValLysSerCysLysCysSer 112 136 c 471.00 5.065 86.916 seq\_name: gb\_est97:BG180040 mRNA sequence. BG180040 seq\_documentation\_block:
LOCUS BG180040 alignment\_block: TGFB3P x AW627667/rev Ratio: Percent Similarity: 11 human. alignment\_scores ESTsource DEFINITION ORGANISM BASE COUNT ACCESSION VERSION. KEYWORDS SOURCE FEATURES ORIGIN

tgfb3p.rst

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FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone_lib="NIH_MGC_91"
/tissue_type="adenocarcinoma, cell line"
/tissue_type="adenocarcinoma, cell line"
/tab_nost="bH10B (phage-resistant).
/note="Organ: prostate; Vector: pCNV-SPORT6; Site_1: Not1; Site_2: Sal1; Cloned unidirectionally; oilsgo-dT primed. Site_2: Sal1; Cloned unidirectionally; oilsgo-dT primed. Average insert size 1.4 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH_MGC Library."
                                                                                                                  Contact: Robert Strausberg, Ph.D.

Email: cgapbs-rémail.nih.gov
Tissue Procurement: DCTD/DTP
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAMIONS row: o column: 23
High quality sequence stop: 338.
Location/Qualifiers
               1 (Dases 1 to 431)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         90 yrTyrValGlyArgThrProLysValGluGlnLeuSerAsnMetValVal 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       267 ACTACGTGGGCCGCAAGCTGGAGCAGCTGTCCAACATGATCGTG 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7 CysPheArgAsnLeuGluGluAsnCysCysValArgProLeuTyrIleAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23 pPheArgGlnAspLeuGlyTrpLysTrpValHisGluProLysGlyTyrT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               40 yrAlaAsnPheCysSerGlyProCysProTyrLeuArgSerAlaAspThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               57 ThrHisSerThrValLeuGlyLeuTyrAsnThrLeuAsnProGluAlaSe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  73 rAlaSerProCysCysValProGlnAspLeuGluProLeuThrIleLeuT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length: 106
Gaps: 0
Percent Identity: 75.472
                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4431214"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  to: 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Align seg 1/1 to: BG180040 from: 1
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                                                                                             Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            468.00
5.087
86.792
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TGFB3P x BG180040
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                       REFERENCE
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seq\_name: gb\_est26:AI927187

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Tunor Gene Index

Unpublished (1997)
Contact: Robert Strausberg, Ph.D.

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NOT-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

Www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 1358 Std Error: 0.00
                                            WOO88C02.X1 NCI_CGAP_Kidll Homo sapiens CDNA clone IMAGE:2462402 3/
similar to gb:X02812_cds1 TRANSFORMING GROWTH FACTOR BETA 1
PRECURSOR (HUMAN);contains element MER22 repetitive element ; mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Organ: Kidney; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eoc RI; Plasmid DNA from the normalized library NCI_CGAP_Kid3 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDS 1322376-1333911, 1456007-1456775, and 150552-1502855). Subtraction by Bento Soares and M. Fatima Bonaldo. "
                                                                                                                                                                                                                                                       Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                            08-MAR-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   475 GCTTTGGATACTAACTATTGNTTTAGCTCTATGGAGAANTGCTGTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length: 112
Gaps: 0
Percent Identity: 72.321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone="IMAGE:2462402"
/clone_lib="NCI_CGAP_Kidll"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Align seg 1/1 to reverse of: AI927187 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seq primer: -400P from Gibco
High quality sequence stop: 394.
Location/Qualifiers
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                                                                                                                                                                             AI927187.1 GI:5663151
                          578 bp
                                                                                                                                                                                                                                                                                                                                (bases 1 to 578)
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84.821
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seq_documentation_block:
LOCUS A1927187
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Ratio:
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                                                                                                                                                                                                                                    human.
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sequence.
AI433146
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TGFB3P x AI430179
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                                                                                                             ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                      seq_documentation_block:
LOCUS A1430179 317 bp mRNA EST 15-MAR-2000
DEFINITION me44004.y1 Soares mouse embryo NbME13.5 14.5 Mus musculus cDNA clone IMAGE:390342 5' similar to gb:x02812_cds1 TRANSFORMING GROWTH FACTOR BETA 1 PRECURSOR (HUMAN); gb:M32745 mouse transforming growth factor beta-3 mRNA, complete (MOUSE); mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Marmalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bass 1 to 317)
Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter Waterston,R. and Wilson,R., Cardenas,M., McCann,R., The WashU-NCI Mouse EST Project 1999
Contact: Marra M/WashU-NCI Mouse EST Project 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This clone is available royalty-free through LLNL; contact the MAGE Consortium (info@image.llnl.gov) for further information. This read is a RESEQUENCE of a previously sequenced mouse clone This read has been verified (found to hit its original self in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Washington University School of Medicine, 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA Pers: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:10090"
/clone="liMAGE:390342"
/clone_lib="Soares mouse embryo NbMEl3.5 14.5"
/sex="unknown"
                                                                                                                                                                     275 GCATAACCCGGGCGCCCTCGGCGCGCCCTGNTGCGTGCCGCAGGGGCTGG 226
                                     325 ATTTGGAGCCTGGACACGCAGTACAGCACGTCCTGGCCCTGTACAACCA 276
51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh
                                                                                    67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue_type="embryo"
/dev_stage="13.5-14.5dpc total fetus"
/lab_host="DH10B"
                                                                                                                                                                                                                                                       /organism="Mus musculus"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       High quality sequence stop: 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Seq primer: -40RP from Gibco
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MGI:242174
                                                                                                                                                                                                                                                                                                                                              seq_name: gb_est20:AI430179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        house mouse.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AI430179
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COMMENT

FEATURES

KEYWORDS

SOURCE

VERSION

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CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A1433146 505 bp mRNA EST 30-MAR-1999
13732411.X1 NCI_CGAP_GAS4 HOMO SAPIENS CHOM CALON HAGES:2132156 3'
similar to gb:x02812_cG51 TRANSFORMING GROWTH FACTOR BETA 1
PRECURSOR (HUMAN);contains element TAR1 repetitive element ; mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

1 (bases 1 to 505)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   α.
Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization, and was constructed by Bento Soares and M. Bartima Roundlo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael
Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97 ysValGluGlnLeuSerAsnMetValValLysSerCysLysCysSer 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          256 AGGTGGAGCAGTTGTCCAACATGATTGTGCGCCTCCTGCAAGTGCAGC 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14 ASnCySCySValArgProLeuTyrIleAspPheArgGlnAspLeuGlyTr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64 LeuTyrAsnThrLeuAsnProGluAlaSerAlaSerProCysCysValPr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   47 roCysProTyrLeuArgSerAlaAspThrThrHisSerThrValLeuGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  oGlnAspLeuGluProLeuThrIleLeuTyrTyrValGlyArgThrProL
                                                                                                                                                                                                                                                                             Length: 99
Gaps: 0
Percent Identity: 78.788
                                                                                                                                           65 t
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                                                                                                                                           89 g
                                                                                                                 M.Fatima Bonaldo.
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Unpublished (1997)
                                                                                                                                                                                                                                                                                                             5.18487.879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seq_name: gb_est20:A1433146
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Mus musculus
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TGFB3P x AU016729/rev
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KEYWORDS
SOURCE
                                                                                                                                                                              FEATURES
                                                                                       COMMENT
                                                                                     /db_xref="taxon:9606"
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Ko,M.S.H,'Kitchen,J.R., Wang,X., Threat,T.A., Sun,T., DePalma,G.E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_documentation_block:
LOCUS AU016729 576 bp mRNA EST 15-OCT-1998
DEFINITION AU016729 Mouse two-cell stage embryo cDNA Mus musculus cDNA clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95 hrProLysValGluGlnLeuSerAsnMetValValLysSerCysLysCys 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28 uGlyTrpLysTrpValHisGluProLysGlyTyrTyrAlaAsnPheCysS 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62 LeuGlyLeuTyrAsnThrLeuAsnProGluAlaSerAlaSerProCysCy 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             erGlyProCysProTyrLeuArgSerAlaAspThrThrHisSerThrVal 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sValProGlnAspLeuGluProLeuThrIleLeuTyrTyrValGlyArgT 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Align seg 1/1 to reverse of: AI433146 from: 1 to: 505
                                                                                                                                                                                                                                                                                                                                                               Length: 101
Gaps: 0
Percent Identity: 76.238
   Std Error: 0.00
                                                                                                                                                                                                                                                                              95 t
Insert Length: 2004 Std Error:
Seq primer: -40UP from Gibco
High quality sequence stop: 376.
                                                   Location/Qualifiers
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                                                                                                                                                                                                                                                                               187
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5.091
87.129
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TGFB3P x AI433146/rev
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Ratio:
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                                                                                                                                                                                                                                                                              BASE COUNT
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KEYWORDS
SOURCE
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                                                     FEATURES
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seq_documentation_block:

LOCUS
AA657145
530 bp mRNA
DEFINITION vr26403.r1 Barstead mousemyctubes MPLRB5 Mus musculus cona clone
IMAGE:1121765 5' similar to gb:.03241 TRANSFORMING GROWTH FACTOR
BETA 3 PRECURSOR (HUMAN); gb:M32745 mouse transforming growth factor_beta-3 mRNA, complete (MOUSE);, mRNA sequence.
                                                                                 Unpublished (1998)

Contact: Hirofumi Doi

Doi Bloosymmetry Project, ERATO

Japan Science and Technology Corporation (JST)

WBG Marive East 12F, 2-6 Nakase, Mihama-ku, Chiba 261-71, Japan

Email: hd@bioa.jst.go.jp.
Liang,Y., Kargul,G.J., Sharara,R. and Doi,H.
Systematic analyses of genes expressed in 2-cell stage mouse
embryos (The ERATO/Doi Project at Wayne State University) (Ko
                                                                                                                                                                                                                                                                                           /db.zref="taxon:10090"
/clone="J0728H08"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          uGluProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluG 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          204 GGAACCACTGACCATTCTCTATTACATTGGAAATACGCCCAAGATCGAAC 155
                                                                                                                                                                                                                                                                                                                                                               /dev_stage="two-cell stage embryo" 123 c 134 g 164 t 11 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGlu.AsnCysCysV 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps: 2
Percent Identity: 76.316
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length:
                                                                                                                                                                                                                           1, .576 /organism="Mus musculus" /strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Align seg 1/1 to reverse of: AU016729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AA657145.1 GI:2593299
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4.298
91.228
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                                                                 et al.
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Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Life Technologies catalog #: 11547-015

Lone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

Wow-bio.llnl.gov/bbrp/Aimage/Aimage.html
Insert Length: 873 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 380.
                                                                                                                                                                                                                         seq_documentation_block:

LOCUS A1434956 567 bp mRNA EST 30-MAR-1999

DEFINITION ti46f04.x1 NCI_CGAP_Lyml2 Homo sapiens cDNA clone IMAGE:2133535 3'

Similar to gb:X02812_cds1 TRANSFORMING GROWTH FACTOR BETA 1

PRECURSOR (HUMAN);contains element TAR1 repetitive element ;, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Organ: lymph node; Vector: pCMV-SPORT6; Site_1:
Sall; Site_2: NotI; Cloned unidirectionally. Primer:
Oligo dr. Average insert size 1.25 kb. Life Technologies
catalog #: 11547-015"
163 c 209 g 107 t 1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1. .567
/Organism="Homo sapiens"
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
          212 AACCCCCAAGGTGGAGCAGCTGTCCAACATGGTGTGAAGTCGTGAAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                AI434956
AI434956.1 GI:4299804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tumor Gene Index
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     438.00
4.761
85.185
                                                                                                                                                                              seq_name: gb_est20:A1434956
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TGFB3P x A1434956/rev
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                                                                                111 ysser 112
                                                                                                                                262 GCAGC 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                            human.
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                ACCESSION
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KEYWORDS
SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13/3; double-stranded CDNA was ligated to Eco RI adaptors [AATTCGGATCCTTG], digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library constructed by Bob Barstead. The C2C12 cell line (available from ATCC, catalog # CRL-1772) differentiates rapidly, forming contractile myotubes and producing characteristic muscle proteins.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 530)
Marra, M. Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@lmage.llnl.gov) for further information.
MGI:611101
                                                                                                                                                                                                                         Unpublished (1996)
Contact: Marna M/Mouse EST Project
Washb-HHMI Mouse EST Project
Washb-HHMI University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Far: 314 286 1800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="IMAGE:1121765"
/clone_lib=Barstead mouse myotubes MPLRB5"
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/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94 gThrProLysValGluGlnLeuSerAsnMetValValLysSerCysLysC 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        44 sSerGlyProCysProTyrLeuArgSerAlaAspThrThrHisSerThrV 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            78 CysValProGlnAspLeuGluProLeuThrIleLeuTyrValGlyAr 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 alLeuGlyLeuTyrAsnThrLeuAsnProGluAlaSerAlaSerProCys 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        162 TGCGTCCCCCAGGACCTGGACCCTGACCATCTTGTACTATGTGGGCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28 LeuGlyTrpLysTrpValHisGluProLysGlyTyrTyrAlaAsnPheCy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length: 85
Gaps: 0
Percent Identity: 98.824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Seq primer: -28ml3 rev2 ET from Amersham
High quality sequence stop: 183.
Location/Qualifiers
1. .530
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                                                                                                                                                                                                    The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /strain="C3H"
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5.214
98.824
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                                                                                                                                                                              Waterston, R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percent Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGFB3P x AA657145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               alignment_scores:
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source

FEATURES

TITLE JOURNAL COMMENT

REFERENCE AUTHORS alignment\_block:

13

BASE COUNT ORIGIN

```
420 CATTGACTTCGCAAAGGACCTCGGCTGNAAGTGGATCCACGAGGCCCAAGG 371
                                                                                                                                                                                                                                                                                                                                                                21 rIleAspPheArgGlnAspLeuGlyTrpLysTrpValHisGluProLysG 38
                                                                                                                                                                                                                                                        5 AsnTyrCysPheArgAsnLeuGluGluAsnCysCysValArgProLeuTy 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                38 lyTyrTyrAlaAsnPheCysSerGlyProCysProTyrLeuArgSerAla 54
                                                                                                                                                                                              Align seg 1/1 to reverse of: AI434956 from: 1 to: 567
Length: 108
Gaps: 0
Percent Identity: 71.296
```

22

```
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: capabs-remail.nih.gov.
Tissue Procurement: CLONTECH Laboratories, Inc.
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1519 row: h column: 05
High quality sequence stop: 562.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone="IMAGE:4694836"
/clone_lib="NIH_MGC_77"
/lab_host="DH10B (Tl phage-resistant)"
/note="Organ: lung; Vector: pDNR-LIB (Clontech); Site_l:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostou Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 889) NIH-WGC http://mgc.nci.nih.gov/. NIH-WGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BG540633 889 bp mRNA EST 03-APR-2001 602570520F1 NIH_MGC_77 Homo sapiens CDNA clone IMAGE:4694836
                                                                                                                                                                                                                    84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17
                                                                                                                                                                                                                                                                               17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
                                                                                                                                                                                                                                                                                                                                                                      34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                           51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG
                                                                                                                                                   to: 559
                                          Percent Identity: 71.429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LeuSerAsnMetValValLysSerCysLysCysSer 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                184 CIGICCAACAIGAICGIGCGCICCIGCAAGIGCAGT 149
                                                                                                                                                   from: 1
                             Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                   Align seg 1/1 to reverse of: BG058804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BG540633.1 GI:13532879
437.50
4.704
83.036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_name: gb_est102:BG540633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mRNA sequence.
BG540633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                       alignment_block:
TGFB3P x BG058804/rev
Quality:
Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            human.
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AUTHORS
TITLE
JOURNAL
COMMENT
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KEYWORDS
SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: cgapbs-remail.nih.gov
Tissue Procurement: M. Bento Soares, Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D. and M.Fatima
Bonaldo, Ph.D.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BGOS0804 559 bp mRNA EST 25-JAN-2001 naf10g09.x1 Soares_NPBMC Homo sapiens cDNA clone IMAGE:4140856 3' similar to SW:TGF1_BOVIN P18341 TRANSFORMING GROWTH FACTOR BETA 1 PRECURSOR; contains element TAR1 repetitive element; , mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 559)
NCI-GAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index Unpublished (1997)
                                                                                                                                               120 TCGTGTACTACGTGGCCGCAAGCCCAAGGTGGAGCAGCTGTCCAACATG 171
88 leLeuTyrTyrValGlyArgThrProLysValGluGlnLeuSerAsnMet 104
                                                              AspThrThrHisSerThrValLeuGlyLeuTyrAsnThrLeuAsnProGl 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       found through the I.M.A.G.E. Consortium/LLNL at: info@image.llnl.gov
Seq primer: -4000 from Gibco
High quality sequence stop: 125.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="taxon:9606"
/clone="IMAGE:4140856"
                                                                                                                                                                                                                                                                                                                                                  170 ATCGTGCGCTCCTGCAAGTGCAGC 147
                                                                                                                                                                                                                                                                                                                         105 ValValLysSerCysLysCysSer 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BG058804.1 GI:12525628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .559
                                                                                                                                                                                                                                                                                                                                                                                                              seq_name: gb_est96:BG058804
                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq_documentation_block:
LOCUS BG058804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         human .
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84

LOCUS DEFINITION

SOURCE

REFERENCE AUTHORS

TITLE

JOURNAL

COMMENT

ACCESSION VERSION KEYWORDS Euteleostomi;

source

FEATURES

BASE COUNT

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alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                            source
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                                                                                                                                                                                                                                          BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACCESSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        54
                                                                      FEATURES
                                                                                                                                                                                                                                                               ORIGIN
Sfil (ggccgctcggcc); Site_2: Sfil (ggccattatggcc); 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGCCATATCGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGGCGGCGCACATG-dT(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.9 kb (range 0.5-4.0 kb). 12/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MCC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Systematic analyses of genes expressed in fertilized mouse eggs(The ERATO/Doi Project at Wayne State University)
Unpublished (1998)
Contact: Hirofumi Doi
Doi Bioasymmetry Project, ERATO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus
Eukaryota, Matazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 589)
Ko,M.S.H. Kitchen,J.R., Wang,X., Wang,X., Threat,T.A., Sun,T.,
Bopalma,G.E., Liang,Y., Kargul,G.J., Sharara,R., Paonessa,P.D. and
Doi,H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seq_documentation_block:
LOCUS C86748 589 bp mRNA EST 11-MAR-1998
DEFINITION C86748 Mouse fertilized one-cell-embryo cDNA mus musculus cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       174 CCATAAATCCAGAAGCATCTGCTTCTCCTTGCTGCGTGTCCCAAGATTTA 523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              84 GluProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGl 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    274 GCTTTGGATGCGCCCTATTGCTTTAGAAATGTGCAGGATAATTGCTGCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             34 HisGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             50 rLeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length: 110
Gaps: 2
Percent Identity: 70.909
                                                                                                                                                                                                                                                                                                                                                                                                                                                 to: 889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      clone J0232C11 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       574 CITTTCIAATATTGATTGTAAAGTCC 599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100 nLeuSerAsn.MetValValLysSer 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Align seg 1/1 to: BG540633 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C86748
C86748.1 GI:2918705
                                                                                                                                                                                                                                                                                               437.00
4.505
88.182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_name: gb_est103:C86748
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       house mouse.
                                                                                                                                                                                                                                                                                                    Quality:
                                                                                                                                                                                                                                                                                                                                        Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                        TGFB3P x BG540633
                                                                                                                                                                                                                                                                              alignment_scores
                                                                                                                                                                                                                                                                                                                                                                                   alignment_block
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                                                                                                                                                                                            BASE COUNT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JOURNAL
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SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMMENT
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Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthomorpha; Terraodontiformes; Tetraodontidae; Tetraodon.

1 (bases 1 to 1168)
Roest-Crollius,H., Jaillon,O., Dasilva,C., Fizames,C., Fisher,C., Weissenbach,J.
Japan Science and Technology Corporation (JST)
WBG Marive East 12F, 2-6 Nakase, Mihama-ku, Chiba 261-71, Japan
Email: hdebioa.jst.go.jp.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CNSO3XHH 1168 bp DNA GSS 18-MAY-2000
Tetraodon nigroviridis genome survey sequence T7 end of clone
066G06 of library G from Tetraodon nigroviridis, genomic survey
                                                                                                      /organism="Mus musculus"
/strain="CS/BL/6J"
/db_xref="taxon:10090"
/clone="J0232C11: 10090"
/clone="J0232C11: Extilized one-cell-embryo CDNA"
/clone_lib="Mouse fertilized one-cell-embryo"
1 123 c 141 g 171 t 9 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              88 IleLeuTyrTyrValGlyArgThrProLysValGluGlnLeuSerAsnMe 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     lyTyrTyrAlaAsnPheCysSerGlyProCys.ProTyrLeuArgSerAl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                aAspThrThrHisSerThrValLeuGlyLeuTyrAsnThrLeuAsnProG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               71 luAlaSerAlaSerProCysCysValProGlnAspLeuGluProLeuThr
                                                                                                                                                                                                                                                                                                                                                               Gaps: 4
Percent Identity: 72.072
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       to: 589
                                                                                                                                                                                                                                                                                                                                          Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Align seg 1/1 to reverse of: C86748 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AL265022
AL265022.1 GI:7986741
GSS; genome survey sequence.
Tetraodon nigroviridis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               104 tValValLysSerCysLysCysSer 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       141 GATTGTCAAGTCTTGTAAATGCAGC 117
                                                                                                                                                                                                                                                                                                                                      433.00
4.330
90.090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                seq_name: gb_gss4:CNS03XHH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sednence.
                                                                                                                                                                                                                                                                                                                                            Quality:
                                                                                                                                                                                                                                                                                                                                                                                Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                               Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                TGFB3P x C86748/rev
                                                                                                                                                                                                                                      145
                                                                                                                                                                                                                                                                                                                       alignment_scores:
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Charaterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis Unpublished (1788)	700 C 700 seq_name: gb_est1
2 (bases I to 1168) Roest-Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C., Rest-Crollius, H., Wincker, P., Brottier, P., Quetier, F., Saurin, W. and Weissenbach, J. Human gene number estimate provided by genome wide analysis using Tetracodon nigroviridis DNA sequence	seq_documentation LOCUS C8688 DEFINITION C8688 , ACCESSION C8681
	Σ
inis sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.	RS
11168 /organism="Tetraodon nigroviridis" /db_xref="taxon:99883" /clone="066G06" /clone 11b="G"	TITLE Syste ERAT JOURNAL Unpuk COMMENT Conte
/note="Genoscope sequence ID : COBG066BD03LP1-end : T7" 308 a 300 c 299 g 258 t 3 others	S
scores:     Quality: 433.00	source
_block: _cns03xHH/rev	BASE COUNT ORIGIN
to reverse of: CNS03XHH from: 1 to: 1168	
12 GluGluAsnCysCysValArgProLeuTyrIleAspPheArgGlnAspLe 28 ::::::	
uGlyTrpLysTrpVal.HisGluProLysGlyTyrTyrAla.AsnPheCy 44             GGGCTGGAGGTGGATCCCATGAGCCTACGAGGCCCAACTTCTG 1001	Percent Similari alignment_block: TGFB3P x C86879/
SSerGlyProCysProTyrLeuArgSerAlaAspThrThrHisSer 59  :::	Align seg 1/1 t
65 59	450 TTGGATGC
TACCGATGAAGGGCTGGGACCCAGCCGGTTGGCCTCGAGTGTCTGTGGGC 901	18 rgProLeu
TICTGGGCTTTCTGGACTTCTGACCGTTTCTCATCTTCAGGTGTT 851	400 GCCNTCTT 34 sGluProl
uGlyLeuTyrAsnThrLeuAsnProGluAlaSerAlaSerProCysCysV 79 	   350 TGAACCCA   51 euArgSer
alproginaspLeuGluProLeuThrIleLeuTyrTyrValGlyargThr 95 	 301 TATGGAGT 68 LeuAsnPr
ProLysValGluGlnLeuSerAsnMetValValLysSerCysLysCysSe 112        ::	251 NTNAATCC 84 uProLeuT
	201 ACCACTGA

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ematic analyses of genes expressed in fertilized mouse eggs(The 'O/Doi Project at Wayne State University)
blished (1988)
act: Hirofuni Doi
Bloasymmetry Project, ERATO
In Science and Technology Corporation (JST)
Marive East 12F, 2-6 Nakase, Mihama-ku, Chiba 261-71, Japan
1. hd@bloa.jst.go.jp.
Location/Qualifiers
                                                                                                                                                                                                                    ryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; alla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. bases I to 583, 1. S.H. Kitchen, J.R., Wang, X., Wang, X., Threat, T.A., Sun, T., Ima, G.E., Liang, Y., Kargul, G.J., Sharara, R., Paonessa, P.D. and
                                 n_block: 583 bp mRNA EST 11-MAR-1998 79 Mouse fertilized one-cell-embryo cDNA Mus musculus cDNA e J0235C05 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Mus musculus"
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/strain="C57BL/GJ"
/db_xref="taxon:10090"
/clone="J0335C05"
/clone="Jnb="Mouse fertilized one-cell-embryo cDNA"
/dev_stage="fertilized one-cell-embryo"
124 c 134 g 166 t 17 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TCAGACACTCAACACACNAAAGTCCTCAGCCTGTACAACACN 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyrL 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnThr 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              oGluAlaSerAlaSerProCysCysValProGlnAspLeuGl 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length: 113
Gaps: 2
Percent Identity: 74.336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         to reverse of: C86879 from: 1 to: 583
                                                                                                                                        79.1 GI:2918836
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4.454
85.841
103:086879
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source DEFINITION ORGANISM AUTHORS TITLE BASE COUNT ACCESSION REFERENCE JOURNAL 51 VERSION KEYWORDS FEATURES COMMENT ORIGIN SOURCE /note="Vector: pT773D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from mammary polylinker; 1st strand cDNA was prepared from mammary polylinker; 1st strand cDNA was prepared, and was then primed with a Not I - Oligo(dT) primer. Double stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT773 vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo." Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 996) morphished (1999)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs.remail.nih.gov
Tissue Procurement: M. Bento Soares, Ph.D.
CDNA Library Preparation: Bento Soares and M. Fatima Bonaldo
CDNA Library Prarayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: They I.M.A.G.E. Consortium (LLNL)
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov h column: 18 BF682484 996 bp mRNA bold MILMG Mus musculus cDNA clone 1MAGE:3468737 3', mRNA sequence. NIH MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC) 2 LeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCys.CysValA 18 35 GluProLysGlyTyrTyrAlaAsnPheCysSerGly.ProCysProTyrL 51 from: 1 to: 996 Gaps: 4 Percent Identity: 72.807 101 euSerAsnMetValValLysSerCysLysCysSer 112 Length: High quality sequence start: 37 High quality sequence stop: 636. Location/Qualifiers Align seg 1/1 to reverse of: BF682484 /lab\_host="DH10B" BF682484.1 GI:11956379 4.559 82.456 428.50 1. .996 seq\_name: qb\_est91:BF682484 seq\_documentation\_block: house mouse. Mus musculus TGFB3P x BF682484/rev Quality: Ratio: Percent Similarity: 239 alignment\_scores: alignment\_block source DEFINITION BASE COUNT ORIGIN ORGANISM REFERENCE AUTHORS TITLE JOURNAL COMMENT ACCESSION VERSION KEYWORDS FEATURES SOURCE

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Anote—"Vector: pT7T3D-pac (Pharmacia) with a modified polylinker; Plasmid DNA from the normalized library NCI_CGAP_GC4 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1257096-1258631, 1469064-1470983, and 1475592-1476743). Subtraction by Bento Soares and M. Fatima Bonaldo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              wb02f01.x1 NCI_CGAP_GC6 Homo sapiens CDNA clone IMAGE:2304505 3' similar to gb:X02812_cds1 TRANSFORMING GROWTH FACTOR BETA 1 PRECURSOR (HUMAN); contains element TAR1 MER22 repetitive element; AI824845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tumor Gene Index
Unpublished (1997)
Contact: Robert Stausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
R. Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I (bases 1 to 44).
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
                                                                                                                      84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
                                                                                                                                                                                                   84
                                                                                     67
                                                                                                                                                                                                   68 Leu. AsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG
                                                                                     euArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone="IMAGE:2304505"
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/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 497 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 347.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                    101 LeuSerAsnMetValValLysSerCysLysCysSer 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  137 TTGTCCAACATGATTGTGCGCTCCTGCAAGTGCAGC 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AI824845.1 GI:5445516
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_name: gb_est25:A1824845
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LOCUS AI824845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
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alignment_block:
TGFB3P x A1654506/rev
                                                                                                                                                                                                                                                                                                                                                                 Percent Similarity:
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                                                                                                                                                                                                                                 BASE COUNT
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KEYWORDS
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                                                                                                                                                                                                                                                   ORIGIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AI654506 460 bp mRNA EST 17-DEC-1999 wb63d04.xl NCI_CGAP_GC6 Homo sapiens CDNA clone IMAGE:2310343 3' similar to gb:X02812_cds1 TRANSFORMING GROWTH FACTOR BETA 1 PRECURSOR (HUMAN);contains PTR5.t3 PTR5 MSR1 repetitive element; mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
R. Emmert-Buck, M.D., Ph.D.
CONA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 460)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                           PValHisGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysP 49
                                                                                                                                                                                                                                                                                                                                                 roTyrLeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyr 65
                                                                                                                                                                                                                                                                                                                                                                                                                             AsnThrLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAs 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       pLeuGluProLeuThrIleLeuTyrTyrValGlyArgThrProLysValG 99
                                                                                                                                                                                         16 CysValArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTr
                                                                                                                                                       to: 441
                                     Gaps: 0
Percent Identity: 76.289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99 luGlnLeuSerAsnMetValValLysSerCysLysCysSer 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         www.bio.llnl.gov/bbrp/image/image.html
Insert Length: 519 Std Error: 0.00
Seq primer: -400P from Gibco
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./db_xref="taxon:9606"
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                                                                                                                                                   Align seg 1/1 to reverse of: AI824845
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             426.00
5.071
86.598
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 _documentation_block:
                                                                                           alignment_block:
TGFB3P x A1824845/rev
               Quality:
Ratio:
Percent Similarity:
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alignment_scores:
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DEFINITION
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VERSION
KEYWORDS
SOURCE
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force—"Vector: P1773D-Pac (Pharmacia) with a modified polylinker; Plasmid DNA from the normalized library NCI_CGAP_GC4 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1257096-1258631, 1469064-1470983, and 1475592-1476743). Subtraction by Bento Soares and M. Fatima Bonaldo. "
131 c 166 g 93 t 2 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seq_documentation_block:
LOCUS AA049522 477 bp mRNA EST 09-SEP-1996
DEFINITION mj35f01.rl Soares mouse embryo NbME13.5 14.5 Mus musculus cDNA clone IMAGE:478105 5' similar to gb:X02812_cds1 TRANSFORMING GROWTH FACTOR BETA 1 PRECURSOR (HUMAN); gb:M32745 mouse transforming growth factor beta-3 mRNA, complete (MOUSE);, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 (bases 1 to 477)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         358 TCGGGCCCTGCCCCTACATTTGGAGCCTGGACACGCAGTACAGCAAGGTC 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         95 hrProLysValGluGlnLeuSerAsnMetValValLysSerCysLysCys 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        208 AGCCCAAGGTGGAGCAGCAGCTGTGAACATGATCGTGCGCTCCTGCAAGTGC 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28 uGlyTrpLysTrpValHisGluProLysGlyTyrTyrAlaAsnPheCysS 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           45 erGlyProCysProTyrLeuArgSerAlaAspThrThrHisSerThrVal 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       78 sValProGlnAspLeuGluProLeuThrIleLeuTyrTyrValGlyArgT 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62 LeuGlyLeuTyrAsnThrLeuAsnProGluAlaSerAlaSerProCysCy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12 GluGluAsnCysCysValArgProLeuTyrIleAspPheArgGlnAspLe
                              /tissue_type="pooled_germ cell tumors"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          to: 460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length: 101
Gaps: 0
Percent Identity: 74.257
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/clone_lib="NCI_CGAP_GC6"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  426.00
4.953
85.149
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Mus musculus
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                               Unpublished (1996)
Contact: Marara MyMouse EST Project
WashD-HHMI Mouse EST Project
WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                      /strain="c57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:478105"
/clone=lib="Soares mouse embryo NbMB13.5 14.5"
/sex="unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           340 ACACAACCGGGGGGTTCGGCGTCACCGTGCTGCGTGCCGCACGTTTTGG 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         142 GCCCTGGATACCAACTATTGCTTCAC.TCCACAGAGAAGAACTGCTGTGT 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17 lArgProLeuTyrlleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG
                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="embryo"
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/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length: 108
Gaps: 0
Percent Identity: 75.926
                                                                                                                                                                                                                                                     Seq primer: -28M13 rev2 from Amersham
High quality sequence stop: 450.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             91 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Align seg 1/1 to: AA049522 from: 1 to: 477
                                                                                                                                                                                                                                                                                                                             /organism="Mus musculus"
                                               The WashU-HHMI Mouse EST Project
                                                                                                                                                                                      Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           126 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           M. Fatima Bonaldo.
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4.532
87.037
                                                                                                                                                                                                                                                                                                               1. .477
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TGFB3P x AA049522
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                                                 TITLE
JOURNAL
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                                                                                   COMMENT
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//note="Organ: mixed (see below); vector: pT7T3D-Pac (Pharmacia) with a modified polylinker: Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (melanocyte 2NbHM, pregnant uterus NbHPU, and fetal heart NbHH19W) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 260232-265223, 340488-345479, and 484488-489479. 1 others
                                                                                                                                                                                                                                                                           A1273619 499 bp mRNA EST 29-JAN-1999 415001.x1 Soarse_NHHMPU_S1 Homo sapiens CDNA clone IMAGE1.1876320 3' similar to 9b:XO2812_cds1 TRNNSFORMING GROWTH FACTOR BETA 1 PRECURSOR (HUMAN);contains PTR5.t3 PTR5 repetitive element; mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
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/clone_lib="Soares_NhHMPu_S1"
/tissue_type="Pooled human melanocyte, fetal heart, and pregnant uterus"
/lab_host="PDH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 (bases 1 to 499)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 760 Std Error: 0.00
Seq primer: -400P from Gibco
Align seg 1/1 to reverse of: AI273619 from: 1 to: 499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps: 2
Percent Identity: 70.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              High quality sequence stop: 366.
Location/Qualifiers
1. 499
                                                                                                                                                   440 TIGICCAACAIGAITGIGCGCICC 463
                                                                                                  LeuSerAsnMetValValLysSer 108
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AI273619.1 GI:3895887
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4.587
83.636
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                                                                                                                                                                                                  seq_name: gb_est18:A1273619
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LOCUS A1273619
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TGFB3P x AI273619/rev
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                                                                                                  101
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seq_name: gb_est18:AI304490
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TGFB3P x AI272940/rev
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Percent Similarity:
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ORIGIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AI272940 292 bp mRNA EST 18-NOV-1998 q156901.x1 Soares_WhHPW_S1 Homo sapiens cobn clone IMAGE:1876368 3' similar to gb:x02812_cds1 TRANSFORMING GROWTH FACTOR BETA PRECURSOR (HUMAN);contains element MER22 repetitive element ; mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 292)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /Organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tumor Gene Index
Uppublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Seq primer: -40UP from Gibco
High quality sequence stop: 1.
Location/Qualifiers
                                              342 TGGACACGCAGTACAGCAAGGTCCTGGCCCTGTACAACCAGCATAACCCG 293
                                                                                                                                                                                                                                                                                                                                                      292 GGGCCTCGGCGCGCGCTTNTGCGTGCCGCAGGCGCTGGAACCCCTGCC 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                     242 CATTGTGTACTACGTGGCCGCAAGCCCAAGGTGGAGCAACTGTCCAACA 193
                                                                                                                                                                                                                                                                                                                                                                                                                         87 rIleLeuTyrTyrValGlyArgThrProLysValGluGlnLeuSerAsnM 104
                                                                                                                                                                                                                        54 laAspThrThrHisSerThrValLeuGlyLeuTyrAsnThrLeuAsnPro 70
                                                                                                                                                                                                                                                                                                                    71 GluAlaSerAlaSerProCysCysValProGlnAspLeuGluProLeuTh 87
                                                                                                                      37 sGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyrLeuArgSerA 54
                    21 TyrlleAspPheArgGlnAspLeuGlyTrpLysTrpValHisGluProLy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      192 TGATCGTGCGCTCCTGCAAGTGCAAC 167
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/lab_host="DH10B"
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AI272940.1 GI:3895208
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LOCUS AI272940
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Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LiNL at:

www-bio.llnl.gov/Dbrp/image/image.html

Insert Length: 933 Std Error: 0.00

Seq primer: -40UP from Gibco

High quality sequence stop: 385.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq_documentation_block:

LOCUS A1304490 449 bp mRNA EST 01-FEB-1999

DEFINITION qo54e06.x1 NCI_CGAP_CO8 Homo sapiens cDNA clone IMAGE:1912354 3'

similar to gb:X02812_cds1 TRANSFORMING GROWTH FACTOR BETA 1

PRECURSOR (HUMAN);contains PTR5.t3 TAR1 repetitive element ;, mRNA
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 (bases 1 to 449)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                           292 TGCGGGCGGCAGTTGTACATTGACTTCCGCAAGGACCTCGGCTGGAAGTG 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 32 pValHisGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysP 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 49 roTyrLeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyr 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            66 AsnThrLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAs 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16 CysValArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTr
                              Gaps: 0
Percent Identity: 74.227
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Unpublished (1997)
416.00
5.012
85.567
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Homo sapiens
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KEYWORDS
SOURCE
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                                                                                 FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORIGIN
                                                                                              /note="Organ: colon; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from colon adenocarcinoma, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo. "
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 348)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq_documentation_block:

LOCUS A1192407 348 bp mRNA EST 28-OCT-1998

DEFINITION qC98c094.1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone
IMAGE:1722256 3' similar to gb:Y00083 TRANSFORMING GROWTH FACTOR
BETA 2 PRECURSOR (HUMAN);, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL ; contact the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                uThrIleLeuTyrTyrValGlyArgThrProLysValGluGlnLeuSerA 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             244 GCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAGCTGTCCA 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    70 ProGluAlaSerAlaSerProCysCysValProGlnAspLeuGluProLe 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    erAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnThrLeuAsn 69
                                                                                                                                                                                                                                                                                                                                                                                                 Gaps: 0
Percent Identity: 77.419
                 /clone="IMAGE:1912354"
/clone_lib="NCL_CGAP_CO8"
/tissue_type="adenocarcinoma"
                                                                                                                                                                                                                                                                                                                                                                              Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Align seg 1/1 to reverse of: AI304490
                                                                             /lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AI192407.1 GI:3743616
                                                                                                                                                                                                                                                                                                                                                                         Quality: 416.00
Ratio: 5.073
nilarity: 88.172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tumor Gene Index
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TGFB3P x AI304490/rev
                                                                                                                                                                                                                                                                                                                                                                                                                Percent Similarity:
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                                                                                                                                                                                                                                                                      99
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                                                                                                                                                                                                                                                                                                                                                        alignment_scores
                                                                                                                                                                                                                                                                                                                                                                                                                                                             alignment_block
                                                                                                                                                                                                                                                                    BASE COUNT
ORIGIN
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VERSION
KEYWORDS
SOURCE
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TITLE
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A1421250 540 bp mRNA EST 28-MAR-1999 tf14d02.x1 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:2096163 3' similar to gb:X02812_cds1 TRANSFORMING GROWTH FACTOR BETA 1 PRECURSOR (HUMAN);contains element TAR1 repetitive element;, mRNA
                                                                                                                                                                                                                                                                                                                                                                Not
                                                                                                                                                                                                                                                                                                                                       double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the No and Eco RI sites of the modified pT/T3 vector. Library went through one round of normalization. Library constructed by M. Fatima Bonaldo.
                                                                                                                                                                                                                                                            /note="Organ: uterus; Vector: pT7T3-Pac; Site_1: Not I
Site_2: Eco RI; 1st strand cDNA was primed with a Not
Oligo(dT) primer [5'
AACTGGAAGATTCGCGGCCCCTTTTTTTTTTTTTTT 3'],
IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 672 Std Error: 0.00 Seq primer: -40UP from Gibco High quality sequence stop: 157.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          215 ACGTCCACTTTACATTGATTTCAAGAGGGATCTAGGGTGGAAATGGATAC 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone_lib="Soares_pregnant_uterus_NbHPU"
/sex="female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     from: 1 to: 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length: 88
Gaps: 0
Percent Identity: 78.409
                                                                                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1722256"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Align seg 1/1 to reverse of: AI192407
                                                                                                                                                                                                                       /dev_stage="adult"
                                                                                                                                                                                                                                         /lab_host="DH10B
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92.045
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seg_documentation_block:
LOCUS A1421250
DEFINITION tf14d02.x1 NC
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Ratio:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            alignment_scores:
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CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

CDNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

Www-bio.lnl.gov/bbrp//image/himage.html

Insert Length: 874 Std Error: 0.00

Seq primer: 40UP from Gibco

High quality sequence stope: 373.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     T 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is normalized, and was constructed by Bento Soares and M.Fatima Bonaldo."
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

(bases 1 to 540)

NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

NAIJONAL Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BTGAP), Tumor Gene Index

Unpublished (1998)

Contact: Robert Strausberg, Ph.D.
Enail: cgapbs-rémail.nih.gov

Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1913 CGTGCCGCAGGCGCTGGAGCCGCTGCCATCGTACTACGTGGGCCGCA 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62 LeuGlyLeuTyrAsnThrLeuAsnProGluAlaSerAlaSerProCysCy 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12 GluGluAsnCysCysValArgProLeuTyrIleAspPheArgGlnAspLe 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        78 sValProGlnAspLeuGluProLeuThrIleLeuTyrTyrValGlyArgT 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               45 erGlyProCysProTyrLeuArgSerAlaAspThrThrHisSerThrVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps: 0
Percent Identity: 74.257
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TGFB3P x AI421250/rev
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                                                                  AUTHORS
TITLE
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                                                REFERENCE
                                                                                                                                                      JOURNAL
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
/clone_lib="BN0014"
/dev_stage="Adult"
/note="Organ: breast_normal; Vector: pucl8; Site_1: Smal;
Site_2: Smal; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
0 a 54 c 63 g 74 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: asimpsoneludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be set in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RCl&t2=RCl-BN0014-210100-012-d06&t3=2000-01-21&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 15
High quality sequence start: 261.
                                                                                                                                                                                                                                  AW600940 261 bp mRNA EST 23-MAR-2000
RC1-BN0014-210100-012-d06 BN0014 Homo sapiens CDNA, mRNA sequence.
AW600940
                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
Subaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 261)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     259 TITAGAAAIGTGCAGGAIAAATGCTGCCTACGTCCACTTTACATTGACTT 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24
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8 PheArgAsnLeuGluGluAsnCysCysValArgProLeuTyrIleAspPh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           to: 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HCGP http://www.ludwig.org.br/ORESTES.
The FAPESP/LICR Human Cancer Genome Project
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length: 85
Gaps: 0
Percent Identity: 77.647
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                                                                                                                                                                                                                                                                                                                    AW600940.1 GI:7305679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tel: +55-11-2704922
Fax: +55-11-2707001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              401.00
5.076
92.941
                                                                                                                                                                                seq_name: gb_est49:AW600940
                                                                                                                                                                                                                             seq_documentation_block:
LOCUS     AW600940
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                                                                                                                                                                                                                                                                                                                                                                     human.
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                                                                                         Ser 112
                                                                                                                                   143 AGC 141
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TITLE
JOURNAL
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KEYWORDS
SOURCE
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                                                                                         112
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102 GCCCTGGACACCAACTATTGCTTCAGCTCCACGGAGAAGAACTGCTGCGT
                                            17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH
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ORGANISM
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AUTHORS
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               //octe="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact: Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax: (1) 301 610 8371 Email: fliang@lifetech.com URL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens

Bukaryota s, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

1 (Moses 1 to 798)

Full (Moses 1 to 798)

Full-length cDMA libraries and normalization

Unpublished (2001)

Contact: Genoscope
                                                                                                                                                                                                                                                                                                                                                                                                                                                       AL530080 798 bp mRNA EST 13-FEB-2001
AL530080 LTI_NFL001_NBC4 Homo sapiens cDNA clone CSODD009YM06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqrefégenoscope.cns.fr, Web : www.genoscope.cns.fr.
Location/Qualifiers
                                         58 HisSerThrValLeuGlyLeuTyrAsnThrLeuAsnProGluAlaSerAl 74
                                                                                                                                    109 CACAGCAGGTCCTGAGCTTATATAATACCATAAATCCAGAAGCATCTGC 60
                                                                                                                                                                                                   74 aSerProCysCysValProGlnAspLeuGluProLeuThrIleLeuTyrT 91
                                                                                                                                                                                                                          41 laAsnPheCysSerGlyProCysProTyrLeuArgSerAlaAspThrThr 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue_type="neuroblastoma cells"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       http://fulllength.invitrogen.com"
228 c 274 g 145 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CSODD009YM06"
/clone_lib="LTI_NFL001_NBC4"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   prime, mRNA sequence.
AL530080
AL530080.1 GI:12793573
                                                                                                                                                                                                                                                                                                                                                                                      seq_name: gb_est29:AL530080
                                                                                                                                                                                                                                                                                                                                                                                                                              seq_documentation_block:
LOCUS AL530080
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              human.
                                                                                                                                                                                                                                                                                           91 yrval 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         alignment_scores:
                                                                                                                                                                                                                                                                                                                                        9 ACATC 5
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AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACCESSION
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Align seg 1/1 to reverse of: AL530080 from: 1 to: 798

TGFB3P x AL530080/rev

alignment\_block

Percent Identity: 66.364

4.500 80.909 400.50

Percent Similarity:

Quality:

Ratio:

Length: Gaps:

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/note="Organ: Dreast_normal; Vector: puc18; Site_1: Smal; Site_2: Smal; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under 10w stringency conditions. " 52 c 62 g 84 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC1&t2=RC1-BN0014-210100-012-c03_1&t3=2000.01-21&t4=1)
Seq primer: puc 18 forward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23-MAR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AWG00938 267 bp mRNA EST 23-MAR-2C RCI-BN0014-210100-012-c03_1 BN0014 Homo sapiens cDNA, mRNA SAWG00938.1 GI:7305677
                                                                                                                                              155 AGCGCTGCCCTTCGTGTACTACGTGGCCGCAAGCCCAAGGTGGGGCCG 106
                                                                                                                                                                                                                                                                                                                                                  84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
                                                                                                                                                                                                                                 84
                                                                                                                51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
                             67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG
34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr
                                                                                                                                                                                                                                                                                      202 GCATAACCCGGGCCTCGGCGCGCC...GTGCGCGTGCCGCAGGCGCTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 (bases 1 to 267)
HCGP http://www.ludwig.org.br/ORESTES.
The FAPESP/LICR Human Cancer Genome Project Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
1. 267
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="BN0014"
/dev_stage="Adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   101 LeuSerAsnMetValValLysSerCysLys 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        High quality sequence stop: 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   105 CTGTCCAACATGGTCGTGCGCTCCTGCAAG 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                seq_name: gb_est49:AW600938
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_documentation_block:
LOCUS     AW600938
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30 12:56:57 2001

Oct

Tue

alignment\_scores

alignment\_block

265

43

115 93 9

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T 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT/T3 vector. Library went through one round of normalization, and was constructed by Bento Soares and M.Fatima Bonaldo."
                                                                                                                                                          /note="Organ: placenta; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              W98872 431 bp mRNA EST 16-JUL-1996
mf89e01.rl Soares mouse embryo NbME13.5 14.5 Mus musculus cDNA
clone IMAGE:421464 5' similar to gb:X02812_cds1 TRANSFORMING GROWTH
FACTOR BETA 1 PRECURSOR (HUMAN);, mRNA sequence.
                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
/db_xref="taxon:10090"
/clone="IMAGE:457739"
/clone="IMAGE:457739"
/clone_lib="Soares mouse placenta 4NbMP13.5 14.5"
/sex="unknown"
/tissue_type="placenta"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps: 2
Percent Identity: 74.757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          to: 558
                                                                                                                    /dev_stage="adult"
                                                                                                                                     /lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            W98872.1 GI:1428996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  399.50
4.540
85.437
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       518 GTTGTCC 524
                                                                                                                                                                                                                                                                                                                                                                              130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alignment_scores:
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ORIGIN
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DEFINITION
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VERSION
KEYWORDS
SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AA021815 558 bp mRNA EST 21-JAN-1997 mN85d06.rl Soares mouse placenta 4NbMPl3.5 14.5 Mus musculus CDNA clone IMAGE:45739 5' similar to gb:X02812_cds1 TRANSFORMING GROWTH FACTOR BETA 1 PRECURSOR (HUMAN); gb:M32745 mouse transforming growth factor beta-3 mRNA, complete (MOUSE);, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Galsel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moroe,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The WashU-HHMI Mouse EST Project
Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
WashU-HHMI Mouse EST Project
WashIngton University School of Medicinep
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Fax: 314 286 1800
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
                                                                                                                                                                                                                 yArgThrProLysValGluGlnLeuSerAsnMetValValLysSerCysL 110
                                                                                                                                                                                                                                                                                                           eCysSerGlyProCysProTyrLeuArgSerAlaAspThrThrHisSerT 60
                                                                                                                                                                                                                                                                                                                                                                                             60 hrValLeuGlyLeuTyrAsnThrLeuAsnProGluAlaSerAlaSerPro 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  77 CysCysValProGlnAspLeuGluProLeuThrIleLeuTyrTyrValGl 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        to: 267
                          Length: 86
Gaps: 0
Identity: 80.233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MGI:274627
Seq primer: -28M13 rev2 from Amersham
High quality sequence stop: 454.
Location/Qualiflers
                                                                                                                                                                                from: 1
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,<organism="Mus musculus"
                                                                                                                                                                           Align seg 1/1 to reverse of: AW600938
                                                                         Percent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AA021815.1 GI:1485570
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                        400.00
5.063
91.860
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         house mouse.
                                                                                                                                   TGFB3P x AW600938/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          110 ysCysSer 112
                               Quality:
                                              Ratio:
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LOCUS DEFINITION

ORGANISM ACCESSION VERSION KEYWORDS SOURCE

REFERENCE AUTHORS JOURNAL COMMENT

TITLE

source

FEATURES

TITLE JOURNAL COMMENT

REFERENCE AUTHORS

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Systematic analyses of genes expressed in fertilized mouse eggs(The ERATO/Doi Project at Wayne State University)
Unpublished (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 (bases 1 to 587)
Ko,M.S.H, Kitchen,J.R., Wang,X., Wang,X., Threat,T.A., Sun,T.,
DePalma,G.E., Liang,Y., Kargul,G.J., Sharara,R., Paonessa,P.D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dol Bloasymmetry Project, ERATO
Japan Science and Technology Corporation (JST)
WBG Marive East 12F, 2-6 Nakase, Mihama-ku, Chiba 261-71, Japan
Email: hdebios.jst.go.jp.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                        C87366 587 bp mRNA EST 11-MAR-1998 C87366 Mouse fertilized one-cell-embryo cDNA Mus musculus cDNA clone J0244610 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="taxon:10090"
/clone="J0244G10"
/clone=lib="Mouse fertilized one-cell-embryo cDNA"
/dev_stage="fertilized one-cell-embryo"
1 128 c 140 g 166 t 6 others
                                                                                                                                248 ATTTGGAGCCTGGACACACAGTACAGCAAGGTCCTTGCCCTCTACAACCA 297
                                          22 IleAsp.PheArgGlnAspLeuGlyTrpLysTrpValHisGluProLysG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6 TyrCysPheArgAsnLeuGlu.GluAsnCysCysVal.ArgProLeuTyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Identity: 71.818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Align seg 1/1 to reverse of: C87366 from: 1 to: 587

    .587
    /organism="Mus musculus"

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /strain="C57BL/6J
                                                                                                                                                                                                                                                                  396 TTGTCCAACATGGATGTGCGC 416
                                                                                                                                                                                                                        101 LeuSerAsnMetValValLys 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Hirofumi Doi
                                                                                                                                                                                                                                                                                                                                                                                                                                           C87366.1 GI:2919323
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4.052
88.182
                                                                                                                                                                                                                                                                                                         seq_name: gb_est103:C87366
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Doi, H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            alignment_scores
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             T 3'], on equal amounts of mRNA from 2 13.5dpc and 2
14.5dpc embryos [total RNA provided by Minoru Ko, Wayne
State Univ., from 2 ]; double-stranded cDNA was ligated to
Eco RI adaptors (Pharmacia), digested with Not I and
cloned into the Not I and Eco RI sites of the modified
pyTT3 vector. Library went through one round of
normalization, and was constructed by Bento Soares and
M.Fatima Bonaldo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (bases 1 to 431)
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Gelsel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                 This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                         Unpublished (1996)
Contact: Marka M/Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:10090"
/clone="IMAGE:421464"
/clone_lib="Soares mouse embryo NbME13.5 14.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               198 ACGAGCCCAAGGCTACCATGCCAACTTCTGTCTGGGACCCTGCCCCTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue_type="embryo"
/dev_stage="13.5-14.5dpc total fetus"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          oaps: 0
Percent Identity: 71.028
                                                                                                                                                                                                                                                                                                                                                                                                                frace considered overall poor quality
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          85 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Mus musculus"
                                                                                                                              Waterston, R.
The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                           Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Align seg 1/1 to: W98872 from: 1 to: 431
                                                                                                                                                                                                                                                                                                                                                                                                                              Seq primer: ETPrimer
High quality sequence stop: 1.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          117 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /sex="unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            138 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4.43883.178
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Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       alignment_block:
TGFB3P x W98872
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BASE COUNT ORIGIN

source

FEATURES

Length: Gaps: 64.865

Percent Identity:

79.279

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Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bonaldo, Ph.D. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:
info@image.linl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT713 vector. Library is normalized; constructed in the laboratory of M. Bento Soares (University of Iowa)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nafidfiz.xl Soares_MPBMC Homo sapiens cDNA clone IMAGE:4140814 3' similar to SW:TGF1_CERAE P09533 TRANSFORMING GROWTH FACTOR BETA 1 PRECURSOR ; contains element PTR5 repetitive element ;, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I (bases 1 to 403)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Organ: blood; Vector: pT7T3D-Pac; Site_1: NotI; Site_2: EcoRI; 1st strand cDNA was primed with a Not I -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cDNA Library Preparation: M. Bento Soares, Ph.D. and M.Fatima
                                                                                                                                                                                                                                                                                                                                                                                                                                                          25-JAN-2001
239 ACT.TCCGCTTCCCCTTGCTGTGTCCCAGGATCTGGAACCACTGACCA 191
                                                                                                                                                                                                                   88 leLeuTyrValGlyArgThrProLysValGluGlnLeuSerAsnMet 104
                                                                                              71 uAlaSerAlaSerProCysCysValProGlnAspLeuGluProLeuThrI 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="lymphocyte"
/lab_host="DH10B (phage-resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: M. Bento Soares, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Trace considered overall poor quality
Seq primer: -400P from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone="IMAGE:4140814"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                High quality sequence stop: 1.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                     mRNA
                                                                                                                                                                                                                                                                                     105 ValValLysSerCysLysCysSer 112
                                                                                                                                                                                                                                                                                                                                     140 ATTGTCAAGTCTTGTAAATGCAGC 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BG058796.1 GI:12525613
                                                                                                                                                                                                                                                                                                                                                                                                                                                        403 bp
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                                                                                                                                                                                                                                                                                                                                                                               seq_name: gb_est96:BG058796
                                                                                                                                                                                                                                                                                                                                                                                                                             seq_documentation_block:
LOCUS BG058796
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Ratio:
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VERSION
KEYWORDS
SOURCE
ORGANISM
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TITLE
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    55
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 339)
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DEFINITION ue48g10.r2 Soares_mammary_gland_NMLMG Mus musculus cDNA clone IMAGE:1494402 5' similar to gb:M32745 mouse transforming growth factor beta-3 mRNA, complete (MOUSE);, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Waterston, R.
The Mashu-HHMI Mouse EST Project
Unpublished (1996)
Contact: Marra M/Mouse EST Project
Washu-HHMI Mouse EST Project
Washu-HHMI Mouse EST Project
Washington University School of Medicinep
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                             234 ACGAGCCCAAGGGCTACCATGCCAACTTCTGCATCGGGCCCTGCCCTAC 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
                                                                                                                                          1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
                                                                                                                                                                                                                                                                                                                                                                                    34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
                                                                                                                                                                                                                                                                                                                                                                                                                  MGI:932006
Seq primer: -28ml3 rev2 ET from Amersham
High quality sequence stop: 267.
Location/Qualifiers
                                                                                          from: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Mus musculus"
/db_xref="taxon:10090"
                                                                                    Align seg 1/1 to reverse of: BG058796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AI157673.1 GI:3686142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_name: gb_est16:A1157673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     house mouse.
alignment_block:
TGFB3P x BG058796/rev
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Page

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Fax: 314 286 1810
rel: 314 286 1800
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TGFB3P x A1604914/rev
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
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                                                                                                                                                                                           source
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                                                                                                                                                                 FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORIGIN
                                                                                                           /note="Vector: pr713D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from mammary gland tissue from a lactating female, and was then primed with a Not I - Oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pr773 vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AI604914 403 bp mRNA EST 21-APR-1999 me44C04.x1 Scares mouse embryo NbWE13.5 14.5 Mus musculus cDNA clone IMAGE:390342 3' similar to gb:X02812_cds1 TRANSFORMING GROWTH FACTOR BETA 1 PRECURSOR (HUMAN); gb:M32745 mouse transforming growth factor beta-3 mRNA, complete (MOUSE);, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 403) Marra, M.; Hillier, L.; Kucaba, T.; Martin, J.; Beck, C.; Wylie, T.; Underwood, K.; Steptoe, M.; Theising, B.; Allen, M.; Bowers, Y.; Person, B.; Swaller, T.; Gibbons, M.; Pape, D.; Harvey, N.; Schurk, R.; Ritter, F.; Kohn, S.; Shin, T.; Jackson, Y.; Cardenas, M.; McCann, R.; The WashU-NCI Mouse EST Project 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (1999)
Contact: Marra M/WashU-NCI Mouse EST Project 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      208 ACGAACCTAAGGGTTACTATGCCAACTTCTGCTCAGGCCCTTNGCCATAC 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              258 CTCCGCAGCGCAGACAACCCATAGCACGGTGCTTGGACTATACAACAC 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17 largProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
                 /clone_lib="Soares_mammary_gland_NMLMG"
/sex="female (lactating)"
/tissue_typ="mammary gland"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Identity: 98.649
                                                                                                                                                                                                                                                                                                                                                                                                                              Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           to: 339
/clone="IMAGE:1494402"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Align seg 1/1 to: AI157673 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AI604914.1 GI:4614081
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5.301
98.649
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LOCUS A1604914
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Ratio:
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T 3'], on equal amounts of mRNA from 2 13.56pc and 2
14.56pc embryos [total RNA provided by Minoru Ko, Wayne
State Oniv., from 2 ]; double-stranded cDNA was ligated to
BCO RI adaptors (Pharmacia), digested with Not I and
cloned into the Not I and Eco RI sites of the modified
pT7T3 vector. Library went through one round of
normalization, and was constructed by Bento Soares and
M.Fatina Bonaldo. "
                                                                                                                                                                                                                                                                                                                                                                                                                          seq_documentation_block:
LOCUS AI360877 328 bp mRNA EST 15-FEB-1999
DEFINITION qy01c06.x1 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:2010730 3'
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
This clone was previously sequenced on the 5' end only, this new
data is from the 3' end.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                             /tissue_type="embryo"
/dev_stage="13.5-14.5dpc total fetus"
/dab_host="PH108"
/note="Vector: pT/T3D-Pac (Pharmacia) with a modified
                                                                                                                                                                                                                  /db_xref="taxon:10090"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             354
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               92 lGlyArgThrProLysValGluGlnLeuSerAsnMetValValLysSerC 109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      76 ProCysCysValProGlnAspLeuGluProLeuThrIleLeuTyrTyrVa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          203 GGGTCGCAAGCCCAAGGTGAACATGTCCCAACATGATTGTGCGCTCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26 GlnAspLeuGlyTrpLysTrpValHisGluProLysGlyTyrTyrAlaAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             42 nPheCysSerGlyProCysProTyrLeuArgSerAlaAspThrThrHisS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               59 erThrValLeuGlyLeuTyrAsnThrLeuAsnProGluAlaSerAlaSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Align seg 1/1 to reverse of: AI604914 from: 1 to: 403
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Percent Identity: 77.011
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                                                                                                                                                                                /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          149 g
                                                                                                                                                                                                     /strain="C57BL/6J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                M.Fatima Bonaldo.
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5.092
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D. CDNA Library Arrayed by: Greg Lennon, Ph.D. CDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                            Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
                                                                                                                                              Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 328) NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BTGAP), Tumor Gene Index Unpublished (1998)
similar to gb:X02812_cds1 TRANSFORMING GROWTH FACTOR BETA 1
PRECURSOR (HUMAN);, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   278 GTACATTGACTTCCGCAAGTACCTCGGCTGGAAGTGGATTCTCGAGCACA 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     228 AGGCTACCATGTCAGGTTCTGCCTCGGCCCTGCCCTACATTTGGAGC 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1. .328
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/clone="IMAGE:2010730"
/tissue_type="glioblastoma (pooled)"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 ThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysValArgProLe
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96 c 104 g 59 t
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                                                                                                                                                                                                                                                                                                                Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
                                                            AI360877.1 GI:4112498
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78.899
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A1634937 408 bp mRNA EST 16-DEC-1999 tz74f0.x1 NCI_CGAP_Panl Homo sapiens cDNA clone 1HAGE:2294345 3's similar to gb:X02812_cd31 TRANSFORMING GROWTH FACTOR BETA 1 PRECURSOR (HUMAN); contains element MER22 repetitive element ; mRNA
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information can be
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 408)
NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
87 hrileLeuTyrTyrValGlyArgThrProLysValGluGlnLeuSerAsn 103
                                                                                                                                 oGluAlaSerAlaSerProCysCysValProGlnAspLeuGluProLeuT 87
                                                                                                                                                                                                                                        18 CCATCGTGTACTACTTGGGCCGCAAGCCCAAGGTGGAGCAGCTGTTCAAC 29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Life Technologies catalog #: 11548-013
DNA Sequencing by: Washington University Genome (Clone distribution: NCI-CGAP clone distribution)
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www.bio.llnl.gov/bbrp/image/image.html
Insert Length: 614 Std Error: 0.00
Seq primer: -400p from Gibco.
Location/Qualifiers
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Gaps: 0
Percent Identity: 76.471
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/clone_lib="NCI_CGAP_Pan1"
/tissue_type="adenocarcinoma"
/lab_host="DH10B"
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LOCUS A1634937
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AA016742 553 bp mRNA EST Mus musculus CDNA mh39e08.rl Scares mouse placenta 4NbMP13.5 14.5 Mus musculus CDNA clone INAGE:444902 5' similar to 9b:X02812_cds1 TRANSFORMING GROWTH FACTOR BETA 1 PRECURSOR (HUMAN); 9b:M37745 mouse transforming growth factor beta-3 mRNA, complete (MOUSE); mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Organ: placenta; Vector: pT773D-Pac (Pharmacia)
with a modified polylinker; Site_1: Not I; Site_2: Eco RI;
1st strand cDNA was primed with a Not I - oligo(dT) primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 553)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone_lib="Soares mouse placenta 4NbMP13.5 14.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Waterston, K.
The WashU-HHMI Mouse EST Project
Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of Medicinep
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Fax: 314 286 1800
Fmx: 314 286 1810
Email: mouseest@watson.wustl.edu
407 CTCGGCTGGAAGTGGATCCACGAGGCCCAAGGCCTACCATGCCAACTTCTG 358
                                                                                       94 gThrProLysValGluGlnLeuSerAsnMetValValLysSerCysLysC 111
                                                                                                                                                                                                                                                                                                                                                            207 CAAGCCCAAGGTGGAGCAGCTGTCCAACATGATCGTGCGCTCCTGCAAGT 158
                                                                                                                                                                                                                                              94
                                                                                                                                                    61 alLeuGlyLeuTyrAsnThrLeuAsnProGluAlaSerAlaSerProCys
                                                                                                                                                                                                                                              78 CysValProGlnAspLeuGluProLeuThrIleLeuTyrTyrValGlyAr
                                                                44 sSerGlyProCysProTyrLeuArgSerAlaAspThrThrHisSerThrV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Seq primer: -28M13 rev2 from Amersham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1. .553
/organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="placenta"
/dev_stage="adult"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                High quality sequence stop: 432.
Location/Qualifiers
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/clone="IMAGE:444902"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /sex="unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AA016742.1 GI:1479043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seq_name: gb_est1:AA016742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq_documentation_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                         111 ysser 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   157 GCAGC 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             source
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SOURCE

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T 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pr773 vector. Library went through one round of normalization, and was constructed by Bento Soares and M.Fatima Bonaldo."
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 245)

HCGP http://www.ludwig.org.br/ORESTES.

The FAPESP/LICR Human Cancer Genome Project
Unpublished (1999)
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Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AW600947 245 bp mRNA EST 23-MAR-2000 RC1-BN0014-210100-012-e04_1 BN0014 Homo sapiens CDNA, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  466 TIGGAGCCACTGCCATCGTCTACTAGTGGGTCGCAAGCTTGAGCA 515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       372 ATTIGGAGCCIGGACACACAGIACAGCAAGGICCTIGCCCTCTACAACCA 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   84 luProLeuThrIleLeuTyrTyr.ValGlyArgThrProLysValGluGl
                                                                                                                                                                                                                                                                                   Length: 113
Gaps: 2
Percent Identity: 65.487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nLeuSerAsnMetValValLysSerCysLysCysSer 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  516 GTTGTC.AACATGATTGTGCGCTCGTGCAGTGCAGCT 551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Align seg 1/1 to: AA016742 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Simpson A.J.G.
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human.
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KEYWORDS
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ORGANISM
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                                                                                                                                                                                                                                                          /note="Organ: breast_normal; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC1&t2=RC1-BN0014-210100-012-e04_lat3=2000-01-216t4=1) Seq primer: puc 18 forward High quality sequence stop: 233.

1. .245
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Ko,M.S.H, Kitchen,J.R., Wang,X., Threat,T.A., Sun,T., DePalma,G.E., Liang,Y., Kargul,G.J., Sharara,R. and Doi,H.
Systematic analyses of genes expressed in 2-cell stage mouse embryos (The ERATO/Doi Project at Wayne State University) (Ko
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AUO16439 465 bp mRNA EST 15-OCT-1998
MOUO16439 Mouse two-cell stage embryo CDNA Mus musculus CDNA clone
AUO16439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GluProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGl 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          34 HisGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTy 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           50 rLeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnT 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             67 hrLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeu 83
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Percent Identity: 83.544
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        44 GCTTCTAATATGATTGTAAAGTCTTGCAAATGCAGC
                                                                                                                                                                           /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="BN0014"
/dev_stage="Adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AU016439.1 GI:3371443
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5.123
92.405
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Ratio:
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                                                                                                                                    FEATURES
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Euteleostomi;
Contact: Hirofumi Doi
Doi Bioasymmetry Project, ERATO
Japan Science and Technology Corporation (JST)
WBG Marive East 12F, 2-6 Nakase, Mihama-ku, Chiba 261-71, Japan
Email: hd@bloa.jst.go.jp.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               seq_documentation_block:
LOCUS AM295761 409 bp mRNA EST 16-JAN-2000
DEFINITION UI-H-BII-afh-a-02-0-UI.S1 NCI_CGAP_Sub3 Homo sapiens cDNA clone
IMAGE:2721675 3', mRNA sequence.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 409)
                                                                                                                                                                                   /db_xref="taxon:10090"
/clone="J0725B08"
/clone_lib="Mouse two-cell stage embryo cDNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          224 IGCIGIGIGICCCAGGAICIGGAACCACIGACCAITCICIATIACATIGG 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    44 CysSerGlyProCysProTyrLeuArgSerAlaAspThrThr.HisSerT 60
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                                                                                                                                                                                                                                                                          6 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27 pLeuGlyTrpLysTrpValHisGluProLysGlyTyrTyrAlaAsn.Phe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   77 CysCysValProGlnAspLeuGluProLeuThrileLeuTyrTyrValGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12 GluGluAsnCysCysValArgPro...LeuTyrIleAspPheArgGlnAs
                                                                                                                                                                                                                                                                                                                                                                         Length: 104
Gaps: 3
Percent Identity: 70.192
                                                                                                                                                                                                                                                 /dev_stage="two-cell stage embryo"
97 c 112 g 127 t 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         to::
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                                                                                                                              1. .465
/organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Align seg 1/1 to reverse of: AU016439
                                                                                                                                                                    /strain="C57BL/6J"
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                                                                                                                                                                                                                                                                                                                                                                       364.50
4.238
82.692
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64

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6

COMMENT

Source

FEATURES

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me44c04.rl Soares mouse embryo NbME13.5 14.5 Mus musculus CDNA clone IMAGE:39034.5 's similar to 9b:x02812_cds1 TRANSFORMING GROWTH PACTOR BETA 1 PRECURSOR (HUMAN); 9b:M3745 mouse transforming growth factor beta 3 mRNA, complete (MOUSE); mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 (bases 1 to 301)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., La,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Washington Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="taxon:10090"
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/clone="INAGE:390342"
/clone_lib="Soares mouse embryo NbME13.5 14.5"
/sex="unknown"
                                          259 CAGGCGCTGGAGCCGCTGCCCATCGTACTACGTGGGCCGCAAGCCCAA 210
                                                                                                                                                                    oCysProTyrLeuArgSerAlaAspThrThrHisSerThrValLeuGlyL
                                                                                               euTyrAsnThrLeuAsnProGluAlaSerAlaSerProCysCysValPro
                                                                                                                                                                                                                                          /tissue_type="embryo"
/dev_stage="13.5-14.5dpc total fetus"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (1996)
Contact: Marra M/Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Mus musculus"/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              High quality sequence stop: 289.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                       mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Seq primer: mob.REGA+ET
                                                                                                                                                                                                                                                                                                                                                                       301 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                W70801.1 GI:1380934
                                                                                                                                                                                                                                                                                                                seq_name: gb_est110:W70801
                                                                                                                                                                                                                                                                                                                                                       seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    house mouse.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MGI:242174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                W70801
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ORGANISM
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VERSION
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JOURNAL
COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AUTHORS
                         47
                                                                                               64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURES
                                                                                                                                                                                                                                                                                                                                                          Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
The sequence contained an oligo-dr track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. cDNA Library Preparation: M.B. Soares Lab Clone distribution: NCI-CGAP Clone distribution information can be found through the I.M.A.G.E. Consortium/Lin. at:
www-bio.llnl.gov/bbrp/image/image.html The following repetitive elements were found in this cDNA sequence: 102-157,
                                                                                                                                                                                                                                                                                                                                 /clone_lib="NCI_CGAP_Sub3"
/lab_host="DH10B (Life Technologies)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       from: 1 to: 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length: 82
Gaps: 0
Percent Identity: 74.390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       84
                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                             /db_xref="taxon:9606"
/clone="IMAGE:2721675"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6, 791-806.
TAG_LIB=NCI_CGAP_Pr22
TAG_TISSUE=prostate
                                                                                                                                                                                                                                        Location/Qualifiers
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                                                                                                                                                                                    >GC_rich#Low_complexity
Seq primer: M13 Forward
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5.014
85.366
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27
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alignment\_block:

BASE COUNT

Align seg 1/1

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112 r 112
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 BASE COUNT
ORIGIN
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VERSION
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TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KEYWORDS
SOURCE
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1 (bases 1 to 878)
Aoki, T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tokyo University of Fisheries
Konan, 4-5-7, Minato 108, Japan
Hell: 03-5463-0556
Email: aoki@tokyo-u-fish.ac.jp
clone WBI1-23:similar to rainbow trout transforming growth factor
 and was constructed by Bento Soares and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                seq_documentation_block:
LOCUS AUG50770 878 bp mRNA EST 08-JUN-1999
DEFINITION AUG50770 Paralichthys olivaceus library (Aoki T) Paralichthys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="Paralichthys olivaceus library (Aoki T)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GlyLeuTyrAsnThrLeuAsnProGluAlaSerAlaSerProCysCysVa 79
                                                                                                                                                                                                                                                                                                                                 YTrpLysTrpValHisGluProLysGlyTyrTyrAlaAsnPheCysSerG 46
                                                                                                                                                                                                                                                                                                                                                                                                  46 lyProCysProTyrLeuArgSerAlaAspThrThrHisSerThrValLeu 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     lProGlnAspLeuGluProLeuThrIleLeuTyrTyrValGlyArgThrP 96
                                                                                                                                                                                                                                                                                    3 AAGAACTGCTGTGCGGCA.CTGTACATTGACTTTAGGAAGGACCTGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13 GluAsnCysCysValArgProLeuTyrIleAspPheArgGlnAspLeuGl
                                                                                                               Length: 100
Gaps: 0
Percent Identity: 76.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Paralichthys olivaceus"
/db_xref="taxon:8255"
/clone="WB11-23"
                                64
                                                                                                                                                                                                                                    to: 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Japanese flounder leukocyte cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                             84 9
normalization, ar
M.Fatima Bonaldo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (1999)
Contact: Takashi Aoki
Genetics and Biochemistry
                                                                                                                                                                                                                                  from: 1
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                                                                                                                               3.966
                                  88
                                                                                                                 349.00
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                                                                                                                                                                                                                                 to: W70801
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                                                                                                               Quality:
Ratio:
Percent Similarity:
                                65
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                                                                                                alignment_scores
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                              BASE COUNT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63
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                                                 ORIGIN
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Fax: +55-11-2704922

Fax: +55-11-2707001

Bmail: ssimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RCl&t2=RCl-BN0014-21010-012-012-18 forward

High quality sequence stop: 258.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,

        seq_documentation_block:
        23-MAR-2000

        LOCUS
        AW600942
        259 bp
        mRNA
        EST
        23-MAR-2000

        DEFINITION
        RC1-BN0014-210100-012-d10_1 BN0014 Homo sapiens cDNA, mRNA

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              481 CACAAGGTGGAGCAGCTGTCCAATATGATCGTGAAGTCCTGCAAGTGTAG 530
                                                                                                                                                                                                                                                                                                                                                                                235 GAGACCTGCTGCGTGCGGAN.CTGTACATCGACTTCAGGAAAGATCTGGG 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96 ProLysValGluGlnLeuSerAsnMetValValLysSerCysLysCysSe 112
                                                                                                                                                                                                                                                                                                                                                                                                                               29 yTrpLysTrpValHisGluPro.LysGlyTyrTyrAlaAsnPheCysSer 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   79 alProGlnAspLeuGluProLeuThrIleLeuTyrTyrValGlyArgThr 95
  others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62 uGlyLeuTyrAsnThrLeuAsnProGluAlaSerAlaSerProCysCysV 79
                                                                                                                                                                                                                                                                                                                                  13 GluasnCysCysValArgProLeuTyrIleAspPheArgGlnAspLeuGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          46 GlyProCysProTyrLeuArgSerAlaAspThrThrHisSerThrValLe
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Percent Identity: 66.337
                                                                                                                   101
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HCGP http://www.ludwig.org.br/ORESTES.

The FAPESP/LICR Human Cancer Genome Project

Unpublished (1999)
  4
                                                                                                                   Length:
                                                                                                                                                                                                                                                                                     to: 878
  186 g
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AW600942.1 GI:7305681
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4.088
84.158
213
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                                                                                                                      Quality:
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256
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                                                                                             alignment_scores
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tgfb3p.rst

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seq_name: gb_est91:BF682938
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KEYWORDS
SOURCE
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                                                                                                                                                              FEATURES
                               /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="BN0014"
/dev_stage="Adult"
/note="Organ: breast_normal; Vector: puc18; Site_1: SmaI;
Site_2: SmaI; A min1-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

99 a 48 c 62 9 80 t
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Bukaryota; Mammalia; Buteleostomi;

Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo...

[ (bases 1 to 560)

Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rikin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,T.R., Williamson,A., Wohldmann,P. and Wilson,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (1995)
Contact: Wilson Ry
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            67 hrLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeu 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34 HisGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               50 rLeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnT
                                                                                                                                                                                                                                                                                                                                                                                    Gaps: 1
Percent Identity: 78.481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100 nLeuSerAsnMetValValLysSerCysLysCysSer 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Align seg 1/1 to reverse of: AW600942 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              44 GCTTTCTAATATGGTTGTAAAGTCTTGCAAATGCAGC 8
                                                                                                                                                                                                                                                                                                                                                                 Length:
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                             Ouality: 343.50
Ratio: 4.838
Percent Similarity: 89.873
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq_name: gb_est106:N36741
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TGFB3P x AW600942/rev
                                                                                                                                                                                                                                                               69
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                                                                                                                                                                                                                                                                                                                                               alignment_scores:
                      source
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DEFINITION
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JOURNAL
COMMENT
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KEYWORDS
SOURCE
FEATURES
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Email: estewatson.wustl.edu
High quality sequence stops: 470
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq_documentation_block:
LOCUS BF682938 748 bp mRNA EST 21-DEC-2000
DEFINITION 602117568F1 Soares_mammary_gland_NMLMG Mus musculus cDNA clone
IMAGE:3468737 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            55 pThrThrHisSerThrValLeuGlyLeuTyrAsnThrLeuAsnProGluA 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            72 laSerAlaSerProCysCysValProGlnAspLeuGluProLeuThrIle 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  39 TyrTyrAlaAsnPheCysSerGlyProCysProTyrLeuArgSerAlaAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="GD868"
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/db_xref="taxon:9606"
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/clone=lib="Soares melanocyte 2NbHM"
/sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Identity: 81.081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length:
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                                                                                                                                1. 560
/organism="Homo sapiens"
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                                                                                Seq primer: T7
High quality sequence stop: 470.
Location/Qualifiers
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5.015
91.892
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Tumor Gene Index
Unpublished (1997)
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81.739
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                                                                sequence.
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DEFINITION
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KEYWORDS
SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from mammary polylinker; 1st strand cDNA was prepared from mammary gland tissue from a lactating female, and was then primed with a Not I - Oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo."
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                      DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov.
Plate: LLAM8476 row: h column: 18
High quality sequence start: 26
High quality sequence stop: 746.
                                    1 (bases 1 to 748)
NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                      Email: cgapbs r@mail.nih.gov
Tissue Procurement: M. Bento Soares, Ph.D.
cDNA Library Preparation: Bento Soares and M. Fatima Bonaldo
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      662 ATTIGGAGCCTGGACACACAGTACAGCAAGGTCCTTGCCCTCTACAACAA 711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          612 ACGAGCCCAAGGGCTACCATGCCAACTTCTGTCTGGGACCCTGCCCCTAT 661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone_lib-"Soares_mammary_gland_NMLMG"
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/tissue_type="mammary gland"
/lab_nost="BH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length: 79
Gaps: 0
Percent Identity: 75.949
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                                                                                                                                                                                                                                                                                                                                                                                           1. .748
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="IMAGE:3468737"
                                                                                                Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Align seg 1/1 to: BF682938 from: 1
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TGFB3P x BF682938
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COMMENT
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                                      REFERENCE
                                                           AUTHORS
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                                                                                 TITLE
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21-AUG-1997

EST

mRNA

542 App

AA533093

seq\_documentation\_block:

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nj19904.sl NCI_CGAP_AA1 Homo sapiens cDNA clone IMAGE:992982 3'
similar to gb:X02812_cds1 TRANSFORMING GROWTH FACTOR BETA 1
PRECURSOR (HUMAN);contains element MER22 repetitive element ;, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CDNA Library Arraying: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 1687 5td Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 142.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 542)
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//clone="IMAGE:992982"
//clone="IMAGE:992982"
//clone=lib="NGI_CGAP_AA1"
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/
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: L. Jeffrey Medeiros, M.D., Michael R.
Emmert-Buck, M.D., Ph.D.
__CDNA Library Preparation: Stratagene, Inc., David B. Krizman,
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Gaps: 5
Percent Identity: 66.957
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67

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seq_documentation_block:
LOCUS AII79582 571 bp mRNA EST 20-JAN-1999
DEFINITION EST223304 Normalized rat spleen, Bento Soares Rattus sp. cDNA clone
RSPCJ23 3' end, mRNA sequence.
ACCESSION AII79582. GI:3730220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rat Genome Project: Generation of a Rat EST (REST) Catalog & Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone_lib="Normalized rat spleen, Bento Soares"
/note="Organ: spleen; Vector: pT7T3Pac; Site_1: EcoRI;
Site_2: NotI"
111 c 121 g 195 t
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Lee, N.H., Glodek, A., Chandra, I., Mason, T.M., Quackenbush, J.
Kerlavage, A.R. and Adams, M.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Lee, NH
The Institute for Genomic Research
9712, Medical Center Drive, Rockville, MD 20850, USA
7121: (301)-838-3529
Fax: (301)-838-0208
Email: nhlee@tigr.org
                                        339 ATTIGGAGCCTGGACACGCAGTACAGCAAGGTCCTGGCCCTGTACAACCA 388
189 GCCCTGGACACCAACTATTGCTTCAGCTCCACGGAGAAGAACTGCTGCGT 238
                                                                                                                                                                                                                              LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh
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                                                                                                                                                                                                                                                                                                                     67 rLeuAsnProGluAla.SerAlaSerProCysCysValProGln 81
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Gaps: 0
Percent Identity: 80.556
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/db_xxref="ARTC (inhost):2033997"
/db_xxref="Rattus sp."
/clone="RSPCJ23"
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4.940
93.056
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TGFB3P x AI179582/rev
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Ratio:
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 915)
                                                                                                                                                                                                                                                                                                                                      seq_documentation_block:
LOCUS BR737006 915 bp mRNA EST 15-SEP-2000
DEFINITION 601306767F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3641081 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue_type="adenocarcinoma"
/lab_nost="DH10B (phage-resistant)"
/note="Organ: pancreas; Vector: pOTB7; Site_1: Xho1;
Site_2: EcoR1; cDNA made by oligo-dT priming.
Directionally cloned into EcoR1/Xho1 sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Ferbhologies)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Context: Robert Strausberg, Ph.D.

Email: gapbs-r@mail.nih.gov
Tissue Procurement: AFCC
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM346 row: e column: 18
High quality sequence stop: 424.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                            euGluProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGlu 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17
                  67 ThrLeuAsn. ProGluAlaSerAlaSerProCysCysValProGlnAspL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps: 2
Percent Identity: 71.951
                                                                                                                                                                                                    Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Align seg 1/1 to: BE737006 from: 1 to: 915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone="IMAGE:3641081"
/clone_lib="NIH_MGC_39"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      276 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                            BE737006.1 GI:10150998
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279 c 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     333.50
4.833
84.146
                                                                                                                                                                                                                                                                                                seq_name: gb_est78:BE737006
                                                                                                                                                                                                                                                                                                                                                                                                             mRNA sequence.
BE737006
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Ratio:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 alignment_block:
TGFB3P x BE737006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            human.
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FEATURES

ORGANISM

SOURCE

ACCESSION VERSION KEYWORDS AUTHORS TITLE JOURNAL

COMMENT

REFERENCE

alignment\_scores:

BASE COUNT

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seq_name: gb_est26:A1918883
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                                                                                                              Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                 AA016946 513 bp mRNA EST 21-JAN-1997 mh35al2.rl Soares mouse placenta 4NbMPl3.5 14.5 Wus musculus CDNA clone IMAGE:444478 5' similar to 9b:X02812_cds1 TRANSFORMING GROWTH FACTOR BETA 1 PRECURSOR (HUMAN); 9b:M32745 mouse transforming growth factor beta-3 mRNA, complete (MOUSE);, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. I (bases 1 to 533)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., La,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moors,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   T 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization, and was constructed by Bento Soares and M.Fatima Bonaldo."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              with a modified polylinker: Site_I: Not I: Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Organ: placenta; Vector: pT7T3D-Pac (Pharmacia)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone_lib="Soares mouse placenta 4NbMP13.5 14.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The WashU-HHMI Mouse EST Project
Unpublished (1996)
Contact: Marra MyMouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Porest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
74 laSerProCysCysValProGlnAspLeuGluProLeuThrIleLeuTyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               primer: -28M13 rev2 from Amersham
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Location/Qualifiers
1 533
/organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue_type="placenta"
/dev_stage="adult"
/lab_host="DH10B"
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/clone="IMAGE:444478"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /strain="C57BL/6J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /sex="unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AA016946.1 GI:1478533
                                                                                                                                                                                                                                             sSerCysLysCysSer 112
                                                                                                                                                                                                                                                                                         369 GICTIGIAAAIGCAGC 354
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LOCUS AA016946
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                                                                                                                                                                                                                                             107
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The bases it of 392)

So NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-rémail.nih.gov

Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R.

Email: cgapbs-rémail.nih.gov

Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., CDNA Library Preparation: M. Bento Soares, Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llh.gov/bbrp/image/image.html

Seq primer: -40UP from Gibco

High quality sequence stop: 335.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 222 GCCCTGGATACCAACTATTGCTTCAGCTCCACAGAGAAGAACTGCTGTGT 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   372 AGGIGGAGCCIGGACACACGGIACAGCAAGGICCIGGCGCTCIACAACGA 421
                                                                                                                                                                                                                                                                      51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr
Length: 92
Gaps: 1
Percent Identity: 64.130
                                                                                                                                                                                                                 to: 533
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/db_xref="taxon:9606"
/clone="IMAGE:2250907"
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321.50
4.465
78.261
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ORIGIN

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human.
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SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    75
                                                                                              FEATURES
                                                                     With a modified polylinker; Plasmid DNA from the normalized library NOT_CGAP_PR22 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool 5,000 clones made from the same library (cloneIDs 985608-986759, 1101192-1101959, and 1217928-1220615). Subtraction by Bento Soares and M. Fatima Bonaldo. " 117 c 150 g 67 t 1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: asimpson@ludwig.org.br This sequence was derived from the FAPESP/LICR Human Cancer Genome \ensuremath{\mathsf{This}}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I (bases 1 to 26) Http://www.ludwig.org.br/ORRSTES. The FAPESP/LICR Human Cancer Genome Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AW600960 266 bp mRNA EST 23-MAR-2000 RC1-BN0014-210100-012-h01_1 BN0014 Homo sapiens cDNA, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     338 CTGCCCCTACATTTGGAGCCTGGACACGCAGTACAGCAAGGTCCTGGCCC 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                47 oCysProTyrLeuArgSerAlaAspThrThrHisSerThrValLeuGlyL 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64 euTyrAsnThrLeuAsnProGluAlaSerAlaSerProCysCysValPro 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               to: 392
                                                                                                                                                                                                                                                                                                                                             Length: 82
Gaps: 0
Percent Identity: 73.171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Align seg 1/1 to reverse of: AI918883 from: 1
/clone_lib="NCI_CGAP_Pr28"
                   /sex="male"
/dev_stage="adult"
                                                         /lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequence.
AW600960
AW600960.1 GI:7305699
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Fax: +55-11-2707001
                                                                                                                                                                                                                                                                                                                                           321.00
4.586
85.366
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LOCUS AW600960
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Ratio:
Percent Similarity:
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VERSION
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//note=_organ: breast_normal; Vector: puc18; Site_1: Smal; Site_2: Smal; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RCl&t2=RCl-BN0014-210100-012-bhl_i&t3=2000-01-21&t4=1) Seq primer: puc 18 forward Righ quality sequence stop: 218.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AW364559 391 bp mRNA EST 04-FEB-2000
RC1-DT0028-131299-011-a06 DT0028 Homo sapiens CDNA, mRNA sequence.
AW364559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26 GlnAspLeuGlyTrpLySTrpValHisGluPro.LysGlyTyTTyrAlaA 42 :::|||||||||| :: ::||||||||| 260 GAGGATTAGGT...GAAATGATACACGAGCCAAAGG...TACAATGCAA 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 92 alGlyArgThrProLysValGluGlnLeuSerAsnMetValValLysSer 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          rProCysCysValProGlnAspLeuGluProLeuThrIleLeuTyrTyrV 92
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HCGP http://www.ludwig.org.br/ORESTES.
The FAPESP/LICR Human Cancer Genome Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps: 4
Percent Identity: 71.591
                                                                                                                                                                             /organism="Homo sapiens"
/db_xref="taxon:9606"
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Contact: Simpson A.J.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AW364559.1 GI:6869209
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4.178
86.364
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               seq_documentation_block:
LOCUS     AW364559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19 TGCAAATGCAGC 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         alignment_block:
TGFB3P x AW600960/rev
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Ratio:
Percent Similarity:
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/note="Organ: denis_drash; Vector: puc18; Site_1: Smal; Site_2: Smal; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
                                                                                                                                                                                                                                                                                                                                               Email: asimpsoneludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RCl&t2=RCl-DT0028-131299-011-a06&t3=1999-12-13&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 42
High quality sequence stop: 345.
                                                                                                                                                            Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="taxon:9606"
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/dev_stage="Adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
Tue Oct 30'12:56:57 2001
                                                                                                                                                                                                                                                                                           Tel: +55-11-2704922
                                                                                                                                                                                                                                                                                                                               Fax: +55-11-2707001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .391
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Gaps: 62.500 Percent Identity: 62.500 313.00 3.771 79.808 Quality:
Ratio:
Percent Similarity: alignment\_block: TGFB3P x AW364559 alignment\_scores:

to: 391 to: AW364559 from: 1 Align seg 1/1

15 CysCysValArgProLeuTyrIleAsp.PheArgGlnAspLeuGlyTrpL 31

31 ysTrpValHisGluProLysGlyTyrTyrAlaAsnPheCysSerGlyPro 47

CysProTyrLeuArgSerAlaAspThrThrHisSerThrValLeuGlyLe 64 48

182

oLysValGluGln.....LeuSerAsnMetValValLysSer.CysLys 110 96

111 CysSer 112

seq\_name: gb\_est20:AI414206 332 TGCAGC 337

seq\_documentation\_block: rochs A1414206

mRNA 465, bp

09-FEB-1999 EST

E 1 (Dases 1 to 465)

Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Boeck,C., Wylie,T., Be, Swaller,T., Steptoe,M., Theising,B., Harvey,M., Schurk,R., Person,B., Swaller,T., Steptoe,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.

The Washu-NcI mouse EST Project 1999

Contact: Marra M/WashU-NCI Mouse EST Project 1999

Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800

Fax: 314 286 1810 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
This clone was previously sequenced on the 5' end only, this new
data is from the 3' end
High quality sequence stop: 256. normalization, and was constructed by Bento Soares and md58e04.xl Soares mouse embryo NbME13.5 14.5 Mus musculus cDNA clone ImAGE:372606 3' similar to qb:Y00083 TRANSFORNING GROWTH FACTOR BETA 2 PRECURSOR (HUMAN); gb:X57413 Mouse mRNA for transforming growth factor-beta2 (MOUSE);, mRNA sequence. /strain="C57BL/6J"
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/clone="IMAGE:372606"
/clone\_lib="Soares mouse embryo NbME13.5 14.5"
/sex="unknown" others Gaps: 5 Percent Identity: 63.636 136 t Length: 109 g M.Fatima Bonaldo. AI414206.1 GI:4257710 103 c 3.682 1. .465 313.00 Mus musculus house mouse TGFB3P x AI414206/rev Quality: Percent Similarity: 116 Ratio alignment\_scores: source DEFINITION ORGANISM TITLE JOURNAL COMMENT BASE COUNT ACCESSION REFERENCE AUTHORS KEYWORDS FEATURES VERSION SOURCE ORIGIN

alignment\_block

Align seg 1/1 to reverse of: AI414206 from: 1 to: 465

22 eAspPheArgGlnAspLeuGlyTrpLysTrpValHisGluProLysGlyT 39 = :::=

55 AspThrThrHisSerThrValLeuGlyLeuTyrAsnThrLeuAsnProGl

to: 517

Align seg 1/1 to: BE074350 from: 1

alignment\_block: TGFB3P x BE074350

Length: 58 Gaps: 0 Percent Identity: 98.276

Quality: 305.00 Ratio: 5.259 Percent Similarity: 100.000

alignment\_scores

106

б

150

υ

131

130 a

BASE COUNT

ORIGIN

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Dias Neto, E., García Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., M.J., Soares, F., Brentani, R.R., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QV3-BT0571-030200-078-d08 BT0571 Homo sapiens cDNA, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 517)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09-JUN-2000
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000) 20202663
                                                                                                                                                                                                                                                                     244 AGCTTCCGCTTCCCCTTGCTGTGTGTCCCAGGATCTGGAACCACTGACCA 195
                                                                                                                                                                                                                                                                                                                                                                                                                                               391 TGATTTAAGAGGGATCTTGGAGGAAATGATCCCCAATAACCCAAAG...G 345
                                                                                                                                                                                  88 leLeuTyrTyrValGlyArgThrProLysValGluGlnLeuSerAsnMet 104
                                                                                                                                                                                                                                                                                                                                   71 uAlaSerAlaSerProCysCysValProGlnAspLeuGluProLeuThrI 88
                                                                                                                                                          39 yrTyrAlaAsnPheCysSerGlyProCysProTyrLeuArgSerAlaAsp
                                                                                                                                                                                                                                             56 ThrThr.HisSer.ThrValLeuGlyLeuTyrAsnThr.LeuAsnProGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          105 ValValLysSerCysLysCysSer 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    144 ATTGTCAAGTCTTGTAAATGCAGC 121
Tue Oct 30 12:56:57 2001
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BE074350.1 GI:8422187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         517 bp
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JS BE074350
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SOURCE
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Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
Pris sequence was quence for an inthe fapesP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=RC3-UM0046-290 200-011-a06st3=2000.02-29&t4=1)
Seq primer: puc 18 forward High quality sequence start: 17
High quality sequence stop: 379.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AW798<u>1</u>67 379 bp mRNA EST 16-MAY-2000 RC3-UM0046-290200-011-a06 UM0046 Homo sapiens cDNA, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Shorgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000) 20202663
                                                                                                    88 leLeuTyrTyrValGlyArgThrProLysValGluGlnLeuSerAsnMet 104
                  57
                                                                        71 uAlaSerAlaSerProCysCysValProGlnAspLeuGluProLeuThrI 88
8 AACACAACCCACAGAGCACGGTGCTGGGACTGTACAACACTCTGAACCCTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                         105 ValValLysSerCysLysCysSer 112
                                                                                                                                                                                                                                                                                                                                         158 GTGGTGAAGTCTTGTAAATGTAGC 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AW798167.1 GI:7850141
                                                                                                                                                                                                                                                                                                                                                                                             seq_name: gb_est51:AW798167
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LOCUS AW798167
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/organism="Homo sapiens"
/db\_xref="taxon:9606"
/clone\_lib="BF0651"
/clone\_lib="BF0651"
/dev\_stage="Adult"
/note="Organ: breast; Vector: pucl8; Site\_1: Smal; Site\_2: Smal; A mini-library was made by cloning products derived from ORESTES PCR (US. Letters Patent application No. 196 from the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low

source

FEATURES

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ACCESSION
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                                                                              ORIGIN
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/dev_stage="Adult"
/note="Organ: uterus; Vector: pucl8; Site_1: SmaI; Site_2:
/note="Organ: uterus; Vector: pucl8; Site_1: SmaI; Site_2:
/note="Organ: uterus; Vector: pucl0 products derived
from ORESTES POR (U.S. Letters Patent application No. 196
/716 - Ludwig Institute for Cancer Research) profiles
/716 - Ludwig Institute for Cancer Research) profiles
/716 - Ludwig Institute for Reverse transcription of tissue
//note puc 18 vector. Reverse transcription of tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 (bases 1 to 400)

Malik, A., Tandon, N., Molski, E., Rohlfs, E., Nyarsik, L., Reinhardt, R., Nietfeld, W. and Lehrach, H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Abt.Lehrach
Max Planck Institut Fuer Molekulare Genetik
Innestrasse 73. Berlin, 14195 Germany
The CDNA libraries ICRFP 522 and 523 were normalized with
oligonuclectide fingerprinting, resulting in a unique subset of
5376 cDNA clones.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AL362754 400 bp mRNA EST 04-AUG-2000
AL362754 ICRFp 522 and 523 Mus musculus cDNA clone K9222B41 5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  , Nietleid,w. and bemach,n.
Tissue gene expression analysis using arrayed normalized CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       163 GCCTGGACACTATTGCTTCAGCTCCACGAGAAGAGCTGCTGCTT 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              313 ATTTGGAGCCTGGACACGCAGTACAGCAAGGTCCTGGCCCTGTACAAC 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsn 66
                                                                                                                                                                                                                                                                                                                                                                                                                          Length: 66
Gaps: 0
Percent Identity: 75.758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="taxon:10090"
/clone="K9222041"
/clone_lib="ICRFp 522 and 523"
/tissue_type="embryo"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  to: 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Mus musculus"
/strain="Black 6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genome Res. (2000) In press
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Align seg 1/1 to: AW798167 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mRNA sequence.
AL362754
AL362754.1 GI:9692237
                                                                                                                                                                                                                                                                                                                                                                                                                          304.00
5.241
87.879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_name: gb_est28:AL362754
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq_documentation_block:
LOCUS AL362754
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                 Quality:
                                                                                                                                                                                                                                                                 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGFB3P x AW798167
                                                                                                                                                                                                                                                                                                                                                                                             alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alignment_block
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                                                                                                                                                                                                                                                                 BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACCESSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMMENT
                                                                                                                                                                                                                                                                                                  ORIGIN
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Another Torgan: pooled: Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from five normalized polylinker; steel: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from five normalized.

Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was extractive hybridization reaction. The driver was FCR-amplified cDNAs from pools of 5,000 clones made from the same 5 libraries. The pools consisted of the following libraries and cloneIDs: Soares NDHSF pool 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 396)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A1452742 396 bp mRNA EST 13-APR-1999 145207.x1 Soares, NBF_R8_9W_OT_PA_PS 146mo sapiens cDNA clone IMAGE:21444432 3' similar to 9b:x02812_cds1 TRANSFORMING GROWTH FACTOR BETA 1 PRECURSOR (HUMAN);contains PTR5.t3 MSR1 repetitive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nh.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 529 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          202 GCTTTGGATGCTGCCTACTGCTTTAGAAATGTGCAGGATAATTGCTGCCT 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2144432"
/clone_lib="Soares_NSF_F8_9W_OT_PA_P_S1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsn 66
                                                                                                                                                Length: 66
Gaps: 0
Percent Identity: 72.727
embryo"
96 t
                                                                                                                                                                                                                                                                                                                                 to: 400
/dev_stage="9 and 12 pc
105 c 91 g 9
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                              Align seg 1/1 to: AL362754 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              element;, mRNA sequence.
A1452742
A1452742.1 GI:4287481
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tumor Gene Index
Unpublished (1997)
                                                                                                                                                302.00
5.033
90.909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seq_name: gb_est20:AI452742
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LOCUS A1452742
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                       108 a
                                                                                                                                                      Quality:
                                                                                                                                                                                                  Percent Similarity:
                                                                                                                                                                          Ratio:
                                                                                                                                                                                                                                                                          TGFB3P x AL362754
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                                                                                                                              alignment_scores
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                         BASE COUNT
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seq_name: gb_est106:N55274
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TGFB3P x AA927529/rev
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Ratio:
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                                                    source
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KEYWORDS
SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           86
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           FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORIGIN
309384-310919, 323208-325895 Soares Nb2HP pool 1:
145032-147335, 147720-148103, 148872-149555, 15002 -
150407, 151176-155237 Soares Nb2HF8-9W pool 1:
758280-760583, 772104-774407 Soares NbHPA pool 1:
304776-306311, 320136-322823, 326280-326663 Soares NbHOT
pool 1: 723720-726407, 739080-740999 Subtraction by Bento
Soares and M. Fatima Bonaldo. " 1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  constitution of the control of the c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
Sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthoria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 428)
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Manall: gapDs-remail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      om71all.s1 NCI_CGAP_GC4 Homosapiens cDNA clone IMAGE:1552604 3/
similar to gb:X02812_cds1 TRANSFORMING GROWTH FACTOR BETA 1
PRECURSOR (HUMAN);, mRNA sequence.
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            296 GCGCCTCGGCGGCGCCGTTNTGCGTTCCGCAGGCGCTGGAACCGCTGCCC 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        88 IleLeuTyrTyrValGlyArgThrProLysValGluGlnLeuSerAsnMe 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 38 GlyTyrTyrAlaAsnPheCysSerGlyProCysProTyrLeuArgSerAl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              71 luAlaSerAlaSerProCysCysValProGlnAspLeuGluProLeuThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       to: 396
                                                                                                                                                                                                                                                                                                                                                                                                                                             Length: 75
Gaps: 0
Percent Identity: 73.333
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             196 GATCGTGCGCTCCTGCAAGTGCAGC 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          104 tValValLysSerCysLysCysSer 112
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AA927529.1 GI:3076426
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4.778
84.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ratio:
                                                                                                                                                                                                                                                             57
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/note="Vector: pr773D-pac (Pharmacia) with a modified polylinker: 1st strand cDNA was prepared from 3 pooled germ cell tumors, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT773 vector. Library is normalized. Library was constructed by Bento Scares and M. Fatima Bonaldo. "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
1 (bases I to 456)
Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B.,
Chissoe,S., Dietrich,N., Dubuque,T., Favello,A., Gish,W., Hawkins,M., Hultman,M., Kucaba,T., Lacy,M., Le,N., Mardis,E., Moore,B., Morris,M., Parsons,J., Prange,C., Rifkin,L., Rohlfing,T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N55274 456 bp mRNA EST 28-JAN-1997 yv46d05.s1 Soares fetal liver spleen lNFLS Homo sapiens cDNA clone IMAGE:245769 3' similar to qb:J03241 TRANSFORMING GROWTH FACTOR BETA 3 PRECURSOR (HUMAN);, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGlnLeuSe 102
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsn.ThrLeuA 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         36 roLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyrLeuArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                69 snProGluAlaSerAlaSerProCysCysValProGlnAspLeuGluPro
                                                                      /db_xref="taxon:9606"
/clone="IMAGE:1552604"
/clone=lib="NCI_GGAP_GG4"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length: 95
Gaps: 3
Percent Identity: 66.316
                                                     /organism="Homo sapiens"
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3.928
80.000
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                                                        ORGANISM
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  ACCESSION
               VERSION
KEYWORDS
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                                                                                                                                                       JOURNAL
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                                                                                                                               TITLE
                                                                                                                                                                       COMMENT
                                           SOURCE
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                                                                                                                                                                                                                                                                                                                                   Schellenberg,K., Soares,M.B., Tan,F., Thierry-Meg,J., Trevaskis,E., Underwood,K., Wohldmann,P., Waterston,R., Wilson,R. and Marra,M. Generation and analysis of 280,000 human expressed sequence tags Genome Res. 6 (9), 807-828 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tel: 314 286 1810
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the Insert Length: 1001 Std Error: 0.00
Seg primer: ml3 -40 forward
High quality sequence stop: 424.
                                                                                  Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                        /clone="IMAGE:245769"
/clone_lib="Soares fetal liver spleen INFLS"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6 TyrCysPheArgAsnLeuGluGluAsnCysCysValArgProLeuTyrIl 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       39 .TyrTyrAlaAsnPheCysSerGlyProCysProTyrLeuArgSerAlaA 55
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Gaps: 2
Percent Identity: 91.379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               to reverse of: N55274 from: 1 to: 456
                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/db_xref="GDB:3795015"
/db_xref*"taxon:9606"
                                                                                                                                                                                                                            Location/Qualifiers
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                                                                     Contact: Wilson RK
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93.103
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                                                        97044478
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TGFB3P x N55274/rev
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JOURNAL
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                                                                      COMMENT
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement. Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrapad by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Organ: stomach; Vector: pCMV-SPORT6; Site_1: Sall; Site_2: Not1; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.69 kb. Life Technologies catalog #:
                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 501)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
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/clone="InAqCE:2188102"
/clone=lib="NCI_CGAP_Gas4"
/tissue_type="poorly differentiated adenocarcinoma with signer ring cell features"
/lab_host="DH108"
                                                                                                                                                                         NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      425 CIGCCCCIACATITGGAGCCIGGACACGCAGTACAGCAAGGIACGICTGG 376
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 1819 Std Error: 0.00
Seq primer: -400P from Gibco
High quality sequence stop: 276
POLYA-No.
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AI610679.1 GI:4619846
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                                                                                                                                                                                                                           Tumor Gene Index
Unpublished (1997)
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TGFB3P x BG247154
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AUTHORS
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JOURNAL
COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="branchial arches"
/dev_stage="embryo. 10.5 dpc"
/lab_host="bHl08 (phage resistant)"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
/note="Vector: pT7T3D-Pac (Pharmacia) was primed pT7T3D-Pac (Pharmacia) was primed with a Not I - oligo(dT) primer [5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacla), digested with Not I and cloned into the Not I and Eco RI sites of the modified pr773 vector. Library constructed and normalized by Bento Soares and M.Fatima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: cgapbs-r@mail.nih.gov
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. I (bases 1 to 639)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
Onpublished (1997)
                                                                                                                                                                                                                                                                           BF723491 639 bp mRNA EST 03-JAN-2001 mab32f06.yl Soares_NMEBA_branchial_arch Mus musculus cDNA clone IMAGE:3972226 5' similar to SW:TGF1_MOUSE P04202 TRANSFORMING GROWTH FACTOR BETA 1 PRECURSOR; mRNA sequence.
                          225 CCGCTGCCCATCGTGTACTACGTGGCCCCAAGCCCCAAGGTGGAGCAGCT 176
85 ProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGlnLe 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5 others
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/clone="IMAGE:3972226"
/clone_lib="Soares_NMEBA_branchial_arch"
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Gaps: 0
Percent Identity: 70.000
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                                                                                                                        175 GTCCAACATGATCGTGCGCTCCTGCAAGTGCAGC 142
                                                                                                101 uSerAsnMetValValLysSerCysLysCysSer 112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Seq primer: -40RP from Gibco
High quality sequence stop: 477.
Location/Qualifiers
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BF723491.1 GI:12024493
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                                                                                                                                                                                                    seq_name: gb_est91:BF723491
                                                                                                                                                                                                                                                   seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                          house mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MGI:1472258
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TGFB3P x BF723491
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DEFINITION
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ORIGIN
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                                                                                                                                                                                                                                                                                                                                                                                   ACCESSION
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KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JOURNAL
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1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17

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BG247154 494 bp mRNA EST 13-FEB-2001
602361136F1 NCI_CGAP_Mam1 Mus musculus cDNA clone IMAGE:4489400 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E (bases 1 to 494)

S NIH-MGC http://mgc.nci.nih.gov/.

NIH-MGC http://mgc.nci.nih.gov/.

Institutes of Health, Mammalian Gene Collection (MGC)

L Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-rémail.nih.gov

Tissue Procurement: Gilbert Smith, Ph.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC. clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:

http://image.llol.gov

Plate: LLAM10337 row: h column: 09

High quality sequence stop: 491.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
577 AINIGGAGCCTGGACACACACATACAAGTCCTTGCCCTCTACAACCA 626
                                                                                                                                                                                   34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
                                                                                                                                                                                                                                                                                          51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
                                                                                                                                                                                                                 17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:10090"
/clone="IMAGE:4489400"
/clone_lib="MXI_CGAP_Maml"
/tissue_type="tumor, biopsy sample"
/dev_stage="3 months, virgin"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length: 54
Gaps: 0
Percent Identity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /strain="FVB/N"
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5.296
100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mRNA sequence.
BG247154
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LOCUS BG247154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  house mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        627 ACACAACCCC 636
                                                                                                                                                                                                                                                                                                                                                                                                    67 rLeuAsnPro 70
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Ratio:
Percent Similarity:
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alignment_scores
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                                                                                                                                                                                                source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                83
                                                                                                                                                                          FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORIGIN
                                      /note="Organ: denis_drash; Vector: pucl8; Site_1: Smal; Site_2: Smal; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dias Neto, E., García Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagal, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deolivelar, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BF901708 255 bp mRNA EST 18-JAN-2001
CM2-WT0190-091200-595-a10 MT0190 Homo sapiens cDNA, mRNA sequence.
BF901708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 255)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               roc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sSerThrValLeuGlyLeuTyrAsnThrLeuAsnProGluAlaSerAlaS 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               erProCysCysValProGlnAspLeuGluProLeuThrIleLeuTyrTyr 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  120 CTCCTTGCTGCGGGTCCCAAGATTTAGAACCTCTAACCATTCTCTACTAC 71
                                                                                                                                                                                                                                                                                             Percent Identity: 73.239
                                                                                                                                                                                                                                                                                                                                                                                                                                                  to: 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Align seg 1/1 to reverse of: AW579188 from: 1
/clone_lib="DT0028"/dev_stage="Adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BF901708.1 GI:12293167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              rel: +55-11-2704922
Fax: +55-11-2707001
                                                                                                                                                                                                                                                                                                                    4.607
85.915
                                                                                                                                                                                                                                                                                                   281.00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequence tags
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20 TTGCAAATGCAGC 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq_documentation_block:
LOCUS BF901708
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Simpson, A.J.
                                                                                                                                                                                                                                                                                                                                                                                   alignment_block:
TGFB3P x AW579188/rev
                                                                                                                                                                                                                                                                                                   Quality:
Ratio:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28
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// Coganism="Homo sapiens"
// Organism="Homo sapiens"
// Ab__xref="taxon:9606"
// Ab__xref="taxo
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=CM2&t2=CM2-MT0190-091200-595-al0&t3=2000-12-09&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 7
High quality sequence stop: 234.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                from: 1 to: 255
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Gaps: 2
Percent Identity: 62.025
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4.574
77.215
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Cerletti, Nico
APPLICANT: McMaster, Gary K.
APPLICANT: Cox, David
APPLICANT: Schmitz, Albert
APPLICANT: Schmitz, Albert
APPLICANT: Myehack, Bernd
TITLE OF INVENTION: Process for Refolding Recombinantly
TITLE OF INVENTION: Produced TGF-beta-like Proteins
                                                                               ADDRESSEE: Merchant & Gould
STREET: 11150 Santa Monica Boulevard, Suite 400
CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PatentIn Release #1.0, Version #1.30
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Henry P. No. 5922846ak
STREET: 520 White Plains Road, P.O. Box 2005
and
Their Use in Wound Healing
                                                                                                                                                                                                                                                                                                                                                                                                                                                               30630-10501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 10591-9005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 43, Application US/08789588 Patent No. 5922846 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Sharp, Janice A.
REGISTRATION NUMBER: 34,051
                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 30
TELECOMMUNICATION INFORMATION:
TELEPHONE: 310-445-1140
TELEFAX: 310-445-9031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 34:
                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 112 amino acids
TYPE: amino acid
                                        NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; MOLECULE TYPE: protein US-08-470-837-34
                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 424
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
                                                                                                                                                                COUNTRY: USA
ZIP: 90025-3395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Tarrytown STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: U.S.A. ZIP: 10591-9005
                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-789-588-43
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 ALDTNYCFRNLEENCCVRPLYIDFRQDLGWKWVHEPKGYYANFCSGPCPYLRSADTTHST 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      No. 6057430el process for the production of biologically active dimeric protein 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 VLGLYNTLNPEASASPCCVPQDLEPLTILYYVGRTPKVEQLSNMVVKSCKCS 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 VLGLYNTLNPEASASPCCVPQDLEPLTLLYYVGRTPKVEQLSNMVVKSCKCS 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 112;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99.8%; Score 633; DB 2; I
100.0%; Pred. No. 2.3e-61;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                      PRILING DATE: 13-CT-1932
PRIOR APPLICATION NUMBER: 13-CT-1932
PRIOR APPLICATION DATA: 67-1932
PRIOR APPLICATION NUMBER: 05-05-1930
PRIOR APPLICATION NUMBER: 68-927546.5
PRIOR APPLICATION NUMBER: 68-927546.5
FILING DATE: 06-DEC-189
ATTORNEY/AGENT INFORMATION:
NAME: No. 592284684, Henry P. RECEISTRATION NUMBER: 33-200
REFERENCE/DOCKET NUMBER: 4-17861/+/Cont3
TELEFAX: (908) 277-5110
TELEFAX: (908) 277-5110
TELEFAX: (908) 277-4306
INFORMATION FOR SEQ ID NO: 43:
                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/486,057
FILING DATE: 07-UN-1995
APPLICATION NUMBER: US 08/201,703
FILING DATE: 25-FEB-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/960,309
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/789,588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Patent No. 6057430
GENERAL INFORMATION:
TITLE OF INVENTION: No. 6057430e1
TITLE OF INVENTION: biologically of SEQUENCES: A COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 112 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 112 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 99.8%
Best Local Similarity 100.0
Matches 112; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 530
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein US-08-789-588-43
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MOLECULE TYPE: protein

US-09-123-233-6
                                                                        CLASSIFICATION:
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                                               FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY:
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US-09-123-233-6
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63 VLGLYNTLNPEASASPCCVPQDLEPLTILYYVGRTPKVEQLSNMVVKSCKCS 114

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                                                                                                                                                                        1 ALDTHYCFRHLEENCCVRPLYIDFRQDLGWKWYHEPKGYYANFCSGPCPYLRSADTHST 60
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                                                                                                                                                                                                                                                                                              61 VLGLXINTLNPEASASPCCVPQDLEPLTILXYVGRTPKVEQLSNMVVKSCKCS 112
DB 3; Le.,
                            Length 112;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: JOHNS HOPKINS UNIVERSITY
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-3
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURREWY APPLICATION DATA:
APPLICATION NUMBER: US/08/481,377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: SPENSLEY HORN JUBAS & LUBITZ
STREET: 1880 CENTURY PARK EAST, FIFTH FLOOR
CITY: LOS ANGELES
STATE: CALIFORNIA
                     99.8%; Score 633; DB
100.0%; Pred. No. 2.3
ive 0; Mismatches
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PRIOR APPLICATION DATA:
PREDETATION NUMBER: PCT/US94/00666
FILING DATE: 12-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: WETHERELL, JR. Ph.D., JOHN R. REGISTRATION NUMBER: FD2279 PCT
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 455-5100
TELEPHONE: (619) 455-5100
TELEFAX: (619) 455-5100
TELEPHONE: (619) 455-5110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 25, Application US/08481377
Patent No. 5808007
               Query Match
Best Local Similarity 100.
Matches 112; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS: single
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IMMEDIATE SOURCE:
CLONE: TGF-beta 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
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Matches 112; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             90067
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                                                                                                                                                                                              APPLICANT: THE JOHNS HOPKINS UNIVERSITY
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-9
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 8
10.509-153-733A-25
11.509-153-733A
12.509-153-733A
12.509-153-733A
13.509-153-733A
13.509-153-73A
13.509-153-73A
14.509-153-73A
15.509-153-73A
15.5
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Pred. No. 2.3e-61;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                   E: Spensley Horn Jubas & Lubitz
1880 Century Park East, Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Wetherell, Jr. Ph.D., John R. REGISTRATION NUMBER: 31,678
REFERENCE/DOCKET NUMBER: FD3288
TELECOMNUTCATION INFORMATION:
TELEPHONE: (619) 455-5100
TELEPHONE: (619) 455-5100
INFORMATION FOR SEQ ID NO: (23)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER REDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: EN PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTION DATA:
CURRENT APPLICATION DATA:
FILLIG DATE: 23-OCT-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/00685
FILLING DATE: 12-JAN-1994
ATTORNEY AGENT INFORMATION:
                                                                            dS/08491835
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100.0%; Pre
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TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 112; Conservative
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                                                                                ; Sequence 23, Application; Patent No. 5821056
                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Los Angeles
STATE: California
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; LOCATION: 1..114
US-08-491-835-23
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IMMEDIATE SOURCE:
CLONE: TGF-beta3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
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                                                                                                                                                            GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          90067
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RESULT 7
US-08-491-835-23
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61 VLGLYNTLNPEASASPCCVPQDLEPLTILYYVGRTPKVEQLSNMVVKSCKCS 112

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; NAME/KEY: Protein
; LOCATION: 1..114
US-08-946-092A-23
                                                                                                                                                                                                                                                                                                                                                                                                              linear
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                                                                                      CLASSIFICATION:
                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY:
        SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-172-062-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 99.8%; Score 633; DB 3; Length 114; Best Local Similarity 100.0%; Pred. No. 2.3e-61; Matches 112; Conservative 0; Mismatches 0; Indels
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Patent No. 6030617
GENERAL INFORMATION:
APPLICANT: THE JOHNS HOPKINS UNIVERSITY
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-9
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Spensley Horn Jubas & Lubitz
                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.25
CORRESPONDENCE ADDRESS:
ADDRESSEE: SPENSLEY HORN JUBAS & LUBITZ
STREET: 1880 CENTURY PARK EAST, FIFTH FLOOR
CITY: LOS ANGELES
STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Spensley Horn Jubas & Lubitz
STREET: 1890 Century Park East, Suite 500
CIIY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                   PRICE APPLICATION DATA:
APPLICATION NUMBER: 08/481,377
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: WETHERELL, JR. Ph. D., JOHN R. REGISTRATION NUMBER: 31,678
REFERENCE/DOCKET NUMBER: FD2279 PCT
TELECOMMUNICATION INFORMATION:
TELEPRONE: (619) 455-5110
TELEPRONE: (619) 455-5110
INFORMATION FOR SEQ ID NO SECOURACE CHARACTERISTICS:
                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/09/153,733A
                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PC-DOS/MS-DOS
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 114 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein
                                                                                                                                             COMPUTER READABLE FORM:
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CLONE: TGF-beta 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
                                                                                                                                                                                                                                                                                     FILING DATE:
CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: LOS
STATE: CZ
COUNTRY:
                                                                                                      COUNTRY:
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1 ALDINYCFRNLEENCCVRPLYIDFRQDLGWKWVHEPKGYYANFCSGPCPYLRSADTIHST 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 114;
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GENERAL INFORMATION:
APPLICANT: THE JOHNS HOPKINS UNIVERSITY
TITLE OF:INVENTION: GROWTH DIFFERENTIATION FACTOR-9
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Spensley Horn Jubas & Lubitz
STREET: 1880 Century Park East, Suite 500
CITY: Los Angeles
STATE: California
COUNTRY: US
ZIP: 90067
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/172,062
PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99.8%; Score 633; DB 3; 1
100.0%; Pred. No. 2.3e-61;
iive 0; Mismatches 0;
                                                                                                                                                                                                                           NAME: Wetherell, Jr. Ph.D., John R. REGISTRATION NUMBER: 31,678
REFERENCE/DOCKET NUMBER: FD3288
TELECOMUNICATION INFORMATION:
TELEPRINE: (619) 455-5100
TELEPRINE: (619) 455-5100
TELEPRINE: (619) 455-5100
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 114 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 23-OCT-1995
APPLICATION NUMBER: PCT/US94/00685
FILING DATE: 12-JAN-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION:
CLASSIFICATION:
PRIOR APPLICATION NUMBER: US/08/491,835
APPLICATION NUMBER: 23-0CT-1995
PCT /US94/0068
                                                  US/08/946,092A
                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/491,835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 23, Application US/09172062 Patent No. 6191261
                                                                                                                                                                           FILING DATE: ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 112; Conservative
                             CURRENT APPLICATION DATA
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IMMEDIATE SOURCE:
CLONE: TGF-beta3
                                                    APPLICATION NUMBER:
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TOPOLOGY: linear MOLECULE TYPE: protein IMMEDIATE SOURCE: CLONE: TGF-beta-3
                                                                                                           NAME/KEY: Protein
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CLONE: TGF-beta 3
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   STRANDEDNESS:
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MOLECULE TYPE:
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PCT-US94-00666-25
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                                                                                                                            ; LOCATION:
US-08-624-635-24
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                                                                                          FEATURE
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APPLICANT: Lee, Se-Jin
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-10
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Spensley Horn Jubas & Lubitz
STREET: 1880 Century Park East, Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: PC-DUS, MS-DUS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/624,635
FILING DATE: 16-AGG-1996
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/134,078
FILING DATE: 08-OCT-1993
ATTORNEY AGENT INFORMATION:
NAME: Wetherell, Jr., Ph.D., John R., REGISTRATION NUMBER: 9D-3054
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 455-5100
TELEPHONE: (619) 455-5100
SEQUENCE CHARACTERISTICS:
LENGTH: 114 amino acids
                                                                                                                                                                                                                                                                                                                                                                              99.8%; Score 633; DB 4; I
100.0%; Pred. No. 2.3e-61;
tive 0; Mismatches 0;
NAME: Wetherell, Jr. Ph.D., John R. REGISTRATION NUMBER: 31,678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                     FD3288
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Patent No. 6204047
                               REFERENCE/DOCKET NUMBER: E032
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 455-5100
TELERX: (619) 455-5140
INFORMATION FOR SEQ ID NG: 23
SEQUENCE CHARACTERISTICS:
LENGTH: 114 antho acid
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                             MOLECULE TYPE: protein
IMMEDIATE SOURCE:
CLONE: TGF-beta3
                                                                                                                                                                              STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                       ; NAME/KEY: Protein
; LOCATION: 1..114
US-09-172-062-23
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STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION
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                                                                                                                                                                                                                                                                                                                                                                                                               Matches 112;
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                                                                                                                                       3 ALDINYCFRNLEENCCVRPLYIDFRQDLGWKWVHEPKGYYANFCSGPCPYLRSADTTHST 62
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Query Match 99.8%; Score 633; DB 4; Length 114; Best Local Similarity 100.0%; Pred. No. 2.3e-61; Matches 112; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 25, Application PC/TUS9400666
GENERAL INFORMATION:
APPLICANT: JOHNS HOPKINS UNIVERSITY
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-3
NUMBER OF SEQUENCES: 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: SPENSLEY HORN JUBAS & LUBITZ
STREET: 1880 CENTURY PARK EAST, FIFTH FLOOR
CITY: LOS ANGELES
STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY AGENT INFORMATION:
NAME: WETHERELL, JR. Ph.D., JOHN R.
REGISTRATION NUMBER: 31,678
REFERENCE/DOOKET NUMBER: FD2279 PCT
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: PCT/US94/00666 FILING DATE: 12-JAN-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
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tive 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (619) 455-5100
TELEFAX: (619) 455-5110
INFORMATION FOR SEQ ID NO: 25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 114 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 99.8 Best Local Similarity 100. Matches 112; Conservative
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1 ALDITNYCFRNLEENCCVRPLYIDFRQDLGWKWVHEPKGYYANFCSGPCPYLRSADTTHST 60
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NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESSES:
ADDRESSEE: SPENSLEY HORN JUBAS & LUBITZ
STREET: 1880 CENTURY PARK EAST, FIFTH FLOOR
CITY: LOS ANGELES
STATE: CALIFORNIA
                     TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-6 NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99.8%; Score 633; DB 1; LA 100.0%; Pred. No. 2.4e-61; iive 0; Mismatches 0;
                                                                                       ADDRESSEE: Fish & Richardson
STREET: 4225 Executive Square, Suite 1400
STREET: 2011a
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Lisa A. Haile, Ph.D. REGISTRATION UNBER: 38,347 REFERENCE, DOCKET NUMBER: 07265/082001 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/581,529B FILING DATE: 15-APR-1996 CLASSIFICATION: 536 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 27, Application US/08455559
Patent No. 5801014
GENERAL INFORMATION:
APPLICANT: LEE, SE-JIN
APPLICANT: HUYNH, THANH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (619) 678-5070
TELEFAX: (619) 678-5099
INFORMATION FOR SEQ ID NO: 71:
SEQUENCE CHARACTERISTICS:
LENGTH: 115 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 100.
Matches 112; Conservative
  Huynh, Thanh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MULECULE TYPE: protein IMMEDIATE SOURCE: CLONE: TGF-beta-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: single
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MEDIUM TYPE: Floppy
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MEDIUM TYPE: Floppy
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MOLECULE TYPE:
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US-08-581-529B-21
    APPLICANT:
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US-08-455-559-27
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                        3 ALDINYCERNLEBINCCVRPLYIDFRQDLGWKWVHEPKGYIANFCSGPCPYLRSADTTHST 62
1 ALDINYCFRNLEENCCVRPLYIDFRQDLGWKWVHEPKGYYANFCSGPCPYLRSADTTHST 60
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                                                                                          VLGLYNTLNPEASASPCCVPQDLEPLTILYYVGRTPKVEQLSNMVVKSCKCS 112
                                                                                                                  63 VLGLYNTLINPEASASPCCVPQDLEPLTILYYVGRTPKVEQLSNMVVKSCKCS 114
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                                                                                                                                                                                                                                          Sequence 23, Application PC/TUS9400685
GENERAL INFORMATION:
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-9
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSE: Spensley Horn Jubas & Lubitz
STREET: 1880 Century Park East, Suite 500
CITY: Los Angeles
STATE: California
COUNTRY: US
21P: 90067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER TEADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: TBM FO Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/00685
FILING DATE: 12-JAN-1994
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99.8%; Score 633; DB 5; I
100.0%; Pred. No. 2.3e-61;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY AGENT INFORMATION:
NAME: Wetherell, Jr. Ph.D., John R.
REGISTRATION NUMBER: 31,678
REFERENCE/COCKET NUMBER: FD3288
TELECOMMINICATION INFORMATION:
TELEPHONE: (619) 455-5100
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 114 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-581-529B-21

; Sequence 21, Application US/08581529B

; Patent No. 577044

; GENERAL INFORMATION:
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Best Local Similarity 100.0
Matches 112; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein
IMMEDIATE SOURCE:
CLONE: TGF-beta3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; NAME/KEY: Protein
; LOCATION: 1.114
PCT-US94-00685-23
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Length 115; Indels

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ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                       protein
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: La Jolla
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                              IMMEDIATE SOURCE:
CLONE: TGF-beta-3
                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: Protein
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Best Local Similarity
                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: pro1
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                                                                                                                                                                                                                                                                                                                                                                                                                                             ; LOCATION:
US-08-581-528A-21
                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
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Sequence 21, Application US/08581528A

Patent No. 59860B

PAPELICANT: Lee, Se-Jin

APPLICANT: Huynh, Thanh

TITLE OF INVENTION:

NUMBER OF SEQUENCES: 21

CORRESPONDENCE ADDRESS:
                      SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATUR SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
RPILICATION NUMBER: US/08/581,528A
FILING DATE: 03-Sept-1993
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99.8%; Score 633; DB 1; 100.0%; Pred. No. 2.4e-61; ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Fish & Richardson, p.C.
STREET: 4225 Executive Square, Suite 1400
                                                            APPLICATION NOMBER: US/08/455,559
FILING DATE: 31-MAY-1995
CLASSIFCATION: 435
PRIOR APPLICATION NATA:
APPLICATION NUMBER: US 08/003,144
FILING DATE: 12-JAN-1993
ATTORNEY AGENT INFORMATION:
NAME: WETHERELL, JR. PH.D., JOHN R. REGISTRATION NUMBER: PD2280
FELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: 619-455-5100
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APPLICATION NUMBER: US 08/089,670
FILING DATE: 09-JUL-1993
PC-DOS/MS-DOS
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Best Local Similarity 100.
Matches 112; Conservative
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CLONE: TGF-beta-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: Protein
  OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
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USA
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US-08-455-559-27
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 ALDINYCFRNLEENCCVRPLXIDFRQDLGWKWVHEPKGYYANFCSGPCPYLRSADTTHST 63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 115;
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Sequence 21, Application US/09097616
Patent No. 6090563
Patent No. 6090563
Patent No. 6090563
Patent Invention
APPLICANT: Lee, Se-Jin
APPLICANT: Huynh, Thanh
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-6
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PC-DOS/MS-DOS SOFTWARE: PC-DOS/MS-DOS CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/097,616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99.8%; Score 633; DB 2; I
100.0%; Pred. No. 2.4e-61;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Fish & Richardson
STREET: 4225 Executive Square, Suite 1400
                                                         07265/081001
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APPLICATION NUMBER: US 08/581,529
FILING DATE: 15-APR-196
ATTORNEY/AGENT INFORMATION:
NAME: Lisa A. Haile, Ph.D.
REGISTRATION NUMBER: 38,347
REFERENCE/DCOKET NUMBER: 07265/0820(
TELEPHONE: (619) 678-5070
TELEPHONE: (619) 678-5070
TELEFAX: (619) 678-5070
TELEFAX: (619) 678-5070
NAME: Lisa A. Haile, Ph.D.
REGISTRATION NUMBER: 38,347
REFRENCE/DOCKET NUMBER: 0726;
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5079
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 115 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
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Matches 112; Conservative
 Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                              Query Match 99.8%; Score 633; DB 3; Length 115; Best Local Similarity 100.0%; Pred. No. 2.4e-61; Matches 112; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Lee, Se-Jin
APPLICANT: Huynh, Thanh
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-5
CORRESPONDENCE: 27
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: FASTEM: Windows95
SOFTWARE: FASTEEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/145,060
FILLING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Fish & Richardson, P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Lisa A. Haile, Ph.D.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07265/057001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/455,559
FILING DATE: 31-MAY-1995
APPLICATION NUMBER: 08/003,144
FILING DATE: 12-JAN-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 27, Application US/09145060 Patent No. 6245896 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 619/678-5099 (172)
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MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 115 amino acids
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TELEFAX: 619/678-5099
                single
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                                              MOLECULE TYPE: protein
                                                                  IMMEDIATE SOURCE:
CLONE: TGF-beta-3
                                                                                                                        NAME/KEY: Protein
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amino acid
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              STRANDEDNESS:
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                                   TOPOLOGY:
                                                                                                                                        ; LOCATION:
US-09-097-616-21
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                                                                                     CLONE:
FEATURE:
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Length 115;

DB 4;

99.8%; Score 633;

Query Match

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                      Gaps
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                                                                  1 ALDITNYCFRNLEENCCVRPLYIDFRQDLGWKWVHEPKGYYANFCSGPCPYLRSADTTHST 60
                                                                                        4 ALDTNYCFRNLEENCCVRPLYIDFRQDLGWKWYHEPKGYYANFCSGPCPYLRSADTTHST 63
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                                                                                                                                                        61 VLGLYNTLNPEASASPCCVPQDLEPLTILYYVGRTPKVEQLSNMVVKSCKCS 112
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                         Indels
                                                                                                                                                                                                                                                                                                                                                       APPLICANT: SE-JIN LEE
APPLICANT: HUNNH, THANH
ITILE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-5
NUMBER OF SEQUENCES: 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/00657
FILING DATE: 1/12/94
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: WETHERELL, JR. PH.D., JOHN R.
REGISTRATION NUMBER: 31,678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 99.8%; Score 633; DB 5; L
Best Local Similarity 100.0%; Pred. No. 2.4e-61;
Matches 112; Conservative 0; Mismatches 0;
100.0%; Pred. No. 2.4e-61; tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: SPENSILY HORN JUBAS & LUBITZ
STREET: 1880 CENTURY PARK EAST, FIFTH FLOOR
CITY: LOS ANGELES
COUNTRY: US
                                                                                                                                                                                                                                                                                                              Sequence 27, Application PC/TUS9400657 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: FD
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/455-5100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 115 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         619-455-5110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IMMEDIATE SOURCE:
CLONE: TGF-beta-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               90067
                                                                                                                                                                                                                                                                     RESULT 19
PCT-US94-00657-27
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PCT-US94-07762-21
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OPERATING SYSTEM:
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PCT-US91-01861-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dp
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Sequence 21, Application PC/TUS9407799
GENERAL INFORMATION:
APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-7
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Spensley Horn Jubas & Lubitz
                                                                 APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-6 NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99.8%; Score 633; DB 5; Length 115; 100.0%; Pred. No. 2.4e-61; Live 0; Mismatches 0; Indels
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SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT_VUS94/07762

FILING DATE: 08-JUL-1994

CLASSIFICATION:

ATOMARKIN, LISA A., PH.D.

REGISTRATION NUMBER: P-38,347

RELECOMMUNICATION INFORMATION:

TELEPHONE: (619) 455-5110

INFORMATION FOR SEQ ID NO: 21: SEQUENCE CHARACTERISTICS:

LENGTH: 115 anino acids

TUBOTH: 115 anino acids
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                                                                                                                                                                                                                                                   ADDRESSEE: Spensley Horn Jubas & Lubitz
STREET: 1880 Century Park East, Suite 500
Application PC/TUS9407762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
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Best Local Similarity 100.(
Matches 112; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
ZIP: 90067
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein
IMMEDIATE SOURCE:
CLONE: TGF-beta-3
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                      CITY: Los Angeles
STATE: California
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                                           GENERAL INFORMATION:
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PCT-US94-07762-21
    Sequence 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   64 VLGLYNTLINPEASASPCCVPQDLEPLILIYYVGRTPKVEQLSNMVVKSCKCS 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Genentech, Inc.
TITLE OF INVENTION: Method of Predisposing Mammals to
TITLE OF INVENTION: Accelerated Tissue Repair
                          PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 633; DB 5; 1
Pred. No. 2.4e-61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. Ser. NO. 07/504,495
FILING DATE: 4 APril 1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                  ATTORNEY ACCULATION:
NAME: TUMARKIN, LISA A., PH.D.
REGISTRATION NUMBER: P-38,347
REFERENCE/DOCKET NUMBER: ED-2348
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 455-5110
TELEPHONE: (619) 455-5110
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/01861
FILING DATE: 19910320
CLASSIFICATION: 514
                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/07799
FILLIO DATE: 08-JUL-1994
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 3, Application PC/TUS9101861 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 63
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99.88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                   single
                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein IMMEDIATE SOURCE: CLONE: TGF-beta-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; NAME/KEY: Protein
; LOCATION: 1..115
PCT-US94-07799-21
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OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: sir
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Best Local Similarity
Matches 112; Conserva
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Matches 112:
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                                                                                                                                                                                                     Length 410;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 3, Application US/08132405
Patent No. 5409896
CENERAL INFORMATION:
APPLICANT: Rudman, Christopher G.
TITLE OF INVENTION: Method of Inducing Bone Growth Using TITLE OF INVENTION:
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                Pred. No. 1.1e-60;
                                                                                                                                                                                                 99.8%; Score 633; DB 5;
100.0%; Pred. No. 1.1e-60
iive 0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/132,405
FILING DATE: 06-0CT-1993
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/063841
FILING DATE: 18-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/790856
FILING DATE: 12-NOV-1991
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/401906
FILING DATE: 01-SEP-1989
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Hasak, Janet E.
REGISTRATION NUMBER: 28,616
REFERENCE/DOCKET NUMBER: 597D
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/952-9881
           TELEFAX: 415/952-9881
TELEX: 910/31-7168
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                     LENGTH: 410 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
415/266-1896
                                                                                                                                                                                                   Query Match 99.8%
Best Local Similarity 100.0
Matches 112; Conservative
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amino acid
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
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TELEPHONE:
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US-08-132-405-3
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APPLICANT: Rudman, Christopher G.
TITLE OF INVENTION: TGF-BETA COMPOSITION FOR INDUCING BONE TITLE OF INVENTION: GROWTH
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
 Length 412;
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99.8%; Score 633; DB 1; 1
100.0%; Pred. No. 1.1e-60;
tive 0; Mismatches 0;
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ilarity 100.0%; Pred. No. 1.1e-60;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P0597D1C2D1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: patin (Genertech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/395,939A
FILLIG DATE: 27-FEB-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 18 MAY 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/790856
FILING DATE: 12-NOV-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/401906
FILING DATE: 1-SEP-1989
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                        Sequence 3, Application US/08395939A Patent No. 5604204 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/132405
FILING DATE: 12-NOV-1993
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REGISTRATION NUMBER: 28,616
REFERENCE/DOCKET NUMBER: PO
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       415/225-1896
415/952-9881
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amino acid
                                       Conservative
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TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO
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APPLICATION NUMBER: (
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SOFTWARE: patin (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 112; Conserv
                   Similarity
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TOPOLOGY:
US-08-395-939A-3
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US-08-395-939A-3
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APPLICANT: Erlander, Mark G.
APPLICANT: Huang, Shaoming
APPLICANT: Jackson, Michael A.
APPLICANT: Peterson, Per A.
TITLE OF INVENTION: PROTEIN GROWTH FACTOR FOR TREATING PROSTATE CANCER, AND REL
NUMBER OF SEQUENCES: 10
                                                                                                                                                                                                                                                                                                                                                                                           ö
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Pred. No. 1.1e-60;
                                                                                                                                                                                                                                                                                                                                                             100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/927,43;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 4, Application US/08927433
; Patent No. 6107476
                                                    APPLICATION NUMBER: 183,410
FILING DATE: 20-APR-1988
APPLICATION NUMBER: 111,022
FILING DATE: 20-OCT-1986
APPLICATION NUMBER: 922,121
FILING DATE: 20-OCT-1986
APPLICATION NUMBER: 847,931
FILING DATE: 07-APR-1986
APPLICATION NUMBER: 725,003
FILING DATE: 19-APR-1986
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REGISTRATION NUMBER: 37,399
REFERENCE/DOCKET NUMBER: OR:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
TELEPHONE: 732-524-3592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Johnson, STREET: One J & J Plaza CITY: New Brunswick STATE: New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 4:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Floppy disk
                                        FILING DATE: 17-MAY-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    112 amino acids
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Best Local Similarity 100.
Matches 112; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein
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                  APPLICATION NUMBER
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  PRIOR APPLICATION
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5262319-2
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Gaps
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                                                                                              161 VIGEYNTLNPEASASPCCVPQDLEPLTILYYVGRTPKVEQLSNMVVKSCKCS 412
                                                                            61 VLGLYNTLNPEASASPCCVPQDLEPLTILYYVGRTPKVEQLSNMVVKSCKCS 112
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                                                                                                                                                                                                                                            APPLICANT: Oncogene Science Inc.
TITLE OF INVENTION: TISSUE DERIVED TUMOR GROWTH INHIBITORS
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99.8%; Score 633; DB 5; Length 412;
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; PETER T.; HALEY, JOHN D.
TITLE OF INVENTION: METHOD FOR OBBTAINING BONE MARROW FREE
; OF TUMOR CELLS USING TRANSFORMING GROWTH FACTOR B3
NUMBER OF SEQUENCES: 9
CURRENT APPLICATION DATA:
FILING DATE: 25-JUN-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1.1e-60;
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)977-9550
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No.
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FILING DATE: 19910625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                              Sequence 2, Application PC/TUS9104541 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Cooper & Dunham STREET: 30 Rockefeller Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.08;
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AMINO ACID
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TELEX: 422523 COOP UI
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; MOLECULE TYPE: protein PCT-US91-04541-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                 CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10112
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Matches 112; Conserv
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5262319-2
;Patent No. 5262319
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REFERENCE/DOCKET NUMBER:
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                                                                                                             1 ALDINYCFRNLEENCCVRPLYIDFRQDLGWKWVHEPKGYYANFCSGPCPYLRSADTIHST 60
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                                                                                                                                                                                         61 VLGLYNTLNPEASASPCCVPQDLEPLTILYYVGRTPKVEQLSNMVVKSCKCS 112
                                 Length 112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99.4%; Score 630; DB 6; Length 203; 99.1%; Pred. No. 9.7e-61; Live 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                 RESULT 28
5168051-12
; Patent No. 5168051
; Patent No. 5168051
; TITLE OF INVENTION: NUCLEIC ACID ENCODING TGF-B ITS USES
; NUMBER OF SEQUENCES: 21
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/389,929
; FILING DATE: 04-AUG-1989
                                                                       Indels
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Patent No. 5827733
GENERAL INFORMATION:
APPLICANT: Huynh, Thanh
TITLE OF INVENTION:
CORRESPONDENCE: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: CA
                                 Score 632; DB 3; L
Pred. No. 2.9e-61;
1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OFFIGATING SYSTEM: Windows95
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/525,596B
FILING DATE: 19-SEP-1995
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Wetherell, Jr., Ph.D, John R.
REGISTRATION NUMBER: 31,678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/07762
FILING DATE: 08-JUL-1994
ATTORNEY/AGENT INFORMATION:
                                 99.7%;
99.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER REALABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: Windows
                 Query Match
Best Local Similarity 99.18
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; LENGTH: 203
5168051-12
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US-08-525-596B-31
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GERERAL INFORMATION:
APPLICANT: Huynh, Thanh
APPLICANT: Lee, Se-Jin
TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR GROWTH DIFFERENTIATION FACTOR-8 AN
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 ALDTNYCFRNLEENCCVRPLYIDFRQDLGWKWVHEPKGYYANFCSGPCPYLRSADTTHST 63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 VLGLYNTLNPEASASPCCVPQDLEPLTILYYVGRTPKVEQLSNMVVKSCKCS 112
                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                              Score 626; DB 2;
Pred. No. 1.3e-60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Gray Cary Ware & Freidenrich LLP STREET: 4365 Executive Drive, Suite 1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM: Windows95
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
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PELLING DATE: 23-OCT-1998
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/525,596
FILING DATE: 19-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: Haile, Ph. D. Lisa A.
RESISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 38,347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 31, Application US/09177860A Patent No. 6096506
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-678-5070
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TELEPHONE: 888-677-1456
TELEPAX: 858-677-1465
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
                                        TELEFAX: 619-678-5099
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 115 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                              98.78;
99.18;
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MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : 115 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 99.13
Matches 111; Conservative
                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: protein
IMMEDIATE SOURCE:
CLONE: TGF-beta-3
                                                                                                                                                                                                                                                             ) NAME/KEY: Protein
; LOCATION: 1.115
US-08-525-5968-31
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STATE: CA
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US-09-177-860A-31
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FILING DATE:
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US-09-123-233-10
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US-09-123-233-12
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                                                                                                                                                                                                                                                                                                                                  1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: DERYNCK, RIK M.A.;GOEDDEL, DAVID V.
TITLE OF INVENTION: NUCLEIC ACID ENCODING TGF-B ITS USES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PatentIn Release #1.0, Version #1.30 (EPO)
                                                                                                                                                                                                                                                         Score 626; DB 3;
Pred. No. 1.3e-60;
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                                                                                                                                                                                                                                                                                                                                  0; Mismatches
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TITLE OF INVENTION.

NUMBER OF SEQUENCES: 14

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

"MEDIUM TYP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/07/389,929
FILING DATE: 04-AUG-1989
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SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/123,233
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                                                                                                                                                                                                                                                         98.7%;
99.1%;
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INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
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TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                    Best Local Similarity 99.1
Matches 111; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 21
                                                                 ; NAME/KEY: Protein
; LOCATION: 1..115
US-09-177-860A-31
TGF-beta-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Patent No. 5168051
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CLONE:
FEATURE:
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                                                                                                                                                                                                                                                             Query Match
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5168051-11
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              Length 112;
Score 595; DB 3; Length 11
Pred. No. 2.9e-57;
5; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 10, Application US/09123233 Patent No. 6057430 GENERAL INFORMATION:
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              93.8%;
92.9%;
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INFORMATION FOR SEO ID NO: 12:
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amino acid
                                                                          Best Local Similarity 92.9
Matches 104; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best_Local Similarity 91.1
Matches 102; Conservative
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; MOLECULE TYPE: protein
US-09-123-233-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION: APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
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1 CCVRPLYIDFRQDLGWKWVHEPKGYYANFCSGPCPYLRSADTTHSTVLGLYNTLNPEASA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 98 amino acids
                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 176
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 87.5
Best Local Similarity 100.
Matches 98; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: MISSOURI
                                                                                                                                                                       US-08-981-739-152
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US-08-478-097A-3
                                                                                                                                                 RESULT
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                                                                                                                                                                                                                                                       1 ALDINYCFRNLEENCCVRPLYIDFRQDLGWKWVHEPKGYYANFCSGPCPYLRSADTTHST 60
                                                                                                                                                                                                                                                                             1 ALDINYCERNLEENCCVRPLYIDFRQDLGWKWVHEPKGYYANFCAGACPYLWSSDTQHSR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                              61 VLGLYNTLNPEASASPCCVPQDLEPLTILYYVGRTPKVEQLSNMVVKSCKCS 112
                                                                                                                                                                   Length 112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            87.5%; Score 555; DB 4; Length 98;
100.0%; Pred. No. 5.1e-53;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: DESAUVAGE, FRED
TITLE OF INVENTION: PERSEPHIN AND RELATED GROWTH FACTOR NUMBER OF SEQUENCES: 239
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/931,858E FILING DATE: CLASSIFICATION: 435
                                                                                                                                                                   Score 577; DB 3;
Pred. No. 2.5e-55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: HOWELL & HAFERKAMP, L.C. STREET: 7733 FORSYTH BOULEVARD, SUITE 1400 CITY: ST. LOUIS STATE: MO
                                                                                                                                                                Query Match 91.0%; Score 577; DE Best Local Similarity 88.4%; Pred. No. 2.5e Matches 99; Conservative 7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 152, Application US/08931858E Patent No. 6222022 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: JOHNSON, EUGENE M
APPLICANT: MILBRANDT, JEFFREY D
APPLICANT: KOTZBAUER, PAUL T
APPLICANT: LAMPE, PATRICIA A
APPLICANT: KLEIN, KOBERT
APPLICANT: DESAUVAGE, FRED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 35,197
REFERENCE/DOCKET NUMBER: 9714
TELECOMUNICATION INFORMATION:
TELEPHONE: 314-727-5188
TELEPHONE: 314-727-6092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 152: SEQUENCE CHARACTERISTICS:
                     : 112 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 98 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 100.
Matches 98; Conservative
  SEQUENCE CHARACTERISTICS
                                                          TOPOLOGY: linear
MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 63105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-931-858E-152
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                                                                                                      US-09-123-233-12
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: JOHNSON JR., EUGENE M.
MILBRANDT, JEFFREY D.
KOTZBAUER, PAUL T.
LAMPE, PATRICIA A.
TITLE OF INVENTION: PERSEPHIN AND RELATED GROWTH FACTORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: HOWELL & HAFERKAMP, L.C.
STREET: 7733 FORSYTH BOULEVARD, SUITE 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      87.5%; Score 555; DB 4; L. 100.0%; Pred. No. 5.1e-53; cive 0; Mismatches 0;
75 SPCCVPQDLEPLTILYYVGRTPKVEQLSNMVVKSCKCS 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SPCCVPQDLEPLTILYYVGRTPKVEQLSNMVVKSCKCS 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: PCT/US97/03461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/981,739
FILING DATE: 31-Aug-1998
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 152:
US-08-981-739-152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: HOLLAND, DONALD R. REGISTRATION NUMBER: 35,197 REFERENCE/DOCKET NUMBER: 976163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
                                                                                                                                                           ; Sequence 152, Application US/08981739; Patent No. 6232449; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
TELEPHONE: (314) 727-5188
TELEFAX: (314) 727-6092
INFORMATION FOR SEQ ID NO: 152:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 3, Application US/08478097A; Patent No. 6040431; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: US
ZIP: 63105-1817
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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1 ALDINYCFRNLEENCCVRPLYIDFRQDLGWKWVHEPKGYYANFCSGPCPYLRSADTTHST 60
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Sequence 42, Application US/08486057B

Patent No. 5650494

GENERAL INFORMATION:
APPLICANT: McMaster, Gary K.
APPLICANT: Cox, David
APPLICANT: Schmitz, Albert
APPLICANT: Schmitz, Albert
APPLICANT: McMast, Bernd
TITLE OF INVENTION: Process for Refolding Recombinantly
TITLE OF INVENTION: Produced TGF-beta-like Proteins
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Henry P. No. 5650494ak
STREET: 520 White Plains Road, P.O. Box 2005
CITY: Tarrytown
STATE: Now York
COUNTRY: U.S.A.
ZIP: 10591-9005

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: TBRD Commatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            84.4%; Score 535; DB 1; Length 112; 79.5%; Pred. No..8.6e-51; tive 14; Mismatches 9; Indels
COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/979,441
FILING DATE: 19921120
CLASSIFICATION: 514
PRIOR APPLICATION: 514
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                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/07/614,306
FILING DATE: 16-NOV-1990
ATTORNEY/AGENT INFORMATION:
NAME: CIOTTI, THOMAS E.
REGISTRATION NUMBER: 21,013
REFERENCE/DOCKET NUMBER: 220952024800
TELECOMMUNICATION INFORMATION:
TELEPAX: 415-494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,057B
FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 415-494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 112 amino acids
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 79.58
Matches 89; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       , MOLECULE TYPE: protein US-07-979-441-2
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US-08-486-057B-42
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 85.3%; Score 541; DB 3; Length 98; 99.0%; Pred. No. 1.7e-51; Live 0; Mismatches 1; Indels
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Patent No. 5462925
GENERAL INFORMATION:
GARA, YASUSHI
APPLICANT: SCHMIDT, DAVID
APPLICANT: SCHMIDT, DAVID
APPLICANT: OF INVENTION: NOVEL BETA-TYPE TRANSFORMING GROWTH
TITLE OF INVENTION: FACTOR
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: MOTTISON & FOOTST
                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/478,097A
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: PITCHER ESQ, EDMUND R
REGISTRATION NUMBER: 27,829
REFERENCE/DOCKET NUMBER: CRP-080
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-248-7000
TELECOMMUNICATION:
TELEPHONE: 617-248-7000
                APPLICANT: SMARY, JOHN
TITLE OF INVENTION: SINGLE-CHAIN ANALOGS OF TGF-B
TITLE OF INVENTION: SUPERFAMILY (MORPHONS)
TUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: PATENT ADMINISTRATOR; TESTA, HURWITZ
ADDRESSEE: THIBEAULT, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   75 SPCCVPQDLEPLTILYYVGRTPKVEQLSNMVKSCKCS 112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: 1..98
CHER INFORMATION: /note= "TGF-B3 SEQUENCE"
US-08-478-097A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3: Morrison & Foerster
755 Page Mill Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 617-248-7100
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                               125 HIGH STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 98 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ouery Match
Best Local Similarity 99.0 Matches 97; Conservative
  APPLICANT: KECK, PETER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 755 Page N
CITY: Palo Alto
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: Protein
                                                                                                                                                                             STREET: 125 H3
CITY: BOSTON
STATE: MA
                                                                                                                                                                                                                                                      USA
                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 38
US-07-979-441-2
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FILING DATE:
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US-08-789-588-42
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-470-837-32
Sequence 32, Application US/08470837
Sequence 32, Application US/08470837
Sequence 32, Application US/08470837
Setent No. 5800811
Sentral No. 1800811
Septicant: Nimni, Marcel E.
APPLICANT: Hall, Frederick L.
APPLICANT: Hall, Frederick L.
APPLICANT: Hall, Transforming Growth Factor B JTILE OF INVENTION: Transforming Growth Factor B JTILE OF INVENTION: Their Use in Wound Healing
TITLE OF INVENTION: Their Use in Wound Healing
SCORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Merchant & Gould
STREET: 11150 Santa Monica Boulevard, Suite 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 84.4%; Score 535; DB 1; L. Best Local Similarity 79.5%; Pred. No. 8.6e-51; Matches 89; Conservative 14; Mismatches 9;
                                                                                   APPLICATION NOMBER: US 0//950,309
FILING DATE: 13-CCT-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0/621,502
FILING DATE: 03-DEC-1990
PRIOR APPLICATION NUMBER: GB 8927546.5
FILING DATE: 06-DEC-1999
ATTORNEY/AGENT INFORMATION:
NAME: NO. 56509484, Henry P.
RECISTRATION NUMBER: 33200
REFERENCE/DOCKET NUMBER: 4-17861/+/Cont3
TELECPHONE: (908) 277-4306
INFORMATION FOR SEQ ID NO: 42: SEQUENCE CHARACTERISTICS:
SEQUENCH: 112 amino acids
TYDE: AMINO acids
TELENTY OR AND ACIDS
TELENTY OF THE AMINO ACIDS
TELENTY OF THE AMINO ACIDS
TELENTY OF THE AMINO ACIDS
TOTAL OF THE AMINO ACIDS
APPLICATION NUMBER: US 08/201,703
FILING DATE: 25-FEB-1994
                                                                      us 07/960,309
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ATTORNEY/AGENT INFORMATION:
NAME: Sharp, Janice A.
REGISTRATION NUMBER: 34,051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                      FILING DATE: 25-FEB-1
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; MOLECULE TYPE: protein US-08-486-057B-42
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CITY: Los Angeles
STATE: California
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ZIP: 90025-3395
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APPLICANT: Certett, Nico
APPLICANT: Cox, David Series
APPLICANT: Cox, David Series
APPLICANT: Schmitz, Albert
APPLICANT: Schmitz, Albert
APPLICANT: Meyhack, Bernd
TITLE OF INVENTION: Process for Refolding Recombinantly
TITLE OF INVENTION: Produced TGF-beta-like Proteins
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Henry P. No. 5922846ak
STREET: 520 White Plains Road, P.O. Box 2005
                                                                                                                                                                                                                                                                                                                                                 Length 112;
                                                                                                                                                                                                                                                                                                                                                 Query Match 84.4%; Score 535; DB 1; Length 11: Best Local Similarity 79.5%; Pred. No. 8.6e-51; Matches 89; Conservative 14; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/789,588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 4-17861/+/Cont3
        30630-10S01
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/621,502
FILING DATE: 03-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 8927546.5
FILING DATE: 06-DEC-1989
ATTORNEY/AGENT INFORMATION:
NAME: NO. 5922846ak, Henry P.
REGISTRATION NUMBER: 33200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/201,703
FILING DATE: 25-FEB-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/960,309
FILING DATE: 13-OCT-1992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 10591-9005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
REFERENCE/DOCKET NUMBER: 30
TELECOMMUNICATION INFORMATION:
TELEPHONE: 310-445-1140
TELEFAX: 310-445-9031
INFORMATION FOR SEQ ID NO: 32:
                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 112 amino acids
TYPE: amino acid
TYPE: amino acid
TYPE: MOLECULE TYPE: protein
US-08-470-837-32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM:
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STATE: New York
COUNTRY: U.S.A.
ZIP: 10591-9005
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APPLICANT: Nguyen, Francis H.
APPLICANT: Nguyen, Francis H.
APPLICANT: Ferrara, Napoleone
APPLICANT: Cunningham, Brian C.
APPLICANT: Wells, James A.
APPLICANT: Li, Bing
TITLE OF INVENTION: Variants of Vascular Endothelial Cell
TITLE OF INVENTION: Growth Factor, Their Uses, and Processes for their
TITLE OF INVENTION: Production
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                    1 ALDINYCFRNLEENCCVRPLYIDFRQDLGWKWVHEPKGYYANFCSGPCPYLRSADTTHST 60
                                                                                                                                                                                                                                                                                                                                                                                              1 ALDAAYCFRNVQDNCCLRPLYIDFKRDLGWKWIHEPKGYNANFCAGACPYLWSSDTQHSR 60
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                                                                                                                                                                                                                                                                         84.4%; Score 535; DB 2; Length 112; 79.5%; Pred. No. 8.6e-51; 1ive 14; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
STREET: Four Embarcadero Center, Suite 3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compartible
OPERATING SYSTEM: FC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A-63758/WHD
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APPLICATION NUMBER: US 60/002,827
FILING DATE: 25-AUG-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/567,200
FILING DATE: 05-DEC-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/691,794
FILING DATE: 02-AUG-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Dreger, Walter H.
REGISTRATION NUMBER: 24,190
REFERENCE/DOCKET NUMBER: A-f
TELECOMMUNICATION INFORMATION-
TELECOMMUNICATION INFORMATION:
              TELEPHONE: (908) 277-5110
TELEFAX: (908) 277-4306
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
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(415) 398-3249
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INFORMATION FOR SEQ ID NO: 5:
                                                                                                               : 112 amino acids
amino acid
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                                                                                                                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: San Francisco
STATE: California
COUNTRY: United States
ZIP: 94111-4187
                                                                                                                                                                             ; MOLECULE TYPE: protein US-08-789-588-42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                          Best Local Similarity
Matches 89; Conserv
                                                                                                                                                               linear
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                                                                                                                                                          TOPOLOGY:
                                                                                                                 LENGTH:
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CITY: Sa
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APPLICANT: Erlander, Mark G.
APPLICANT: Huang, Shaoming
APPLICANT: Jackson, Michael A.
APPLICANT: Jackson, Michael A.
APPLICANT: Peterson, Per A.
TITLE OF INVENTION: PROTEIN GROWTH FACTOR FOR TREATING PROSTATE CANCER, AND REL
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: No. 6057430el process for the production of TITLE OF INVENTION: biologically active dimeric protein NUMBER OF SEQUENCES: 14
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Floppy Flore
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                Length 112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match

84.4%; Score 535; DB 3; Length 112;
Best Local Similarity 79.5%; Pred. No. 8.6e-51;
Matches 89; Conservative 14; Mismatches 9; Indels
                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO) CURRENT APPLICATION DATA:
                                                                                                                              84.4%; Score 535; DB 3; I illarity 79.5%; Pred. No. 8.6e-51; Conservative 14; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US/09/123, 233
                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 4, Application US/09123233 Patent No. 6057430 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 3, Application US/08927433
; Patent No. 6107476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Johnson & Johnson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 112 amino acids
                               TOPOLOGY: unknown
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   , MOLECULE TYPE: protein US-09-123-233-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
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                                                                                                                              Query Match
Best Local Similarity
Matches 89; Conserv
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             STRANDEDNESS:
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                                       ; TOPOLOGY
; MOLECULE T'
US-08-691-794-5
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US-09-123-233-4
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TOPOLOGY: linear
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; LOCATION:
US-08-481-377-24
                                                                                                                                                                                         TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-491-835-22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 24, Application US/08481377
Fatent No. 5808007
GENERAL INFORMATION
TITLE OF INVERTION: GROWTH DIFFERENTIATION FACTOR-3
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: SPENSIEY HORN JUBAS & LUBITZ
STREET: 1880 CENTURY PARK EAST, FIFTH FLOOR
STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/481,377
                                                                                       COMPOTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               84.4%; Score 535; DB 3; L
illarity 79.5%; Pred. No. 8.6e-51;
Conservative 14; Mismatches 9;
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CLASSIFICATION: 514
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: PCT/US94/00666
FILING DATE: 12-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: WETHERELL, JR. Ph.D., JOHN R.
                                                                                                                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/927,433
                                                                                                                                                                                                                                                                                                                       ORT-849
                                                                                                                                                                                                                                                                             NAME: Morrison, Alan J. REGISTRATION NUMBER: 37,399
                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: OR
TELECOMMUNICATION INFORMATION:
TELEPHONE: 732-524-3592
TELEFAX: 732-524-2808
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                         FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 112 amino acids
TYPE: amino acid
STRANDEDNESS: single
: One J & J Plaza
New Brunswick
                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; MOLECULE TYPE: protein US-08-927-433-3
                                      New Jersey
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Best Local Similarity
Matches 89; Conserva
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                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
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1 ALDINYCFRNLEENCCVRPLYIDFRQDLGWKWVHEPKGYYANFCSGPCPYLRSADTTHST 60
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84.4%; Score 535; DB 1; Length 114;
Best Local Similarity 79.5%; Pred. No. 8.8e-51;
Matches 89; Conservative 14; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: THE JOHNS HOPKINS UNIVERSITY
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-9
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Spensley Horn Jubas & Lubitz
STREET: 1880 Century Park East, Suite 500
CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/491,835
FILING DATE: 23-OCT-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Wetherell, Jr. Ph.D., John R. REGISTRATION NUMBER: 31,678
REFERENCE/DOCKET NUMBER: FD3288
                           FD2279 PCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/00685
FILING DATE: 12-JAN-1994
TICNING DATE: 12-JAN-1100:
NAME: Wetherell, Jr. Ph.D., John R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TELEPHONE: (619) 455-5100
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 114 amino acids
TYPE: amino acid
TYPE: amino acids
STRANDEDNESS: single
REGISTRATION NUMBER: 31,678
REFERENCE/DOCKET NUMBER: FD22
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 455-5100
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                           LENGIH: 114 amino acids
                                                                                                                                                                                                                        single
                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein
IMMEDIATE SOURCE:
CLONE: TGF-beta 2
                                                                                                                                                                                                                                                                                                                                                                     Protein
                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: sir
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Matches
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                                                                                                                                                                                                                                                                 3 ALDAAYCERNVQDNCCLRPLYIDFKRDLGWKWIHEPKGYNANFCAGACPYLWSSDTQHSR 62
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                                                                                                                                                                                                                                                                                                                                        Length 114;
                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: JOHNS HOPKINS UNIVERSITY
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-3
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/153,733A
FILING DATE:
                                                                                                                                                                   84.4%; Score 535; DB 2; Lr
79.5%; Pred. No. 8.8e-51;
ive 14; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: SPENSLEY HORN JUBAS & LUBITZ
STREET: 1880 CENTURY PARK EAST, FIFTH FLOOR
CITY: LOS ANGELES
CONTIFORNIA
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY JAGENT INFORMATION:
NAME: WETHERELL, JR. Ph.D., JOHN R.
REGISTRATION NUMBER: 31,678
RECISTRATION NUMBER: FD2279 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 455-5110
TELEPHONE: (619) 455-5110
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 114 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 24, Application US/09153733A Patent No. 6025475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/481,377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                   Query Match
Best Local Similarity 79.5%
Matches 89; Conservative
     protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein
IMMEDIATE SOURCE:
CLONE: TGF-beta 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               single
                                                                         NAME/KEY: Protein
MOLECULE TYPE: prot
IMMEDIATE SOURCE:
CLONE: TGF-beta2
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LOCATION:
                                                                                            ; LOCATION:
US-08-491-835-22
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Length 114;

Score 535; DB 3; Pred. No. 8.8e-51;

84.4%; 79.5%;

Query Match Best Local Similarity

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    Gaps
                                                                 3 ALDAAYCFRNVQDNCCLRPLYIDFKRDLGWKWIHEPKGYNANFCAGACPYLWSSDTQHSR 62
                                        1 ALDINYCFRNLEENCCVRPLYIDFRQDLGWKWVHEPKGYYANFCSGPCPYLRSADTTHST 60
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                                                                                                                                                      61 VLGLYNTLNPEASASPCCVPQDLEPLTILYYVGRTPKVEQLSNMVVKSCKCS 112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 84.4%; Score 535; DB 3; Length 114; illarity 79.5%; Pred. No. 8.8e-51; Conservative 14; Mismatches 9; Indels
9; Indels
                                                                                                                                                                                                                                                                                                                                                                        GROWTH DIFFERENTIATION FACTOR-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIOW TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURREW APPLICATION DATA:
APPLICATION NUMBER: US/08/946,092A
                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Spensley Horn Jubas & Lubitz
STREET: 1880 Century Park East, Suite 500
14; Mismatches
                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: THE JOHNS HOPKINS UNIVERSITY
TITLE OF INVENTION: GROWTH DIFFERENTIATINUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Wetherell, Jr. Ph.D., John R. REGISTRATION NUMBER: 31,678
REFERENCE/DOCKET NUMBER: ED3288
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                Sequence 22, Application US/08946092A Patent No. 6030617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/491,835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IELEPHONE: (619) 455-5100
TELERAX: (619) 455-5110
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 114 amino acids
TYPE: amino acid
STRANDENNESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: ATTORNEY/AGENT INFORMATION:
Conservative
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CITY: Los Angeles
STATE: California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: prot
IMMEDIATE SOURCE:
CLONE: TGF-beta2
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Best Local Similarity
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CLASSIFICATION:
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                                                                                                                                                                                                                                       RESULT 48
US-08-946-092A-22
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89;
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PatentIn Release #1.0, Version #1.25
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 90067
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
SOFTWARE: PatentIn Release #
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (619) 455-5100
TELEFAX: (619) 455-5110
INPERATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 114 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein IMMEDIATE SOURCE: CLONE: TGF-beta-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           single
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: LOS ANGELES
STATE: CALIFORNIA
COUNTRY: US
ZIP: 90067
                                                               CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino a STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: li
MOLECULE TYPE:
                                                                                                                            90067
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                                                                                                        COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 ALDINYCFRNLEENCCVRPLYIDFRQDLGWKWVHEPKGYYANFCSGPCPYLRSADTTHST 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       84.4%; Score 535; DB 4; Length 114; 79.5%; Pred. No. 8.8e-51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 23, Application US/08624635
Patent No. 6204047
GENERAL INFORMATION:
APPLICANT: Lee, Se-Jin
APPLICANT: Cunningham, No. 6204047een
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-10
NUMBER OF SEQUENCES: 26
                                                                                             APPLICAM: THE JOHNS HOPKINS UNIVERSITY
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-9
NUMBER OF SEQUENCES: 26
CORRESPONDENCE DADRESS:
ADDRESSEE: Spensley Horn Jubas & Lubitz
STREET: 1880 Century Park East, Suite 500
CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                         ZIP: 90067
ZIP: 90067
ZIP: 90067
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/172,062
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
PRIOR APPLICATION:
PRIOR APPLICATION NUMBER: US/08/491,835
FILING DATE: 23-0CT-1995
APPLICATION NUMBER: PCT/US94/00685
FILING DATE: 12-JAN-1994
ATTORNEY AGENT INFORMATION:
REGISTRATION NUMBER: PD3288
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION FOR SEQ ID NO: 22:
                                Sequence 22, Application US/09172062 Patent No. 6191261 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 114 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 89; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; LOCATION:
US-09-172-062-22
               US-09-172-062-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-624-635-23
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 ALDAAYCFRNVQDNCCLRPLYIDFRRDLGWKWIHEPKGYNANFCAGACPYLWSSDTQHSR 62
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                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/624,635
FILING DATE: 16-AUG-1996
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEBULE 1

Sequence 24, Application PC/TUS9400666

Sequence 24, Application PC/TUS9400666

GENERAL INFORMATION:
GENERAL INFORMATION:
GROWTH DIFFERENTIATION FACTOR SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: SPENSLEY HORN JUBAS & LUBITZ
STREET: 1880 CENTURY PARK EAST, FIFTH FLOOR
ADDRESSEE: Spensley Horn Jubas & Lubitz
STREET: 1880 Century Park East, Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR PAPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/134,078
FILING DATE: 08-0CT-1993
ATTORNEY AGENT INFORMATION:
NAME: Wetherell, Jr., Ph.D., John R.,
REGISTRATION NUMBER: 31,678
REFERENCE/DOCKET NUMBER: PD-3054
TELECOMMUNICATION INFORMATION:
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      84.4%; Score 535; DB 5; Length 114; 79.5%; Pred. No. 8.8e-51; rive 14; Mismatches 9; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Lee, Se-Jin
APPLICANT: Huynh, Thanh
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/581,529B
FILING DATE: 15-APR-1996
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Fish & Richardson
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 07265/082001
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; Patent No. 5770444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Lisa A. Haile, Ph.D.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 0726;
TELECOMMUNICATION INFORMATION:
TELEPAX: (619) 678-5070
TELEPAX: (619) 678-509
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTER.ESTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 115 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                             89; Conservative
             TOPOLOGY: linear
MOLECULE TYPE: protein
IMMEDIATE SOURCE:
CLONE: TGF-beta2
  STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein
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CORRESPONDENCE ADDRESS:
                                                                                                                               NAME/KEY: Protein
LOCATION: 1..114
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IMMEDIATE SOURCE:
CLONE: TGF-beta-2
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Best Local Similarity
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Best Local Similarity
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US-08-581-529B-20
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LOCATION:
PCT-US94-00685-22
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US-08-581-529B-20
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                                                                                                               FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         63 VLSLYNTINPEASASPCCVSQDLEPLTILYYIGKTPKIEQLSNMIVKSCKCS 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 VLGLYNTLNPEASASPCCVPQDLEPLTILYYVGRTPKVEQLSNMVVKSCKCS 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     84.4%; Score 535; DB 5; Length 114; 79.5%; Pred. No. 8.8e-51; Live 14; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: THE JOHNS HOPKINS UNIVERSITY
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-9
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Spensley Horn Jubas & Lubitz
STREET: 1880 Century Park East, Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFFWARE: PAtentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                 ATTORNEY AGENT INFORMATION:
NAME: WETHERELL, JR. Ph.D., JOHN R. REGISTRATION NUMBER: 31,678
REFERENCE/DOCKET NUMBER: FD2279 PCT
TELECOMMUNICATION INFORMATION: (619) 455-5100
TELEFAX: (619) 455-5100
TELEFAX: (619) 455-5100
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 114 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Wetherell, Jr. Ph.D., John R.
REGISTATION NUMBER: 31,678
REFERENCE/DOCKET NUMBER: FD2288
TELECOMMUNICATION INFORMATION:
TELEPHORE: (619) 455-5100
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 114 amino acids
TYPE: amino acid
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/00666
FILING DATE: 12-JAN-1994
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: PCT/US94/00685 FILING DATE: 12-JAN-1994 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PCT-US94-00685-22; Sequence 22, Application PC/TUS9400685; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 79.5
Matches 89; Conservative
                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein
IMMEDIATE SOURCE:
CLONE: TGF-beta 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Los Angeles
STATE: California
COUNTRY: US
ZIP: 90067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; NAME/KEY: Protein
; LOCATION: 1..114
PCT-US94-00666-24
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MOLECULE TYPE: protein
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MEDIUM TYPE: Diskett
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CLONE: TGF-beta-2
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                                                                                             GENERAL INFORMATION:
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                                       US-08-525-596B-30
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                                                                                                                                                                                                                                                              STATE: CA
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 0; Gaps
                                                         4 ALDAAYCFRNVQDNCCLRPLYIDFKRDLGWKWIHEPKGYNANFCAGACPYLWSSDTQHSR 63
                                    1 ALDINYCFRNLEENCCVRPLYIDFRQDLGWKWVHEPKGYYANFCSGPCPYLRSADTTHST 60
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                                                                                                                             61 VLGLYNTLNPEASASPCCVPQDLEPLTILYYVGRTPKVEQLSNMVVKSCKCS 112
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 9; Indels
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                                                                                                                                                                                                                                                                                           APPLICANT: LEE, SE-JIN
APPLICANT: HUYNH, THANH
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-5
WUMBER OF SEQUENCES: 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
APPLICATION NUMBER: US/08/455,559
FILING DATE: 31-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    84.4%; Score 535; DB 1; L
79.5%; Pred. No. 8.9e-51;
iive 14; Mismatches 9;
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STREET: 1880 CENTURY PARK EAST, FIFTH FLOOR
CITY: LOS ANGELES
STATE: CALIFORNIA
COUNTY: US
ZIP: OCCU
 14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 31-MAY-1995
CLASSIECATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/003,144
FILING DATE: 12-JAN-1993
ATTONEY/AGENT INFORMATION:
NAME: WETHERELL, JR. PH.D., JOHN R.
REGISTRATION NUMBER: 31,678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PD2280
                                                                                                                                                                                                                   US-08-455-559-26; Sequence 26, Application US/08455559; Patent No. 5801014; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: PD TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: 619/455-5100
TELEFAX: 619-455-5110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 619-455-5110
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 115 amino acids:
 Conservative
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Best Local Similarity 79.59
Matches 89; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
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US-08-455-559-26
89;
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 Matches
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 ALDINYCFRNLEENCCVRPLYIDFRQDLGWKWVHEPKGYYANFCSGPCPYLRSADTTHST 60
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Patent No. 5986058
GENERAL INFORMATION:
APPLICANT: Lee, Se-Jin
APPLICANT: Huynh, Thanh
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-7
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
                                                       APPLICANT: Huynh, Thanh
APPLICANT: Lee, Se-Jin
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-8
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           84.4%; Score 535; DB 2; L
79.5%; Pred. No. 8.9e-51;
ive 14; Mismatches 9;
                                                                                                                                                                                                                                                                                                                          07265/075001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Wetherell, Jr., Ph.D, John R. REGISTRATION NUMBER: 31,678
Sequence 30, Application US/08525596B Patent No. 5827733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 07
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-678-5070
TELEFAX: 619-678-5099
                                                                                                                                                                                                                                                                                                         COMPUTER: IBM Compatible
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INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 79.59
Matches 89; Conservative
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COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9; Indels
                                                                                                                                                                              OPERATING SISTEM: PC-LUS/MS-LUS
SOFTWARE: Patentin Release #1.0, Version #1.25
CUBRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/581,528A
FILING DATE: 03-Sept-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/089,670
FILING DATE: 09-UL-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Lisa A. Haile, Ph.D.
REGISTRATION NUMBER: 38,347
REGISTRATION NUMBER: 38,347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 20, Application US/09097616
Patent No. 6090563
GENERAL INFORMATION:
APPLICANT: Let, Se-Jin
APPLICANT: HUYDh, Thanh
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-6
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 4225 Executive Square, Suite 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Score 535; DB 2;
; Pred. No. 8.9e-51;
14; Mismatches 9
ADDRESSEE: Fish & Richardson, P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
                                                                                                                                                                                                                                                                                                                                                                                                                              07265/081001
                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 0726
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
TELEFAX: 619/678-5099
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENTH: 115 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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79.58;
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Best Local Similarity 79.5%
Matches 89; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: protein
IMMEDIATE SOURCE:
CLONE: TGF-beta-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: La Jolla
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: Protein LOCATION: 1.115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: sir
                                                                                             92037
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                                                       STATE: C
COUNTRY:
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APPLICANT: Huynh, Thanh
APPLICANT: Lee, Se-Jin
TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR GROWTH DIFFERENTIATION FACTOR-8 AN
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Gray Cary Ware & Freidenrich LLP
STREET: 4365 Executive Drive, Suite 1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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84.4%; Score 535; DB 3; Length 115;
Best Local Similarity 79.5%; Pred. No. 8.9e-51;
Matches 89; Conservative 14; Mismatches 9; Indels
                SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/097,616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/177,860A
FILING DATE: 23-OCT-1998
CLASSIFICATION: 424
                                                        APPLICATION:
FILING DATE:
CLASSIFICATION:
CLASSIFICATION DATA:
PRIOR APPLICATION NUMBER: US 08/581,529
FILING DATE: 15-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Lisa A Halle, Ph.D.
REGISTRATION NUMBER: 38,347
REFERENCE/COCKET NUMBER: 38,347
REFERENCE/COCKET NUMBER: 07265/082001
TELEPHONE: (619) 678-509
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 115 amino acids
TYPE: amino acid
STRANDEDNESS: single
PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-177-860A-30; Sequence 30, Application US/09177860A; Patent No. 6096506; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      IMMEDIATE SOURCE:
CLONE: TGF-beta-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ns
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US-09-097-616-20
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Gaps

FEATURE

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1 ALDITNYCFRNLEENCCVRPLYIDFRQDLGWKWVHEPKGYYANFCSGPCPYLRSADITHST 60
                                                                                                                                                                                                                                                                       4 ALDAAYCFRNVQDNCCLRPLYIDFKRDLGWKWIHEPKGYNANFCAGACPYLWSSDTQHSR 63
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                                                                                                                                                                                                                                                                                                                                                            84.4%; Score 535; DB 4; Length 115; 79.5%; Pred. No. 8.9e-51; Live 14; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 115;
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84.4%; Score 535; DB 5; Length 11

Best Local Similarity 79.5%; Pred. No. 8.9e-51;

Matches 89; Conservative 14; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                         PCT-US94-00657-26

Sequence 26, Application PC/TUS9400657

Sequence 26, Application PC/TUS9400657

SENERAL INFORMATION

TITLE OF INVENTION GROWTH DIFFERENTIATION FACTOR-5

TORRESPONDENCE ADDRESS:

ADDRESSEE: SPRENSLEY HORN JUBAS & LUBITZ

STATE: LOS ANGELES

STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: PCT/US94/00657 FILING DATE: 1/12/94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FD3256 CIP OF PD2280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY AGENT INFORMATION:
NAME: WETHERELL, JR. PH.D., JOHN R.
REGISTRATION NUMBER: 31,678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: FD
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/455-5100
TELEPAX: 619-455-5110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 115 amino acids TYPE: amino acid
                                                                                                                                                       Query Match
Best Local Similarity 79.54
Matches 89; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 619-455-5110
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                      ; IMMEDIATE SOURCE:
; CLONE: TGF-beta-2
US-09-145-060-26
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IMMEDIATE SOURCE:
CLONE: TGF-beta-2
FEATURE:
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        TOPOLOGY: linear
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LOCATION:
PCT-US94-00657-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: CA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64 VLSLYNTINPEASASPCCVSQDLEPLTILYYIGKTPKIEQLSNMIVKSCKCS 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 VLGLYNTLNPEASASPCCVPQDLEPLTILYYVGRTPKVEQLSNMVVKSCKCS 112
                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Lee, Se-Jin
APPLICANT: Lee, Se-Jin
TITLE OF INVENTION GROWTH DIFFERENTIATION FACTOR-5
WIDMER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 84.4%; Score 535; DB 3; La
Best Local Similarity 79.5%; Pred. No. 8.9e-51;
Matches 89; Conservative 14; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastESG for Windows Version 2.0
CURTERNY APPLICATION DATA:
APPLICATION NUMBER: US/09/145,060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Fish & Richardson, P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: CA
NAME: Haile, Ph.D, Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07265/075003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 858-677-1456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 07265/057001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
TELEPHONE: 619/678-5099
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRICE APPLICATION DATA:
PRICE APPLICATION DATA:
APPLICATION NUMBER: 08/455,559
FILING DATE: 31-MAY-1995
APPLICATION NUMBER: 08/003,144
FILING DATE: 12-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Lisa A. Haile, Ph.D.
REGISTRATION NUMBER: 38 347
REGISTRATION NUMBER: 38 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 26, Application US/09145060 Patent No. 6245896 GENERAL INFORMATION:
                                                                                                      TELEFAX: 858-677-1465
INFORMATION FOR SEQ ID NO: 30: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                           : 115 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 115 amino acids TYPE: amino acid
                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                IMMEDIATE SOURCE:
CLONE: TGF-beta-2
                                                                                                                                                                                                                                                                                                                                 ; NAME/KEY: Protein
; LOCATION: 1..115
US-09-177-860A-30
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APPLICATION NUMBER: US/08/132,405
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                                                                       ZIP: 90067
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION:
                                                   COUNTRY:
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US-08-132-405-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 VLGLYNTLNPEASASPCCVPQDLEPLTILYYVGRTPKVEQLSNMVVKSCKCS 112
                        61 VLGLYNTLNPEASASPCCVPQDLEPLTILYYVGRTPKVEQLSNMVVKSCKCS 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-6 NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 84.4%; Score 535; DB 5; Length 115; Best Local Similarity 79.5%; Pred. No. 8.9e-51; Matches 89; Conservative 14; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-7 NUMBER OF SEQUENCES: 21 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/07762
FILING DATE: 08-JUL-1994
CLASSIFICATION:
                                                                                                                                                                                                                                                                               ADDRESSEE: Spensley Horn Jubas & Lubitz
STREET: 1880 Century Park East, Suite 500
CITY: Los Angeles
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Spensley Horn Jubas & Lubitz
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY AGENT INFORMATION:
NAME: TUMARKIN, LISA A., PH.D.
REGISTRATION NUMBER: P-38,347
REFERENCE/DOCKET NUMBER: FD2349
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 455-5100
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERERSTICS:
LENGTH: 115 amino acids
TYPE: amino acid
                                                                                                                                                   Sequence 20, Application PC/TUS9407762 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PCT-US94-07799-20; Sequence 20, Application PC/TUS9407799; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 single
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CLONE: TGF-beta-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                        90067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; LOCATION:
PCT-US94-07762-20
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2, Application US/08132405
Patent No. 5409896
GENERAL INFORMATION:
APPLICANT: Admann, Arthur J.
APPLICANT: Admann, Christopher G.
TITLE OF INVENTION: Method of Inducing Bone Growth Using
TITLE OF INVENTION: TGF-Beta
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               84.4%; Score 535; DB 5; Length 11:
79.5%; Pred. No. 8.9e-51;
Micmatches 9; Indels
                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURREWY APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/07799
FILING DATE: 08-JUL-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
1880 Century Park East, Suite 500
                                                                                                                                                                                                                                                   FILING DATE: 08-JUL-1994
CLASSIFTCATION:
ATTORNEY/AGENT INFORMATION:
NAME: TUMARKIN, LISA A., PH.D.
REGISTRATION NUMBER: P-38,347
REPERENCE/DOCKET NUMBER: FD-2348
TELEPHONE: (619) 455-5100
TELEPHONE: (619) 455-5100
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 115 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 460 Point San Bruno Blvd CITY: South San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM: PC_DOS/MS-DOS SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-
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                                                                                                           COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein
                        Los Angeles
California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IMMEDIATE SOURCE:
CLONE: TGF-beta-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: California
COUNTRY: USA
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PCT-US91-01861-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application US/08395939A
Patent No. 5604204
GENERAL INFORMATION:
APPLICANT: Admann, Arthur J.
APPLICANT: Rudmann, Christopher G.
TITLE OF INVENTION: TGF-BETA COMPOSITION FOR INDUCING BONE TITLE OF INVENTION: GROWTH
NUMBER SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match

84.4%; Score 535; DB 1; Length 414;
Best Local Similarity 79.5%; Pred. No. 4.1e-50;
Matches 89; Conservative 14; Mismatches 9; Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
CORPARE: patin (Genentech)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 28,616
REFERENCE/DOCKET NUMBER: 597DLC2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/252-1896
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 414 amino acids
TOPOLACY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PAPLICATION NUMBER: US/08/395,939A
FILING DATE: 27-FEB-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/132405
FILING DATE: 12-NOV-1993
APPLICATION NUMBER: 08/063841
FILING DATE: 18-MAY-1993
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                          APPLICATION NUMBER: 08/063841
FILING DATE: 18-MAY-1993
PRIOR APPLICATION DATA: 07/790856
FILING DATE: 12-NOV-1991
PRIOR APPLICATION DATA: 07/701006
FILING DATE: 07/401906
FILING DATE: 01-SEP-1989
AFTONNEY/AGGENT INFORMATION: NAME: Hasak, Janet E. REGISTRATION NUMBER: 28,616
FILING DATE: 06-OCT-1993
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-395-939A-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 79.5%; Pred. No. 4.1e-50;
Matches 89; Conservative 14; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2. Application PC/TUS9101861
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
TITLE OF INVENTION: Method of Predisposing Mammals to
TITLE OF INVENTION: Accelerated Tissue Repair
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:

MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA: APPLICATION NUMBER: PCT/US91/01861
FILING DATE: 19910320
CLASSIFICATION DATA: 514
PRIOR PAPLICATION DATA: APPLICATION NUMBER: U.S. Ser. No. 07/504,495
FILING DATE: 4 April 1990
ATTORNEY/AGENT INFORMATION:
NAME: Hasak, Janet E.
REGISTRATION NUMBER: 28,616
                                                                                                                                                                                              P0597D1C2D1
               FILING DATE: 12 NOV-1991
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 07/401906
FILING DATE: 1-SEP-1989
ATTORNEY/AGENT INFORMATION:
NAME: Hasak, Janet E.
REGISTRATION NUMBER: 28,616
REFERENCE/DOCKET NUMBER: P0597D1
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
APPLICATION NUMBER: 07/790856
                                                                                                                                                                                                                                                            TELERAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 414 amino acids
TYPE: amino acid
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/266-1896
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INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: IENGTH: 414 amino acids TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            415/952-9881
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US-08-395-939A-2
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1 ALDINYCFRNLEENCCVRPLYIDFRQDLGWKWVHEPKGYYANFCSGPCPYLRSADTTHST 60
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61 VLGLYNTLNPEASASPCCVPQDLEPLTILYYVGRTPKVEQLSNMVVKSCKCS 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 414;
                                                                                                             5221620-4
;Patent No. 5221620
;Patent No. 5221620
APPLICANT: PURCHIO, ANTHONY F.; MADISEN, LINDA; WEBB, NANCY
TITLE OF INVEWTION: CLONING AND EXPRESSION OF TRANSPORMING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5221620-2; Patent No. 5221620; Patent No. 5221620; APPLICANT: PURCHIO, ANTHONY F.; MADISEN, LINDA; WEBB, NANCY TITLE OF INVENTION: CLONING AND EXPRESSION OF TRANSFORMING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 442;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 84.4%; Score 535; DB 6;
79.5%; Pred. No. 4.4e-50;
iive 14; Mismatches 9.
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APPLICATION NUMBER: US/07/446,020
FILING DATE: 05-DEC-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 285,140
FILING DATE: 16-DEC-1988
APPLICATION NUMBER: 234,065
FILING DATE: 18-AGG-1988
APPLICATION NUMBER: 148,267
FILING DATE: 25-JAN-1988
APPLICATION NUMBER: 160,752
FILING DATE: 25-JAN-1988
APPLICATION NUMBER: 106,752
FILING DATE: 06-OCT-1987
                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/446,020
FILING DATE: 05-DEC-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 285,140
                                                                                                                                                                                                                                                                                                                     FILING DATE: 16-DEC-1988
APPLICATION NUMBER: 234,065
FILING DATE: 18-AUG-1988
APPLICATION NUMBER: 148,267
FILING DATE: 25-JAN-1988
APPLICATION NUMBER: 106,752
FILING DATE: 06-OCT-1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 84.4%;
Best Local Similarity 79.5%;
Matches 89; Conservative 1
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                                                                                                                                                                                        GROWTH FACTOR BETA-2
NUMBER OF SEQUENCES: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GROWTH FACTOR BETA-2
, NUMBER OF SEQUENCES: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 414
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                                                                                                                                                1 ALDTNYCFRNLEENCCVRPLYIDFRQDLGWKWVHEPKGYYANFCSGPCPYLRSADTTHST 60
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                                                                                                                                                                                                                           61 VLGLYNTLNPEASASPCCVPQDLEPLTILYYVGRTPKVEQLSNMVVKSCKCS 112
                                                                                                                                                                                                                                              Length 414;
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                                                                                                             9; Indels
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4.1e-50;
                                                                      84.4%; Score 535; DB 5;
79.5%; Pred. No. 4.1e-50;
ive 14; Mismatches 9
                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Mark A. Perrella
TITLE OF INVENTION: TRANSFORMING GROWTH
TITLE OF INVENTION: PACTOR- INHIBITS
TITLE OF INVENTION: INDUCTBLE NITRIC OXIDE
TITLE OF INVENTION: SYNTHASE GENE
TITLE OF INVENTION: TRANSCRIPTION
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 52 or 555X
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/03705
FILING DATE: 5 April 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14; Mismatches
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ER: 05433/007001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              84.4%; Score 535; 79.5%; Pred. No. 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           UMBER: PCT/US94/03705
5 April 1994
                                                                                                                                                                                                                                                                                                                                                        Sequence 6, Application PC/TUS9403705
GENERAL INFORMATION:
APPLICANT: Mu-En Lee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3: Fish & Richardson 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Janis K. Fraser
REGISTRATION NUMBER: Reg. N
REFERENCE/DOCKET NUMBER: 05
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (617) 542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: (
SEQUENCE CHARACTERISTICS:
                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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APPLICATION NUMBER:
FILING DATE:
linear
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                                                                                        Best Local Similarity
Matches 89; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 89; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS:
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; TOPOLOGY:
PCT-US91-01861-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TOPOLOGY:
PCT-US94-03705-6
                                                                                                                                                                                                                                                                                                                                        PCT-US94-03705-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET:
CITY: Bo
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TITLE OF INVENTION: Nucleic Acid Encoding the Alpha or Beta Chains of Inhibin a
                                                                                                                               USA
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TOPOLOGY:
US-08-197-792-36
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US-08-486-057B-41
                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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0
                VLGLYNTLNPEASASPCCVPQDLEPLTILYYVGRTPKVEQLSNMVVKSCKCS 112
                                   Sequence 1, Application US/07979441

Patent No. 5462925

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: GCHNIDT, DAVID
APPLICANT: CAMIDT, DAVID
TITLE OF INVENTION: FACTOR
TITLE OF INVENTION: FACTOR
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESSS:
STREET: 755 Page Mill Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  78.9%; Score 500; DB 1; Length 112; 76.8%; Pred. No. 5.2e-47; Live 11; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               220952024800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/07/979,441
FILING DATE: 19911120
CLASSIPEICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/614,306
FILING DATE: 16-NOV-1990
ATTORNEY/AGENT INFORMATION:
NAME: CIOTII, THOMAS E.
REGISTRATION NUMBER: 21,013
REFERENCE/DOCKET NUMBER: 22095202480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 36, Application US/08197792
Patent No. 5525408
GENERAL INFORMATION:
APPLICANT: Anthony J. Mason
APPLICANT: Peter H. Seeburg
                                                                                                                                                                                                                                                                                                                                                                                             COMPUTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-813-5600
TELEFAX: 415-494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEX: 706141
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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AMINO ACID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                 CITY: Palo Alto
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 86; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 ALDTHYCESSTERNCCVRQLYIDFRKDLGWRWIHEPKGYHANFCLGPCPYIWSLDTQYSK 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           78.9%; Score 500; DB 1; 76.8%; Pred. No. 5.2e-47;
                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          86; Conservative 11; Mismatches
                                                                                                                                                                                                                                                                                OURMEATURE STRIEMS: C. LOUGHES
SUCTIONERS PATING STRIEMS: C. LOUGHES
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/197,792
FILING DATE: 16-FEB-1994
CLASSIFICATION NUMBER: U7/958414
FILING DATE: 08-0CT-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/744207
FILING DATE: 12-AUG-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/215466
FILING DATE: 105-0JU-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 06/906729
FILING DATE: 31-DEC-1986
PRIOR APPLICATION NUMBER: 06/827710
FILING DATE: 31-DEC-1986
FILING DATE: 31-DEC-1986
FILING DATE: 07-FEB-1986
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSE: Genentech, Inc.
STREET: 440 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 41, Application US/08486057B

Patent No. 5650494

GENERAL INFORMATION:

APPLICANT: Cerletti, Nico

APPLICANT: McMaster, Gary K.
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1896
TELEFAX: 415/952-9881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 36:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 07-FEB-1986
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 06/76
FILING DATE: 03-0CT-1985
ATTORNEY/AGENT INFORMATION:
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RESULT 72
US-08-459-850-36
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                                                                                                                         sequence 36, Application US/08459850
Patent No. 5665568
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                                                                    GENERAL INFORMATION:
APPLICANT: Anthon
APPLICANT: Peter |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (908) 277-430 INFORMATION FOR SEQ ID NO:
                TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 4-17861/+/Cont3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 277-5110
TELEFAX: (908) 277-4306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 03-DEC-1990 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 07/960,309 FILING DATE: 13-OCT-1992 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/201,703
FILING DATE: 25-FEB-1994
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
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NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 06-DEC-1989
ATTORNEY/AGENT INFORMATION:
NAME: NO. 5650494ak, Henry P.
REGISTRATION NUMBER: 33200
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                                                                                                                                                                                                                              Local Similarity 76.8 nes 86; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 07 CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH:
                                                                                                                                                                                                                                                                                                                      1 ALDTNYCFRNLEENCCVRPLYIDFRQDLGWKWVHEPKGYYANFCSGPCPYLRSADTTHST 60
                                                                                                                                                                                                                                                                                                      ALDTNYCFSSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSK 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    112 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E: Henry P. No. 5650494ak
520 White Plains Road, P.O. Box 2005
            Anthony J. Mason
Peter H. Seeburg
Peter H. Seeburg
VENTION: Nucleic Acid Encoding the Alpha or
VENTION: Beta Chains of Inhibin and Method
VENTION: Using such Nucleic Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Meyhack,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Schmitz,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IBM PC compatible SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 UMBER: US/08/486,057B
07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                        78.9%; Score 500; DB 1; 76.8%; Pred. No. 5.2e-47; tive 11; Mismatches 15
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                               for Synthesizing Polypeptide
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RESULT 73
US-08-459-214-36
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                                                   Sequence 36, Appl
Patent No. 571681
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                                                                                                                                                                                                                                                                                                                               Query Match
GENERAL INFORMATION:
APPLICANT: Anthon
APPLICANT: Peter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: 415/225-1896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/197792
FILING DATE: 17-FEB-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 06/8: FILING DATE: 07-FEB-1986 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: 06/827710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 05-JUL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 17-FEB-PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA: US/08/459,850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS: ADDRESSEE: Genentech,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 08-OCT-1992
PRIOR APPLICATION DATA:
                                                                                                                                                          61
                                                                                                                                                                          61 VLGLYNTINPEASASPCCVPQDLEPLTILYYYGRTPKVEQLSNMVVKSCKCS 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 06/9 FILING DATE: 31-DEC-1986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 07/74 FILING DATE: 12-AUG-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 02
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH:
                                                                                                                                                                                                                                            1 ALDTNYCFRNLEENCCVRPLYIDFRQDLGWKWVHEPKGYYANFCSGPCPYLRSADTTHST 60
                                                                                                                                                        VLALYNQHNPGASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 112
                                                                                                                                                                                                                          ALDTNYCFSSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSK 60
                                                                                                                                                                                                                                                                                             86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               T: 460 Point San Bruno Blvd South San Francisco : California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94080
                                                                                                                                                                                                                                                                                                                                                                                                                 amino acid
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                                                                   Application US/08459214
                                                                                                                                                                                                                                                                                                                                                                                                                                    112 amino acids
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                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              patin (Genentech)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Janet E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             03-OCT-1985
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                                                                                                                                                                                                                                                                                                             78.9%;
76.8%;
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                                                                                                                                                                                                                                                                                               11;
                                                                                                                                                                                                                                                                                                             Score 500; DB 1; Pred. No. 5.2e-47;
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                                                                                                               APPLICANT: War, Lington
APPLICANT: War, Lington
APPLICANT: Cheung, David T.
TITLE OF INVENTION: Transforming Growth Factor B Fusion
TITLE OF INVENTION: Their Use in Wound Healing
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marchant & Gould
STREET: 11150 Santa Monica Boulevard, Suite 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 4.1. Application US/08789588
| Patent No. 5922846
| GENERAL INFORMATION:
| APPLICANT: Cerletti, Nico | APPLICANT: Cox, David | APPLICANT: Schmitz, Albert | APPLICANT: Schmitz, Albert | APPLICANT: Meyback, Bernd | TITLE OF INVENTION: Produced TGF-beta-like Proteins | UNDBER OF SEQUENCES: 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TIPE: FIDEN WISH
MEDIUM TIPE: FIDEN WISH
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILLING DATE:
FILLING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Sharp, Janice A.
REGISTRATION NUMBER: 34,051
REFRENCE/POCKET NUMBER: 30630-1US01
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E: Henry P. No. 5922846ak
520 White Plains Road, P.O. Box 2005
                                                Nimni, Marcel E.
Hall, Frederick L.
Tuan, Tai-Lan
                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 90025-3395
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : 310-445-1140
310-445-9031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : 112 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 310-445-9031 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein US-08-470-837-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS: ADDRESSE: Henry P. 1
                                                                                                                                                                                                                                                                                                                                   CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90025-3395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
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                                                   APPLICANT:
APPLICANT:
                                                                                                 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET:
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Nucleic Acid Encoding the Alpha or
Beta Chains of Inhibin and Method for Synthesizing Polypeptide
Using such Nucleic Acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 VLGLYNTLNPEASASPCCVPQDLEPLTILYYVGRTPKVEQLSNMVVKSCKCS 112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 78.9%; Score 500; DB 1; Length 112; Best Local Similarity 76.8%; Pred. No. 5.2e-47; Matches 86; Conservative 11; Mismatches 15; Indels
                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 0.2-JUN-1995
CLASSIFICATION NUMBER: 08/19792
FILING DATE: 17-FEB-1994
PRIOR APPLICATION NUMBER: 08/197792
FILING DATE: 17-FEB-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 0/9/58414
FILING DATE: 08-OCT-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 0/7/44207
FILING DATE: 12-AUG-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 0/9/58416
FILING DATE: 12-AUG-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 0/9/50729
FILING DATE: 05-JUL-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 0/9/527710
FILING DATE: 07-FEB-1986
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 0/9/527710
FILING DATE: 07-FEB-1986
PRIOR APPLICATION DATE: 0/9/527710
FILING DATE: 07-FEB-1986
PRIOR APPLICATION DATE: 0/9/527710
FILING DATE: 07-FEB-1985
ATTORNEY AGENT INFORMATION:
ANDER: 15-50-1
                                                                                                                  ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 297P2D6
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-470-837-30 ; Sequence 30, Application US/08470837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELERA: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 36:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 112 amino acids IYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Hasak, Janet E.
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      415/952-9881
                                                                      NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                      California
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TOPOLOGY: linear
US-08-459-214-36
                                                                                                                                                                                                                   USA
                                                                                                                                                                                                                                    ZIP: 94080
                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                        STATE:
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CITY: Tarrytown

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1 ALDINYCESSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDFQYSK 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: No. 6057430el process for the production of TITLE OF INVENTION: biologically active dimeric protein NUMBER OF SEQUENCES: 14
COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 VLGLYNTLNPEASASPCCVPQDLEPLTILYYVGRTPKVEQLSNMVVKSCKCS 112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               78.9%; Score 500; DB 2; Length 112; 76.8%; Pred. No. 5.2e-47; ative 11; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 112;
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATE: PSYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Score 500; DB 3;
; Pred. No. 5.2e-47;
11; Mismatches 15;
                                                                                                                                                             CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/860,704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/123,233
                                                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/410,57:
                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: BROWN, THERESA A.
REGISTRATION NUMBER: 32,547
REFERENCE/DOCKET NUMBER: P31
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-535-9001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2, Application US/09123233; Patent No. 6057430; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 619-535-8949
; INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: ; LENGTH: 112 anino acids ; TYPE: amino acid ; TOPOLOGY: linear US-08-410-573-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              78.9%;
76.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 78.9%
Best Local Similarity 76.8%
Matches 86; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : 112 amino acids
amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; MOLECULE TYPE: protein US-09-123-233-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 530
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Best Local Similarity
Matches 86; Conserv
                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-123-233-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: LOGAN, ANN
APPLICANT: BAIRD, ANDREW
TITLE OF INVENTION: METHONS OF INHIBITING OR ENHANCING SCAR
TITLE OF INVENTION: FORMATION IN THE CNS
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: PRETTY, SCHROEDER, BRUEGGEMANN & CLARK
STREET: 444 SO. FLOWER STREET, SUITE 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          78.9%; Score 500; DB 2; Length 112; 76.8%; Pred. No. 5.2e-47;
                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/789,588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 4-17861/+/Cont3 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                            PRICE APPLICATION DATA:
APPLICATION NUMBER: US 07/960,309
FILING DATE: 13-007-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/621,502
FILING DATE: 03-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9927546.5
FILING DATE: 06-DEC-1989
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                       CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/486,057
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/201,703
FILING DATE: 25-FEB-1994
                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1, Application US/08410573 Patent No. 5958411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: NO. 5922846ak, Henry P. REGISTRATION NUMBER: 33200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (908) 277-5110
TELEFAX: (908) 277-4306
INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acids
TYPE: amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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COUNTRY: UNITED STATES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; MOLECULE TYPE: protein US-08-789-588-41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
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STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
Matches 86; Conserv
                        X: U.S.A.
10591-9005
  New York
                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-410-573-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            78.9%; Score 500; DB 5; Length 112; 76.8%; Pred. No. 5.2e-47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 23, Application US/08481377
; Patent No. 5808007
; GENERAL INFORMATION:
; APPLICANT: JOHNS HOPKINS UNIVERSITY
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-3
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
; ADDRESSE: SPENSLEY HORN JUBAS & LUBITZ
STREET: LOS ANGELES
CITY: LOS ANGELES
STATE: CALIFORNIA
                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/03068
FILING DATE: 19930401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/481,377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15;
                   4370 LA JOLLA VILLAGE DRIVE, SUITE 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                     FP-LA 9589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: WETHERELL, JR. Ph.D., JOHN R. REGISTRATION NUMBER: 31,678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/00666
FILING DATE: 12-JAN-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 90067
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                            PC-DOS/MS-DOS
  CAMPBELL AND FLORES
                                                                                                                                                                                                                                                                                             CLASSIFICATION:
ATORNEY/AGENT INFORMATION:
NAME: CAMPBELL, CATHRYN A.
RECISTRATION NUMBER: 31.815
REFERENCE/DOCKET NUMBER: FP-LI
TELECHONICATION INFORMATION:
TELEPHONE: 619-535-9001
TELEPAX: 619-535-8949
                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 619-535-8949
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : 112 amino acids
AMINO ACID
                                                                                   UNITED STATES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      86; Conservative
                                                                 CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                         SAN DIEGO
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                                                                                                         92122
ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
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                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                               STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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                                                                                                                                                                                                                             APPLICANT: Erlander, Mark G.
APPLICANT: Huang, Shaoming
APPLICANT: Jackson, Michael A.
APPLICANT: Peterson, Per A.
TITLE OF INVENTION: PROTEIN GROWTH FACTOR FOR TREATING PROSTATE CANCER, AND RELATE
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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             61 VLGLYNTLNPEASASPCCVPQDLEPLTILYYVGRTPKVEQLSNMVVKSCKCS 112
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GENERAL INFORMATION:
APPLICANT: THE WHITTIER INSTITUTE FOR DIABETES
APPLICANT: AND ENDOCRINGLOGY
TITLE OF INVENTION: METHODS OF INHIBITING OR ENHANCING SCAR TITLE OF INVENTION: FORMATION IN THE CNS
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 78.9%; Score 500; DB 3; Length 112; Best Local Similarity 76.8%; Pred. No. 5.2e-47; Matches 86; Conservative 11; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE:
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Morrison, Alan J.
REGISTRATION NUMBER: 37,399
REFRENCE/DOCKET NUMBER: ORT-849
TELECOMMUNICATION INFORMATION:
TELEPHONE: 732-524-2808
                                                                                                                                                                Sequence 5, Application US/08927433 Patent No. 6107476 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Johnson & Johnson
STREET: One J & J Plaza
CITY: New Brunswick
STATE: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 732-524-2808 INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 112 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        amino acid
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                                                                                                                                            US-08-927-433-5
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                                                                                                                                                                                                                                                                                                                                                                                                        Length 114;
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                                                                                                                                                                                    Score 500; DB 2; Length 11:
Pred..No. 5.3e-47;
1; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: JOHNS HOPKINS UNIVERSITY
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-3
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: SPENSLEY HORN JUBAS & LUBITZ
STREET: 1880 CENTURY PARK EAST, FIFTH FLOOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/153,733A
                                                                                                                                                                                    Ouery Match 78.9%; Score 500; DB Best Local Similarity 76.8%; Pred. No. 5.3e-Matches 86; Conservative 11; Mismatches
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8-09-153-733A-23
Sequence 23, Application US/09153733A
Patent No. 6025475
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORIES AGENT INFORMATION:
NAME: WETHERELL, JR. Ph.D., JG
REGISTATION NUMBER: 31,678
REPERENCE/DOCKET NUMBER: FD227
TELECOMMUNICATION INFORMATION:
TELEFAX: (619) 455-5100
TELEFAX: (619) 455-5100
INFORMATION FOR SEQ ID NO: 23:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 114 amino acids
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Best Local Similarity 76.88
Matches 86; Conservative
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                                                             NAME/KEY: Protein
; LOCATION: 1.114
US-08-491-835-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: LOS ANGELES
STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IMMEDIATE SOURCE:
CLONE: TGF-beta 1
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  IMMEDIATE SOURCE:
CLONE: TGF-bet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS
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US-09-153-733A-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
                                                   FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 VLGLYNTLNPEASASPCCVPQDLEPLTILYYVGRTPKVEQLSNMVVKSCKCS 112
                                                                                                                                                                                                                                                                                                                                                                                                                                             78.9%; Score 500; DB 1; Length 114; 76.8%; Pred. No. 5.3e-47; ive 11; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 21, Application US/08491835
Patent No. 5821056
GENERAL INFORMATION:
APPLICANT: THE JOHNS HOPKINS UNIVERSITY
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-9
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTE: SUCO.

COMPUTE: FLODPY disk
COMPUTER: FLODPY disk
COMPUTER: IBM PC compatible
COMPUTER: TBM PC compatible
COMPUTER: TBM PC compatible
COMPUTER: DATE: PC-DOS/MS-DOS
SOFTWARR: PATE: PC-DOS/MS-DOS
SOFTWARR: PATE: DS-ORT-1995
FILING DATE: 23-ORT-1995
FILING DATE: 23-ORT-1995
FILING APPLICATION NUMBER: US-VOS94/00685
FILING DATE: 12-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: WETHERELI, Jr. Ph.D., John R.
REGISTRATION NUMBER: 31,678
FEFERENCE/DOCKET NUMBER: FD3288
TELECOMMUNICATION INFORMATION:
TOTAL COMPUTER: TOTAL COMPUTER: TD3288
TELECOMMUNICATION INFORMATION:
TOTAL COMPUTER: TOTAL COMPUTER: TD3288
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Spensley Horn Jubas & Lubitz
STREET: 1800 Century Park East, Suite 500
CITY: CITY: Callifornia
REFERENCE/DOCKET NUMBER: FD2279 PCT
              TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 455-5100
TELEPAX: (619) 455-5100
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 114 aniho acids
TYPE: amino acid
TYPE: amino acids
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TELEFAX: (619) 455-5110
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 114 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: protein
IMMEDIATE SOURCE:
CLONE: TGF-beta 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 86; Conserv
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90067
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                                                                                                                                                                                                                                                                                                                          ; NAME/KEY:
; LOCATION:
US-08-481-377-23
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                      3 ALDINYCFSSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSK 62
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1 ALDINYCFRNLEENCCVRPLYIDFRQDLGWKWVHEPKGYYANFCSGPCPYLRSADTTHST
                                                                                                     61 VLGLYNTLNPEASASPCCVPQDLEPLTILYYVGRTPKVEQLSNMVVKSCKCS 112
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                                                                                                                                                                                                                     Sequence 21, Application US/08946092A
Patent No. 6030617
GENERAL INFORMATION:
APPLICANT: THE JOHNS HOPKINS UNIVERSITY
TITLE OF INVERTION: GROWTH DIFFERENTIATION FACTOR-9
NUMBER OF SEQUENCES: 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Spensley Horn Jubas & Lubitz
STREET: 1880 Century Park East, Suite 500
STREET: Los Angeles
STATE: California
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Wetherell, Jr. Ph.D., John R. REGISTRATION NUMBER: 31,678
REFERENCE/DOCKET NUMBER: FD3288
TELECOMNINICATION INFORMATION:
TELEPHONE: (619) 455-5100
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 114 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/946,092A
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/491,835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: ATTORNEY/AGENT INFORMATION:
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Matches 86; Conservative
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IMMEDIATE SOURCE:
CLONE: TGF-betal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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APPLICANT: Cunningham, No. 6204047een
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-10
NUMBER OF SEQUENCES: 26
                                                                    APPLICANT: THE JOHNS HOPKINS UNIVERSITY TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-9 NUMBER OF SEQUENCES: 26 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                ADDRESSEE: Spensiey Horn Jubas & Lubitz
STREET: 1880 Century Park East, Suite 500
CITY: Los Angeles
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NOMBER:
APPLICATION NOMBER: US/08/491,835
FILING DATE: 12-704.1994
APPLICATION NUMBER: PCT/US94/00685
FILING DATE: 12-704.1994
ATTORNEY/AGENT INFORMATION:
NAME: Wetherell, Jr. Ph.D., John R.
REGISTRATION UNMBER: 31,678
                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/09/172,062
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Sequence 21, Application US/09172062 Patent No. 6191261
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: FD32
TELECOMMUNICATION INFORMATION:
TELERAN: (619) 455-5100
TELERAX: (619) 455-5110
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 76.8%
Matches 86; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein
IMMEDIATE SOURCE:
CLONE: TGF-betal
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                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE
                                                                                                                                                                                                                                                                                           90067
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APPLICATION NUMBER: PCT/US94/00666
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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TELEFAX: (619) 455-5110
INFORMATION FOR SEQ ID NO: 21:
                        12-JAN-1994
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Best Local Similarity 76.8%
Matches 86; Conservative
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                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein
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CLONE: TGF-beta 1
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                                              CLASSIFICATION:
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PCT-US94-00666-23
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PCT-US94-00685-21
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Query Match

78.9%; Score 500; DB 4; Length 114;
Best Local Similarity 76.8%; Pred. No. 5.3e-47;
Matches 86; Conservative 11; Mismatches 15; Indels
                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppd disk
COMPUTER: IBM PC compatible
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/624,635
FILING DATE: 16-AUG-1996
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/134,078
FILING DATE: 08-0CT-1993
ATTORNEY/AGENT INFORMATION:
NAME: Wetherell, Jr., Ph.D., John R.,
REFERENCE/DOCKET NUMBER: PD-3054
TELECOMMUNICATION INFORMATION:
TELECHONE: (619) 455-5110
INFORMATION FOR SEQ ID NO: 22:
SEQUIENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: JOHNS HOPKINS UNIVERSITY
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-3
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: SPENSLEY HORN JUBAS & LUBITZ
STREET: 1880 CENTURY PARK EAST, FIFTH FLOOR
CITY: LOS ANGELES
STATE: CALIFORNIA
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
3: Spensley Horn Jubas & Lubitz
1880 Century Park East, Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PCT-US94-00666-23; Sequence 23, Application PC/TUS9400666; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 114 amino acids
TYPE: amino acid
STRANDEDNESS: single
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; NAME/KEY: Protein
; LOCATION: 1..114
US-08-624-635-22
                                     CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IMMEDIATE SOURCE:
CLONE: TGF-beta-1
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MOLECULE TYPE:
  ADDRESSEE:
                                                                                 COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               78.9%; Score 500; DB 5; Length 114; 76.8%; Pred. No. 5.3e-47; Live 11; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 21. Application PC/TUS9400685
GENERAL INFORMATION:
APPLICANT: THE JOHNS HOPKINS UNIVERSITY
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-9
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/00685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Spensley Horn Jubas & Lubitz
STREET: 1880 Century Park East, Suite 500
CITY: Los Angeles
STATE: Callfornia
                                                                     REFERENCE/DOCKET NUMBER: FD2279 PCT TELECOMMUNICATION INFORMATION: FELECOMMUNICATION INFORMATION: FOR SEQ ID NO: 23: SEQUENCE CHARACTERISTICS: LENGTH: 114 amino acids TYPE: amino acids TYPE: amino acids modernow.
ATTORNEY AGENT INFORMATION:
NAME: WETHERELL, JR. Ph.D., JOHN R.
REGISTRATION NUMBER: 31,678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: WECHERELL, Jr. Ph.D., John R.
REGISTRATION NUMBER: 31,678
REFERENCE/DOCKET NUMBER: FD3288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 UMBER: PCT/US94/00685
12-JAN-1994
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US-08-455-559-25
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                                                                                                                                                                                                                                 3 ALDINYCESSTEKNCCVRQLYIDFRKDLGWKWIHEPRGYHANFCLGBCPYIWSLDTQYSK 62
                                                                                                                                                                                                                 1 ALDINYCFRNLEENCCVRPLYIDFRQDLGWKWVHEPKGYYANFCSGPCPYLRSADTTHST 60
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                                                                                                                                                                                                                                                                           61 VLGLYNTLNPEASASPCCVPQDLEPLTILYYVGRTPKVEQLSNMVVKSCKCS 112
                                                                                                                                                                                                                                                                                             Length 114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 78.9%; Score 500; DB 1; Length 115; Best Local Similarity 76.8%; Pred. No. 5.3e-47; Matches 86; Conservative 11; Mismatches 15; Indels
                                                                                                                                                                                    15; Indels
                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: PC_DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                      Score 500; DB 5;
Pred. No. 5.3e-47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Fish & Richardson
STREET: 4225 Executive Square, Suite 1400
                                                                                                                                                                                   11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGERT INFORMATION:
NAME: 1.15a A. Haile, Ph.D.
REGISTRATION NUMBER: 38,347
REFERENCE/POCKET NUMBER: 07265/082001
TELECOMMUNICATION: INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      UMBER: US/08/581,529B
15-APR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (619) 678-5070
TELEFAX: (619) 678-5070
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 115 amino acids
TYPE: amino acid
STRANDEDNESS: sinc.
TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                      78.9%;
76.8%;
                                                                                                                                                    Query Match 78.9°
Best Local Similarity 76.8°
Matches 86; Conservative
           MOLECULE TYPE: protein
IMMEDIATE SOURCE:
CLONE: TGF-betal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER:
FILING DATE: 15-APR
CLASSIFICATION: 536
                                                                       ) NAME/KEY: Protein
; LOCATION: 1..114
PCT-US94-00685-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; NAME/KEY: Protein
; LOCATION: 1..115
US-08-581-529B-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: La Jolla
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IMMEDIATE SOURCE:
CLONE: TGF-beta-1
linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    92037
TOPOLOGY:
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                                                            FEATURE
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4 ALDINYCESSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSK 63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 ALDINYCFSSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDIQYSK 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 VLGLYNTLNPEASASPCCVPQDLEPLTILYYVGRTPKVEQLSNMVVKSCKCS 112
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                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: LEE, SE-JIN
APPLICANT: HUYNH, THANH
TITLE OF SEQUENCES: 27
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: SPENSLEY HORN JUBAS & LUBITZ
STREET: 1880 CENTURY PARK EAST, FIFTH FLOOR
CITY: LOS ANGELES
STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US. 08/455,559
FILING DATE: 31-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/003,144
FILING DATE: 12-JAN-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: WETHERELL, JR. PH.D., JOHN R. REGISTRATION NUMBER: 31,678
REFERENCE/POCKET NUMBER: PD2280
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/455-5110
TELEPRAX: 619-455-5110
                                                                                                                                                                                                                      ; Sequence 25, Application US/08455559; Patent No. 5801014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : 115 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 619-455-5110
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein
IMMEDIATE SOURCE:
CLONE: TGF-beta-1
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4225 Executive Square, Suite 1400
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MEDIUM TYPE: Floppy disk
MEDIUM TYPE: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 78.9%
Best Local Similarity 76.8%
Matches 86; Conservative
                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IMMEDIATE SOURCE:
CLONE: TGF-beta-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
                    La Jolla
                                                           USA
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                                                       COUNTRY: U
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US-08-581-528A-19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 ALDTNYCFSSTEKNCCVRQLYIDFRKDLGWKWIHEPRGYHANFCLGPCPYIWSLDJQYSK 63
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Pred. No. 5.3e-47;
L; Mismatches 15; Indels
                                Sequence 29, Application US/08525596B
Patent No. 5827733
GENERAL INFORMATION, Thanh
APPLICANT: Huynh, Thanh
APPLICANT: Lee, Se-Jin
TITLE OF INVENTION: 3ROWTH DIFFERENTIATION FACTOR-8
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 19. Application US/08581528A
Patent No. 5986058
GENERAL INFORMATION:
APPLICANT: Lee, Se-Jin
APPLICANT: Huynh, Thanh
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-7
NUMBER OF SQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM COMPATIBLE
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: Windows95
SOFTWARE: FASIENG for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/525,596B
FILING DATE: 19-SEP-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/07762
FILING DATE: 08-JUL-1994
ATORNEY/AGENT INFORMATION:
NAME: Wetherell, Jr., Ph.D, John R.
REGISTRATION NUMBER: 31,678
REGISTRATION NUMBER: 31,678
REGISTRATION NUMBER: 07265/075001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-678-5070
                                                                                                                                                                                               ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    78.9%; Score 500; 76.8%; Pred. No. 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11;
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INFORMATION FOR SEQ ID NO: 29:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : 115 amino acids amino acid
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                                                                                                                                                                                                                                                                                                                                             Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: protein
IMMEDIATE SOURCE:
CLONE: TGF-beta-1
                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
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US-08-525-596B-29
RESULT 90
US-08-525-596B-29
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US-08-581-528A-19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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APPLICANT: Lee, Se-Jin
APPLICANT: Lee, Se-Jin
APPLICANT: Huynh, Thanh
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-6
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSE: Fish & Richardson
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
CITY: La Jolla
COUNTRY: USA
                                                                                                                                                                                                                                07265/081001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 19, Application US/09097616; Patent No. 6090563; GENERAL INFORMATION:
                                                                                                                                                                                                                            REFERENCE DOCKET NUMBER: 07
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
TELEFAX: 619/678-5099
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                      LENGTH: 115 amino acids TYPE: amino acid
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Gaps

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1 ALDINYCFRNLEENCCVRPLYIDFRQDLGWKWVHEPKGYYANFCSGPCPYLRSADTTHST 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 VLGLYNTLNPEASASPCCVPQDLEPLTILYYVGRTPKVEQLSNMVVKSCKCS 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    78.9%; Score 500; DB 3; Length 115; 76.8%; Pred. No. 5.3e-47; ive 11; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Lee, Se-Jin
APPLICANT: Huynh, Thanh
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-5
WUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: La Jolla
CITY: La Jolla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFWARE: FastSED for Windows Version 2.0
CURRENT APPLICATION DATA:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/455,559
FILING DATE: 31-MAY-1995
APPLICATION UNBER: 08/003,144
FILING DATE: 12-JAN-1993
ATTORNEY AGENT INFORMATION:
NAME: Lisa A. Haile, Ph.D.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07265/057001
                          07265/075003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 25, Application US/09145060
; Patent No. 6245896
                          REFERENCE/DOCKET NUMBER: 07
TELECOMMUNICATION INFORMATION:
TELEPHONE: 858-677-1456
TELEFAX: 858-677-1465
      REGISTRATION NUMBER: 38,347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
TELEFAX: 619/678-5099
INFORMATION FOR SEQ ID NO: 25:
                                                                                         TELEFAX: 858-677-1465
INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 115 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : 115 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 78.9°
Best Local Similarity 76.8°
Matches 86; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                        protein
                                                                                                                                                                                                                                            IMMEDIATE SOURCE:
CLONE: TGF-beta-1
                                                                                                                                                                                                                                                                                                             NAME/KEY: Protein
                                                                                                                                                                              amino acid
                                                                                                                                                                                                      linear
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                                                                                                                                                                              TYPE: amino a
TOPOLOGY: lin
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US-09-177-860A-29
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US-09-145-060-25
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                                                                                                                                                                                                                                                                                         FEATURE
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Sequence 29, Application US/09177860A
Patent No. 6096506
GENERAL INFORMATION:
APPLICANT: Huynh, Thanh
APPLICANT: Lee, Se-Jin
TITLE OF INVENTION:
UNMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 ALDTNYCFRNLEENCCVRPLYIDFRQDLGWKWVHEPKGYYANFCSGPCPYLRSADTTHST 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 ALDINYCESSTERNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSK 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 VLGLYNTLNPEASASPCCVPQDLEPLTILYYVGRTPKVEQLSNMVVKSCKCS 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           78.9%; Score 500; DB 3; Length 115; 76.8%; Pred. No. 5.3e-47; tive 11; Mismatches 15; Indels
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/097,616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: Diskette
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 08/525,596
FILING DATE: 19-SEP-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Gray Cary Ware & Freidenrich LLP STREET: 4365 Executive Drive, Suite 1600 CITY: San Diego STATE: CA
                                                                       FILING JULE.

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
TILING DATE: 15-APR-1996
ATTORNEY AGENT INFORMATION:
NAME: Lisa A. Haile, Ph.D.
REGISTRATION NUMBER: 38.347
REFERENCE/DOCKET NUMBER: 07265/082001
TELECOMMUNICATION INFORMATION:
TELEPANE: (619) 678-570
TELEPANE: (619) 678-509
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LIS amino acids
TYPE: amino acids
TYPE: amino acids
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Best Local Similarity 76.8
Matches 86; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: protein
IMMEDIATE SOURCE:
CLONE: TGF-beta-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 92121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION:
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                                                                                                                                                           Gaps
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                                                                                                                      Length 115;
                                                                                                Score 500; DB 4; Length 11. Pred, No. 5.3e-47;
                                                                                                                                                                                                                                                                                                                                                                                     Sequence 25, Application PC/TUS9400657
GENERAL INFORMATION:
APPLICANT: SE-JIN LEE
APPLICANT: HUYNH; THANH;
TITLE OF INFUNTION: GROWTH DIFFERENTIATION FACTOR-5
CORRESPONDENCE ADDRESS:
ADDRESSE: SPENSLEY HORN JUBAS & LUBITZ
STREET: 1880 CENTURY PARK EAST, FIFTH FLOOR
CITY: LOS ANGELES
STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE PATENTIAN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/00657
FILING DATE: 1/12/94
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: WETHERELL, JR. PH.D., JOHN R.
REGISTRATION NUMBER: 13,678
REFERENCE/DOCKET NUMBER: FD3256 CIP OF PD2280
TELECOMMULICATION INFORMATION:
TELECOMMULICATION INFORMATION:
TELEPHAN: 619/455-5110
INFORMATION POR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                     11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 90067
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                  78.98;
76.88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 115 amino acids
                                                                                                              Query Match 78.9 Best Local Similarity 76.8 Matches 86; Conservative
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein IMMEDIATE SOURCE: CLONE: TGF-beta-1
               ; IMMEDIATE SOURCE:
; CLONE: TGF-beta-1
US-09-145-060-25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
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F-US94-00657-25
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1 ALDINYCFRNLEENCCVRPLYIDFRQDLGWKWVHEPKGYYANFCSGPCPYLRSADTTHST 60
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61 VLGLYNTLNPEASASPCCVPQDLEPLTILYYVGRTPKVEQLSNMVVKSCKCS 112
                                                                                                                                                       Sequence 19, Application PC/TUS9407762
GENERAL INFORMATION:
APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-6
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 19, Application PC/TUS9407799
GENERAL INFORMATION:
APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-7
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             78.9%; Score 500; DB 5; Length 115; 76.8%; Pred. No. 5.3e-47; ive 11; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/07762
FILING DATE: 08-JUL-1994
                                                                                                                                                                                                                                                                                                           E: Spensley Horn Jubas & Lubitz
1880 Century Park East, Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Spensley Horn Jubas & Lubitz
STREET: 1880 Century Park East, Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY AGENT INFORMATION:
NAME: TUMARKIN, LISA A., PH.D.
REGISTRATION NUMBER: P.38,347
REFERENCE/DOCKET NUMBER: FD2349
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 455-5100
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 115 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                              STREET: 1880 Centu
CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: Protein
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Best Local Similarity
Matches 86; Conserv
                                                                                                                                                                                                                                                                                                        ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                          90067
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279 ALDTHYCFSSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSK 338
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 VLGLYNTLNPEASASPCCVPQDLEPLTILYYVGRTPKVEQLSNMVVKSCKCS 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             78.9%; Score 500; DB 1; Length 390; 76.8%; Pred. No. 2.3e-46; tive 11; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1; Application US/08132405
Patent No. 5409896
GENERAL INFORMATION:
APPLICANT: Annuan, Arthur J.
TITLE OF INVENTION: Method of Inducing Bone Growth Using
TITLE OF INVENTION: TGF-Beta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
                                                                                                             5624-159-999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patin (Geneticch)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/132,405
FILING DATE: 06-OCT-1993
CLASSIFFICATION NUMBER: 08/063841
FILING DATE: 18-WAY-1993
FRICKATION NUMBER: 07/790856
FILING DATE: 18-WAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/790856
FILING DATE: 12-NOV-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/401906
FILING DATE: 01-SEP-189
ATTORNEY/AGENT INFORMATION:
NAME: HASAK, JANGE E.
REGISTRATION NUMBER: 28,616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Method of Inducin
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   597D1C2
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OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                      REFERENCE DOCKET NUMBER: 562x
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
TELERAX: 212-869-9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
LENGTH: 390 amino acids
TYPE: AMINO ACID
                      CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MISROCK, S. LESLIE
REGISTRATION NUMBER: 18,872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 59
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 76.8%
Matches 86; Conservative
    19910314
                                                                                                                                                                                                                                                                                                                         , MOLECULE TYPE: protein US-07-669-171-2
                                                                                                                                                                                                                                                                                                            linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2, Application US/07669171
Patent No. 5304541
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: PURCHIO, ANTHONY F.
APPLICANT: MADISEN, LINDA
APPLICANT: MERWIN, JUNE RAE
TITLE OF INVENTION: TGF-bJ/D2: A NOVEL CHIMERIC TRANSFORMING
TITLE OF INVENTION: GROWTH FACTOR-BETA
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 78.9%; Score 500; DB 5; Length 115; Best Local Similarity 76.8%; Pred. No. 5.3e-47; Matches 86; Conservative 11; Mismatches 15; Indels
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ZIP: 10036
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC compatible
COMPUTER: 1BM PC compatible
COMPUTER: Patentin Release #1.0, Version #1.25
                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/07799
FILING DATE: 08-JUL-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: PENNIE & EDMONDS
STREET: 1155 AVENUE OF THE AMERICAS
                                                                                                                                                                                                                                              CLASSIFICATION:
CLASSIFICATION:
ATTORNEY AGENT INRORMATION:
NAME: TUMARKIN, LISA A., PH.D.
REGISTRATION NUMBER: P-234,8
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 455-5100
TELEPHONE: (619) 455-5100
TELEFAX: (619) 455-5110
TELEFAX: (11) 455-5110
SEQUENCE CHARACTERISTICS:
LENGTH: 115 amino acids
                                                                                                                                                                                                                                                                                                                                                  FD-2348
                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein
IMMEDIATE SOURCE:
CLONE: TGF-beta-1
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Los Angeles
California
Y: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: Protein
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                                                                9006
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PCT-US94-07799-19
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                                          COUNTRY:
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                      STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/08395939A
Patent No. 5604204
GENERAL INFORMATION:
APPLICANT: Ammann, Arthur J.
APPLICANT: Rudman, Christopher G.
TITLE OF INVENTION: TGF-BETA COMPOSITION FOR INDUCING BONE
TITLE OF INVENTION: GROWTH
                                                                                                                                                                                                          78.9%; Score 500; DB 1; Length 390; 76.8%; Pred. No. 2.3e-46; Live 11; Mismatches 15; Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk COMPUTER: IEM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: patin (Genericch)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/395,939A
FILING DATE: 27-FEB-1995
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28,616
BRR: P0597DIC2DI
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CLASSIFICATION: 514
PRIOR APPLICATION: 514
PRIOR APPLICATION DATA:
RILING DATE: 12-NOV-1993
PRIOR APPLICATION NUMBER: 08/132405
FILING DATE: 12-NOV-1993
PRIOR APPLICATION DATA: 08/663841
FILING DATE: 18-MAY-1993
PRIOR APPLICATION NUMBER: 07/790856
FILING DATE: 12-NOV-1991
PRIOR APPLICATION NUMBER: 07/790856
FILING DATE: 12-NOV-1991
PRIOR APPLICATION NUMBER: 07/401906
FILING DATE: 1-SEP-1989
ATTORNEY/AGENT INFORMATION:
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TELEPHONE: 415/225-1896
                                               ...
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TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ 1D NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 390 amino acids
TYPE: amino acid
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REGISTRATION NUMBER: 28,
REFERENCE/DOCKET NUMBER:
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Matches 86; Conservative
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech
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TOPOLOGY:
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279 ALDINYCESSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSK 338
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                                                                                          78.9%; Score 500; DB 1; Length 39076.8%; Pred. No. 2.38-46; Live 11; Mismatches 15; Indels
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US-08-395-939A-1
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Length 390;

Search completed: October 30, 2001, 08:53:20 Job time: 139 sec

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                                                                                 NOVEL PROCESS FOR THE PRODUCTION OF BIOLOGICALLY ACTIVE DIMERIC
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CIBA GEIGY AG (CH)
Other publication AU 3109595 960222
Location/Qualifiers
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    .339
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    /db_xref="taxon:32644"

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/note="Protein sequence
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Sequence 5 from Patent W09603433.
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Cerletti, N.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 339)
McMaster,G.K., Cox,D., Cerletti,N. and Kuhla,J.
Novel hybrid transforming growth factors
Patent: EP 0542679-A 3 19-MAY-1993;
CIBA-CBIGY AG
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/db_xref="taxon:9606"
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Sequence 5 from Patent WO9603432.
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TGF-beta3 coding region.
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07-MAR-1997

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RESULT A48553

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conflict with the

SOURCE Human placental and umbilical cord (cell line A673), cDNA to mRNA, from library lambda-gtl0.  ORGANISM Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  REFERENCE 1 (bases 1 to 25.9) AUTHORS ten Dijke, P., Hansen, P., Iwata, K.K., Pieler, C. and Foulkes, J.G.  TITLE Identification of another member of the transforming growth factor type beta gene family.  JOURNAL Proc. Natl. Acad. Sci. U.S.A. 85 (13), 4715-4719 (1988) MEDLINE 88263019 COMMENT Draft entry and computer-readable sequence [1] kindly submitted by proc. Draft entry and computer-readable sequence [1] kindly submitted by	FEATURES  FOURTH factor contains multiple growth inhibitory elements.  Location/Qualifiers  12529  AD_xref="taxon:9606"  AD_xref="taxon:9606"  Agene="TGFB3"  CDS  Gene="TGFB3"  Agene="TGFB3"  Agene"  Agene="TGFB3"  Agene"  Agene="TGFB3"  Agene"  A	/ ADD_XTEEF=71339523 / ADD_XTEEF=71339523 / ADD_XTEEF=71339523 / ADD_XTEEF=71339523 / ADD_XTEEF=7139523   ADD_XTEEF=714504   ADD_XTEEF=71450	IN Chromosome 14.  ITY Match 100.0%; Score 339; St. Local Similarity 100.0%; Pred. No. 2. Sches 339; Conservative 0; Mismatches	Oy 1 gctttggacaccaattactgcttccgcaacttggaggaaactgctgtgtgcgcccctc 60	Qy         121 gccaacttctgctcaggcccttgcccatacctccgcagtgcagacacaaccacagcacg 180	OY 241 caggacctggaccctgaccatcctgtactatgttgggaggaccccaaagtggagcag 300 	Oy 301 ctctccaacatggtggtgaagtcttgtaaatgtagctga 339
OY 181 gtgctgggactgtacaacactctgaaccttgcttgcttgc	PAT 07-0CT-19	AL Patent: US 5650494-A 3 22-JUL-1997; S	Local Similarity 100.0%; Pred. No. 2.7e-83; es 339; Conservative 0; Mismatches 0; Indels 1 gctttggacaccaattactgcttccgcaacttggaggagaactgctgtgtgcclillillillillillillillillillillillilli	Oy 61 tacattgacttccgacaggatctgggctggaagtgggtccatgaacctaagggctactat 120	Qy         181 gtgctgggactgtacaacactctgaaccctgaagcatctgccttgctgctgctgctgccc 240	Oy 301 ctctccaacatggtggaagtcttgtaaatgtagctga 339 	RESULT 8 HUMTGFB3A 2529 bp mRNA PRI 14-JAN-1995 LOCUS HUMARA PRI 14-JAN-1995 DEFINITION Human transforming growth factor-beta 3 (TGF-beta3) mRNA, complete cds. ACCESSION J03241 VERSION J03241.1 GI:339551 KEYWORDS transforming growth factor.

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TCCATGAACCTAAGGCTACTAT 1282
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DB 97; Length 2529;
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Best Local Similarity 99.7
Matches 338; Conservative
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/db_xref="G1:37096"
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                                                                                                                                                                                                                            Direct Submission
Submitted (23-MR-1989) Chen E.Y., Genentech Inc., 460 Pt. San Bubmitted (23-MR-1989) Chen E.Y., Genentech Inc., 460 Pt. San Bruno Blvd., San Francisco, CA 94080, USA
2 (bases 1 to 2574)
Derynck,R., Lindquist,P.B., Lee,A., Wen,D., Tamm,J., Graycar,J.L., Rhee,L., Mason,A.J., Miller,D.A., Coffey,R.J., Moses,H.L. and Chen, B.Y.
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                                                                                                                                              Euteleostomi;
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X14149
X14149.1 GI:37095
growth factor; transforming growth factor; transforming growth
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2574)
                                                                                                                                                                                                                                                                                                                                                                   A new type of transforming growth factor-beta, TGF-beta 3
EMBO J. 7 (12), 3737-3743 (1988)
89091120
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/cell_line="A172 glioblastoma"
254. 1492
/note="TGF-beta 3 (AA 1-412)"
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100.0%; Pred. No. 2.1e-83;
ive 0; Mismatches 0;
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/db_xref="taxon:9606"
/chromosome="14q24"
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Matches 339; Conservative
                                                                       factor-beta 3.
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Marda,K.K., Gold,L.I. and Stephenson,J.R.
Tissue-derived tumor growth inhibitors, methods of
uses thereof
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                                                                                              Unclassified.

1 (bases 1 to 1899)

1 (bases 1 to 1899)

Nucleic acid encoding TGF. beta. and its uses Patent: US 4886747-A 11 12-DEC-1989;
Genentech, Inc.;cco, CA
  PAT
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Pred. No. 6e-83;
0; Mismatches 1;
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103320 1899 bp ss-DNA
Sequence 11 from Patent US 4886747.
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Sequence 2 from Patent EP 0267463
105432
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425 c 452 g
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137 c 129 q
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ORIGIN

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LEISIHCPCHTFQPNGDILENIQEVMEIKFKGVDSEDDPGRGDLGRLKKKKEHSPHLI
LMMIPPDRLDNPGLGAQRKKRALDTNYCFRNLEENCCVRPLYIDFRQDLGWKWVHEPK
GYYANFCSGPCPYLRSADTTHSSVLGLYNTLNPEASASPCCVPQDLEPLTILXYVGRT
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1 (bases 1 to 336)

McMaster,G.K., Cox,D., Cerletti,N. and Kuhla,J.

Novel hybrid transforming growth factors

Patent: EP 0542679-A 5 19-MAY-1993;

CIBA-GEIGY AG
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                                                                                                                     Score 302.2; DB 7;
Pred. No. 3.1e-73;
0; Mismatches 23;
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Pred. No. 7.7e-
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/organism="Homo sapiens"
/db_xref="taxon:9606"
a 109 c 86 g 6
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TGF-betal(44/45)beta3 hybrid
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ilarity 93.2%;
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/note="Protein sequence is in conflict with the conceptual
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SGPCPYLRSADTTHSTVLGLYNTLNPEASASPCCVPQDLEPLTILYYVGRTPKVEQLS
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                                                                                                                                                                                                                                                                                                                                                                          /organism="unidentified"
/db_xref="taxon:32644"
1. .132
/product="N-TERMINAL 44 AMINO ACIDS OF HUMAN TGF-BETAl"
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1 gctttggacaccaattactgcttccgcaacttggaggagaactgctgtgtgcgcccctc
                    121 GCCAACTTCTGCTCAGGCCCTTGCCCATACCTCCGCAGTGCAGACACACAACCCACAGGACG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="HYBRID TGF-BETA NAMED TGF-BETAL-3"
/protein_id="CAA03116.1"
/db_xref="GI:2302326"
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                                                                                                                         PRODUCTION OF
                                                                                                                                                                                                                                                                                                                                              Other publication AU 3109595 960222
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                          Patent: WO 9603432-A 7 08-FEB-1996;
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Sequence 7 from Patent WO9603432.
A48555
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109 c 86 g 6
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Cerletti, N.
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/translation="ALDTNYCFSSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Protein sequence is in conflict with the conceptual
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                133. .336
/product="C-TERMINAL 68 AMINO ACIDS OF HUMAN TGF-BETA3"
109 c 86 g 66 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="N-TERMINAL 44 AMINO ACIDS OF HUMAN TGF-BETAl"
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                                                                                                                                                                                                                                                                                                                                                                                                                                              NEW PROCESS FOR THE PRODUCTION OF BIOLOGICALLY ACTIVE PROTEIN Patent: WO 9603433-A 7 08-FEB-1996; CIBA GEIGY AG (CH) Other publication AU 3109695 960222.
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                                        caggacctggagccctgaccatcctgtactatgttgggaggaccccaaagtggagcag
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/prodonc="HYRBRID TGF-BETA NAMED TGF-BETA1-3"
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                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="unidentified"
/db_xref="taxon:32644"
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A48569
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Cerletti, N.
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Matches 312; Conserv
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SKRTEQRIELFOILRPDEHTAKQRYIGGKNLPTRGTAEMLSRESN
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EPKGYYANFCSGPCPYLRSSDTTHSTVLGLYNTLNPEASASPCCVPQDLEDITILXYV
lung fibroblasts. Transforming growth factor-beta 3
J. Biol. Chem. 270 (6), 2722-2728 (1995)
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                                                                                                                        Submitted (16-NOV-1993) M. Post, The Hospital for Sick Children, Paediatrics & Research Institute, 555 University Avenue, Toronto, Ontario M5G 1X8, Canada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1359 TACATTGACTTCCGGCAGGATCTAGGCTGGAAATGGGTCCACGAACCTAAGGGTTACTAT 1418
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                                                                                                                                                                                                                          /strain="Wister"
/db_xref="taxon:10116"
/clone="clones Fib12N1, TGF18 and TGF5' 3-3"
/clone_lib="glucocrticoid treated fetal rat lung fibroblast library"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   241 caggacctggagccctgaccatcctgtactatgttgggaggaccccaaagtggagcag
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Pred. No. 5.1e-71;
0; Mismatches 28; Indels 0;
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                                                                                                                                                                                                            /organism="Rattus norvegicus"
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/dev_stage="day 20 fetus"
399. 1637
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ilarity 91.7%;
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Wang,J., Kuliszewski,M., Yee,W., Sedlackova,L., Xu,J., Tseu,I. and
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Rodentia; Sciurognathi; Muridae; Murinae;
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Rattus norvegicus Wistar transforming growth factor beta-3 mRNA,
complete cds.
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0; Mismatches 26; Indels
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   1 (bases 1 to 1981)
Derynck, R.M.A. and Goeddel, D.V.
Nucleic acid encoding TGF-.beta. and
Patent: US 4886747-A 10 12-DEC-1989,
                                                                                                                                                                                                                                                                                                                                                                                                                    389
                                                                                                                       103319 1981 bp ss-DNA
Sequence 10 from Patent US 4886747.
103319
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Location/Qualifiers
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Best Local Similarity 92.3%;
Matches 313; Conservative
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Mammalia; Eutheria;
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WIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Tel: (301) 496-1550
Tissue Procurement: Gilbert Smith, Ph.D.
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.AG. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: http://www-shgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Clone distribution: MGC clone distribution information can be found through the I.M. A.G. E. Consortium/Link at: http://image.llnl.gov Series: IRAK Plate: 8 Row f Column: 13.

Location/Qualifiers
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 2164)
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/protein_id="AAH05513.1"
/db_xref="GI:13529608"
                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
Submitted (27-MAR-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              812 TATATTGACTTCCGGCAGGATCTAGGCTGGAAATGGGTCCACGAACCTAAGGGTTACTAT
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/clone="IMAGE:3492763"
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beta-3 (TGF-beta-3) precursor and the comparative expression of TGF-beta-3 and TGF-beta-1 messenger RNA in murine embryos and adult
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ILSKIALTSPPEPSYWTHYPYQVLALINIATISLEEMIGEREEGCTQFTSEEYTYRE
IHKFDMIQGLABHREAVCPRGITSKVFRFRYSSVERNGTMLFRAEFRYLRVPRPSSK
RTEQRIELFQILRPDEHIAKQRYIGGKNLPTRGTAEWLSFDVTDTVREWLLRRESNLG
ILEISIHCPGTFTQPNGDILENVHEVMEYWTRTRGTAEWLSFDVTDTVREWLINPHL
ILMAIPPHRLDSPGGGSQNTKRALDMYCFRILEENCCVRPLYIDFRQDLGWKWVHEP
KGYYANFCSGPOPYIGNTYGLINTLANFAENGENCOVRPLYIDFRGDLGWKWVHEP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
                                                                                                  991
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//note="transforming growth factor beta-3 (TGF beta-3)
precursor (start site 611 could be 368 or 477)"
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                    241 caggacctggagccctgaccatcctgtactatgttgggaggaccccaaagtggagcag
    gtgctgggactgtacaacactctgaaccctgaagcatctgcctcgccttgctgcgtgccc
                                                                                                                                                                                                                                                                                                             mouse transforming growth factor beta-3 mRNA, complete cds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 (bases 1 to 2879)
Miller, D.A., Lee, A., Matsui, Y., Chen, E.Y., Moses, H.L. and
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/note="transforming growth factor beta-3"
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Pred. No. 3.8e-70;
                                                                                                                                                                                                                                                                                                                                                                   transforming growth factor.
Mouse cell line AKR-2B, cDNA to mRNA.
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/db_xref="G1:201950"
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/organism="Mus
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91.2%;
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90190650
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ACCESSION A48557 VERSION KEYWORDS SOURCE SOURCE ORGANISM unidentified. ORGANISM unclassified.  REFERENCE 1 (bases 1 to 336) AUTHORS Carletti,N. TITLE NOVEL PROCESS FOR THE PRODUCTION OF BIOLOGICALLY ACTIVE DIMERIC PROTEI JOURNAL Patent: WO 9603432-A 9 08-FEB-1996; COMMENT COMME	eptide //db  //db  //tra //cc //pr //pr //pr //pr //pr //pr //pr	attactgcttccgcaacttggi 	RESULT 22 A48571 LOCUS DA9571 LOCUS DEFINITION Sequence 9 from Patent W09603433. ACCESSION A48571 VERSION VERSION A48571 VERYWORDS SOURCE Unidentified ORGANISM unidentified
	RESULT 20 A23757 A23757 A23757 A23757 BEFINITION TOFF-beta2(44/45)beta3 hybrid coding region. ACCESSION VERSION A23757.1 GI:825591 VERSION A23757.1 GI:825591 Numan. OKGANISM Homo sapiens Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. REFERENCE AUTHORS MCMASter, G.K., Cox, D., Cerletti, N. and Kuhla, J. TITLE NOVAL hybrid transforming growth factors JOURNAL Patent: EP 0542679-A 7 19-MAY-1993; CLOCATION/Qualifiers LOCATION/Qualifiers ADDARE COUNT ADDARE COUNT ALSO A COMMINISM LOCATION/Qualifiers ADDARE COUNT ADDARE COUNT ADDARE COUNT ADDARE COUNT ASSOURCE ASSOUR	Query Match Best Local Similarity Best Local	Oy 301 ctctccaacatggtggtgaagtcttgtaaatgtagc 336

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human.
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                                                                                                                                                                                                                                   /product="HYBRID TGF-BETA2-3"
/protein_id="CAA03124.1"
/db_xref="G1:2302342"
/translation="ALDAAYCFRNVQDNCCLRPLYIDFKRDLGWKWIHEPKGYNANFC
SGPCPYLRSADTTHSTVLGLYNTLNPEASASPCCVPQDLEPLTILYYVGRTPKVEQLS
NMVVKSCKCS"
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Chicken transforming growth factor beta (TGF-beta-3) mRNA, complete

    336
/note="Protein sequence is in conflict with the conceptual

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1 (bases 1 to 2187)
Jakowlew, S. B., Dillard, P. J., Kondaiah, P., Sporn, M. B. and
                                                                                                                                                                                                                                                                                                                           133. .336
/product="C-TERMINAL 68 AMINO ACIDS OF HUMAN TGF-BETA3"
94 c 84 g 77 t

    .132
'product="N-TERMINAL 44 AMINO ACIDS OF HUMAN TGF-BETA2"

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                                      NEW PROCESS FOR THE PRODUCTION OF BIOLOGICALLY ACTIVE PROTEIN PATENT: WO 9603433-A 9 08-FEB-1996; CIBA GEIGY AG (CH) Other publication AU 3109695 960222. Location/Qualifiers
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Pred. No. 4.3e-66;
0; Mismatches 37; Indels
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Chicken embryo chondrocyte, cDNA to mRNA.
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                                                                                                                                       /db_xref="taxon:32644"
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89.0%;
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             (bases 1 to 336)
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nes 299; Conservative
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Cerletti,N.
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/ CPCOTE 10.1d="AAA49089.1"

/BD xref="G1:212759"

/db_xref="G1:212759"

/db_xref="G1:21759"

/db_xref
Roberts, A.B. Complementary deoxyribonucleic acid cloning of a novel transforming growth factor-beta messenger ribonucleic acid from chick embryo
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/note="transforming growth factor beta signal peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                    /note="transforming growth factor beta precursor"
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/organism="Gallus gallus"
/db_xref="taxon:9031"
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Pred. No. 2.2
                                                                                                            chondrocytes
Mol. Endocrinol. 2, 747-755 (1988)
89096966
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40. .93
/note="transforming
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ilarity 87.3%;
Conservative
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/codon_start=1
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    .336
/note="Protein sequence is in conflict with the conceptual

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1. .336
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                                                    caggacctggagccctgaccatcctgtactatgttgggaggacccccaaagtggagcag 300
                                                                                                                                                                                                                                       61 tacattgacttccgacaggatctgggctggaagtgggtccatgaacctaagggctactat 120
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               gecaacttetgeteaggecettgeceatacetecgeagtgeagacacaacceaggeagg
                                                                                                                                                                                 getttggacaccaattactgettccgcaacttggaggagaactgetgtgtgcgcccctc
                                                                                                                                                                    gtgctgggactgtacaacactctgaaccctgaagcatctgcctcgccttgctgcgtgccc
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90 t
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82.1%; Pred. No. 6.5e-56;
Live 0; Mismatches 60; Indels
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                                                                                                                                                                                                                                                                                             Patent: WO 9603432-A 11 08-FEB-1996;
CIBA GEIGY AG (CH)
Other publication AU 3109595 960222.
                                                                                                                                                                                                                                                                                                                                                                            A48559 336 bp DNA
Sequence 11 from Patent W09603432.
A48559.1 GI:2302329
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/db_xref="taxon:32644"
1. 132
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87 c 71 g 9
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        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

[ (bases 1 to 336)

McMaster,G.K., Cox,D., Cerletti,N. and Kuhla,J.

Novel; hybrid transforming growth factors

Patent: EP 0542679-A 8 19-MAY-1993;

CIBA-GEIGY AG
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/organism="Homo sapiens"
/db_xref="taxon:9606"
a 109 c 98 g 6
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TGF-BETA2"

OY 181 gtgctggg; Db 181 GTCCTGAGG OY 241 Caggacct; Db 241 CAAGATTT OY 301 CtCtCaac OY 301 CTTCTAAC OY 301 CTTCTAAC AF152592 LOCUS DEFINITION CAPPED		P-1031: SOURCE gene CDS	BASE COUNT 52 ORIGIN	Query Match Best Local Simila Matches 230; Cc Qy 34 gaggagaac Qy 164 tgggtccat Qy 94 tgggtccat Cy 94 tgggtccat Db 61 TGGGTCAT Cy 154 cgcagtgca
	RESULT 27 A48573 A48573 A48573 A48573 A48573 A48573 ACCESSION A48573 A48	mat_peptide /db_xxel="taxon:32644"  mat_peptide /db_xxel="taxon:32644"  CDS /product="N-TERMINAL 44 AMINO ACIDS OF HUMAN TGF-BETA3"  1. :336	3336 roduct-"C-TERMINAL 68 AMINO AC 87 c 71 g 90 t	Query Match         70.8%;         Score 240;         DB 9;         Length 336;           Best Local Similarity 82.1%;         Pred. No. 6.5e-56;         Additional Similarity 82.1%;         Pred. No. 6.5e-56;           Matches 276;         Conservative 0;         Mismatches 60;         Indels 0;         Gaps 0;           QY         1 gctttggacaccaattactgcttccgcaacttgggagaacttggggaacttggggaacttggggaacttggggaacttgggaacttgggaacttgggaacttgggaacttgggaacttgggaacttgggaacttgggaacttgggaacttgggaacttgggaacttgggaacttgggaagtgggaacttgggaacttgggaacttgggaagtgggaacttggaacttgaacttcaactccgaacttcaactc

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TTHSTYLGLYTRINBASASPCCVPQDLEPLFILYTV"
84 c 57 g 51 t
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dae; Odocoileinae; Capreolus.
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ttion of growth factors in the testis of roe deer (Capreolus colus)
Reprod. Sci. 64 (1-2), 65-75 (2000)
2592 244 bp mRNA MAM 28-MAR-2001 solus capreolus transforming growth factor beta 3 (TGF-b3) partial cds.
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/db_xref="taxon:9858"
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<1. >244
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<1. .>244
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/codon_start=1
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X12373.1 GI:63808
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/translation="MPPSGLRLLPLLPLLWLLVLPGRPAAGLSTCKTIDMELVKRK
RIEARGGLISKLRRASPPSGGDVPPGPLPENTALYNSTRDRYAGESYEPEPERAD
RYAKEVTRVLLGSGNOIVPRGKTPHSLYMLFNTSELREAVPEPVLLSRAELRLRLR
KLKVRDGHVELYQKYSNOSWRYLSNRLAPSDSPEWLSFDYTGVWRQWLTRREAIEGFR
LSAHCSCDSKDNTLHVEINGFNSGRRGDLATHGMNRPFLLLMATPLERRAQHLHSSRH
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QYSKVLALYNQHNPGASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS"
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Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
1 (bases 1 to 1605)
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                              121 CGCAGCTCAGACACACACACACAGCACGGTGCTGGGCCTGTACAACACCCTGAACCCTGAA 180
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404. .1576
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/note="pot. N-glycosylation site"
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/note="pot. N-glycosylation site"
1238. .1573
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Sequence of the porcine transforming gr
Nucleic Acids Res. 15 (7), 3187 (1987)
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572 c 437 g 298
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/db_xref="G1:2130"
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/organism="Sus scrofa"
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Best Local Similarity 76.1%;
Matches 258; Conservative (
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HRRALDTNYCFSSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLD
TQYSKVLALYYQHNPGASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS"
1284. . 1619
/gene="TGF-beta 1"
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/protein_id="CAA30933.1"
/protein_id="CAA30933.1"
/db_xref="SWISS-PROT:P07200"
/db_xref="SWISS-PROT:P07200"
/translation="MPPSGPGLLPLLPLLWLIPGRPAAGLSTCKTIDMELVKRK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YYAKEVTRVLAVVESGNQIYDKFKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLLRL
KLKVEQHVELYQKYSNDSWGYLSNRLLAPSDSPEWLSFDVTGVVRQWLTRREAIEGFR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
Submitted (14-JUL-1988) Jakowlew S.B., National Institute of health, National Cancer Institute, Laboratory of Chemoprevention, Building 41, Room B902, Bethesda, Maryland 20892, USA 2 (bases 1 to 1750)
2 (bases 1 to 1750)
2 Natowlew, S.B., Dillard, P.J., Sporn, M.B. and Roberts, A.B.
Nucleotide sequence of chicken transforming growth factor-beta 1 (TGF-beta 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The submitters believe that the chicken cDNA library was contaminated with porcine cDNA, and that the sequence is infact porcine TGF-beta-1.

Location/Qualifiers
Gaps
                                                                                                                                                                                                                                                                                                                                                                         AMM 27-MAR-1996 MRNA MAM 27-MAR-1996 PROTAINE for transforming growth factor-beta 1.
                                                                             241 caggacctggagccctgaccatcctgtactatgttgggaggacccccaaagtggagcag
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Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae;
1 (bases 1 to 1750)
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Pred. No. 1.5e-47;
0; Mismatches 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic Acids Res. 16 (17), 8730 (1988)
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/organism="Sus scrofa"
/strain="white leghorn"
/db_xref="taxon:9823"
/cell_type="chondrocyte"
/clone="pTGFB-ChX119"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       transforming growth factor-beta 1.
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/gene="TGF-beta 1"
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/gene="TGF-beta 1"
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Best Local Similarity 76.1%;
Matches 258; Conservative (
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Query Match Local Best Loca Matches source RESULT 32 OCAF000133 DEFINITION 241 ORGANISM BASE COUNT ORIGIN 121 181 301 AUTHORS TITLE JOURNAL REFERENCE 61 ACCESSION VERSION KEYWORDS SOURCE REFERENCE AUTHORS JOURNAL FEATURES CDS TITLE rocus qq q g ò Ω g Ω Pp οy δ KLKVEQHVELYQXYSNISWRYLSNRLLAPSDSPEWLSFDYTGVYRQWLTRREAIEGFR
LSAHCSCDSRDNTLHYEINGFNSGRRGDLATIHGMNRPFLLLMATPLERAQHLHSSRH
RSAHCSCDSSCDNTLHYEINGFNSGRRGDLATIHGMNRPFLLLMATPLERAQHLHSSRH
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3186. 3191 /translation="MPPSGLRLLPLLPLLWLLVLTPGRPAAGLSTCKTIDMELVKRK RIEAIRGQILSKLRLASPPSQGDVPPGPLPEAVLALYNSTRDRVAGESVEPEPEAD YYAKEVTRVLMVESGNQIYDKFKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLLRL Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

( pases 1 to 3206)

Kondaiah,P., van Obbershen-Schilling,E., Ludwig,R.L., Dhar,R.,
Sporn,M.B. and Roberts,A.B.

CDNA cloning of porcine transforming growth factor-beta 1 mRNAs.
Evidence for alternate splicing and polyadenylation
J. Biol. Chem. 263 (34), 18313-18317 (1988) PIGTGFB1A 3206 bp mRNA MAM 31-MAR-1995 Sus scrofa transforming growth factor beta-1 mRNA, complete cds. 1343 1524 CAGGCGCTGGAGCCACTGCCCATCGTGTACGTGGGCCGCAAGCCCAAGGTGGAGCAG 1583 180 9 getttggaeaccaattactgettcegeaacttggaggagaactgetgtgtgegeecete 1284 GCCCTGGATACCAACTACTGCTTCAGGTCCACGGAGAAGAACTGCTGCGGGGGGCTC 241 caggacctggagccctgaccatcctgtactatgttgggaggacccccaaagtggagcag gccaacttctgctcaggcccttgcccatacctccgcagtgcagacacaacccacagcacg On Apr 1, 1995 this sequence version replaced gi:341017. Location/Qualifiers /product="transforming growth factor-beta-1" /protein\_id="AAAA64616.1" /db\_xref="GI:755045" /strain="miniature swine" /db\_xref="taxon:9823" /cell\_type="peripheral blood lymphocyte" 906, 3191 CDNA to mRNA. 301 ctctccaacatggtggtggaagtcttgtaaatgtagctga 339 u transforming growth factor-beta-1. Sus scrofa (strain miniature swine) Sus scrofa 596 /organism="Sus scrofa" 906. .2078 /gene="TGF-beta-1" /gene="TGF-beta-1" 906. .2078 /gene="TGF-beta-1" 3206 /gene="TGF-beta-1" 1041 c 924 g /codon\_start=1 M23703.1 GI:755044 1. .3206 ಹ 645 polyA\_signal polyA\_site ACCESSION VERSION KEYWORDS SOURCE ORGANISM LOCUS DEFINITION source RESULT 31 PIGTGFBIA Н BASE COUNT REFERENCE AUTHORS 121 MEDLINE gene JOURNAL cdsFEATURES TITLE COMMENT ORIGIN qq g 셤 g δ g Ω g οy δ ò

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LGPCPYIWSLDTQYSKVLALYNQHNPGASAAPCCVPQALEPLPIVYYVGRKPKVEQLS
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
1 (bases 1 to 319)
Taylor, T.K., James, E.R., McGonigle, S. and Yoho, E.R.
Rabbit transforming growth factor beta-1 active region
Unpublished
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                                                                                                                                                                                                                                                          1919
                                                                                                                                                                                                                                                                                                               1800 TACATTGACTTCCGGAAGGACCTGGGCTGGAAGTGGATTCATGAACCCAAGGCTACCAT 1859
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                                     Gaps
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Oryccolagus cuniculus transforming growth factor beta-1 mRNA,
partial cds.
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 Length 3206;
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/product="transforming growth factor beta-1"
/protein_id="AbB53806.1"
/db_xref="G1:2072532"
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Submitted (16-APR-1997) Ophthalmology, Med.Univ. S. Avenue, Charleston, SC 29464, USA
Location/Qualifiers
                                     Indels
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Pred. No. 1.4e-46;
); Mismatches 83;
 DB 7;
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/db_xref="taxon:9986"
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Score 209.4; DB 7
Pred. No. 1.4e-47;
0; Mismatches 81
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 61.8%;
76.1%;
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75.5%;
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                                    Conservative
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Best Local Simi
Matches 256;
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1 (bases 1 to 339)
Hall,F.L., Nimni,M.E., Tuan,T., Wu,L. and Cheung,D.T.
Artificial skin prepared from coclagen matrix containing
transforming growth factor. beta. having a collagen binding site
Patent: US 5800811-A 29 01-SEP-1998;
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                                                         GCCCTGGACACCAACTACTGCTTCAGCTCCACAGAAGAACTGCTGTGTGCGGCAGCTG
                                                                                               GTCCTGGCCCTGTACAACCAGCACAACCCGGGCGCGTCGCAGCGCCGTGCTGTGTGCCA
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113 c 100 a
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US
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AR036686
AR036686.1 GI:5954542
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nes 256; Conserv
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Best Local S
Matches 256
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VERSION
KEYWORDS
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/translation="MPPSRIRLLPLLDLLWLLVLAPGRPASGLSTCKTIDMELVKRK
RIEAIRGOILSKILKLASPPSGDVPPGPLPRAVLALYNSTRDRVAGESABPEPEPEP
YYAKEVIRVLAWDNSHNIYKSIETVAHSIYMFFNTSELREAVPDPLLLSRAELRMQRL
YYAKEVIRVLAWDNSHNIYKSIETVAHSIYMFNTSELREAVPDPLLLSRAELRMQRL
FSAHCSCDSKDNTLRVEINGIGPKRRGDLATHGMNRPFLLLMATPLERRQHLHSSRH
RRGLDTWTCFSSTEKNCVRQLYIDFRKDLGMKWHIBEKGYHANCLGPCFYIWSLDF
OYSKUTALYNGHRGASAAPCCVPQALEPLFIVYYVGRKAKVEQLSNMIVRSCKCS"

542 436 9 301 t

542 ò; Cavia porcellus – Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia. 1 (bases 1 to 1597)
Jeevan, A., McMurray, D.N. and Yoshimura, T.
Guinea pig transforming growth factor-beta in peritoneal exudates AF191297 1597 bp mRNA ROD 16-OCT-1999 Cavia porcellus transforming growth factor-beta (TGF-beta) mRNA, Submitted (01-CT-1999) Medical Microbiology & Immunology, Texas A&M Univ. System Hlth. Sci. Ctr., 407 Reynolds Medical Building, College Station, TX 77843-1114, USA 1316 1436 1376 ttgacttccgacaggatctggggctggaagtgggtccatgaacctaagggctactatgcca 124 184 244 Gaps 64 1377 CGTTGGAGCCACTGCCCATCGTGTACTACGTGGGCCGCAAAGCCAAGGTGGAGCTCT DB 94; Length 1597; ; 0 /product="transforming growth factor-beta" /protein\_id="AAF02780.1" /db\_xref="G1:6049851" 81; Indels Jeevan, A., McMurray, D.N. and Yoshimura, T. Direct Submission 60.6%; Score 205.4; DB 9.75.8%; Pred. No. 1.9e-46; iive 0; Mismatches 81 305 ccaacatggtggtgaagtcttgtaaatgtagctga 339 /organism="Cavia porcellus" /db\_xref="taxon:10141" Location/Qualifiers 1. .1597 /strain="Hartley /gene="TGF-beta" 299. .1471 299. .1471 /gene="TGF-beta" /codon\_start=1 AF191297.1 GI:6049850 after BCG vaccination Unpublished 2 (bases 1 to 1597) domestic guinea pig. 254; Conservative 1. .1597 complete cds. AF191297 Best Local Similarity 318 Query Match KEYWORDS SOURCE ORGANISM source BASE COUNT ORIGIN DEFINITION 34 ACCESSION VERSION AUTHORS TITLE REFERENCE AUTHORS TITLE Matches 65 gene REFERENCE JOURNAL JOURNAL RESULT 3 AF191297 CDS FEATURES g g g ò à q ò ò ò δ

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/prodein_id="CaA01385.1"
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IGPCPYIWSLDTQYSKVLALYNQHNPGASAAPCCVPQALEPLDYYVGRKPKVFQLS
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 339)

McMaster,G.K., Cox,D., Cerletti,N. and Kuhla,J.

McMaster,G.K., Tox,D., Cerletti,N. and Coxel phybrid transforming growth factors

Patent: EP 0542679-A 1 19-MAY-1993;

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CIBA GEIGY AG (CH)
Other publication AU 3109595 960222.
Location/Qualifiers
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NEW PROCESS FOR THE PRODUCTION OF BIOLOGICALLY ACTIVE PROTEIN PATENT: WO 9603433-A 1 08-FEB-1996;
CIBA GEIGY AG (CH)
Other publication AU 3109695 960222.
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1 (bases 1 to 699)
Iwata,K.K., Gold,L.I. and Stephenson,J.R.
Tissue-derived tumor growth inhibitors, methods of preparation and
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Derynck, R.M.A. and Goeddel, D.V.
Nucleic acid encoding TGF-.beta. and its uses
Patent: US 4886747-A 3 12-DEC-1989;
Genentech, Inc.;
South San Francisco, CA
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Patent: EP 0267463-A2 4 18-MAY-1988;
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Sequence 3 from Patent US 4886747.
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221 c 204 g
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284 c 231 q
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                                  105434 699 bp
Sequence 4 from Patent
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Best Local Similarity 75.2%;
Matches 255; Conservative
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LGPCPYIWSLDTQYSKVLALYNQHNPGASAAPCCVPQALEPLPIVYYVGRKPRVEQLS
NMIVRSCKCS"
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Cloning and expression of the gene for human transforming growth factor-beta in Escherichia coli
Tumor Res. 22, 41-55 (1987)
Location/Qualifiers
                                                                                                             HUMTGFBA 650 bp mRNA PRI 03-AUG-1993
Human transforming growth factor-beta mRNA, complete cds, clone
pTGF-beta-trp114.
M38449 M55656
M38440.1 GI:339557
transforming growth factor-beta.
Human masopharyngeal carcinoma cell line KB, cDNA to mRNA.
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Pred. No. 3.6e-46;
0; Mismatches 84; Indels
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301 ctctccaacatggtggtgaagtcttgtaaatgtagctga 339
                   119 t
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/db_xref="taxon:9606"
/cell_line="KB"
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<1. .339
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/bprotein_id="aAAA3078 l"
/db_xref="G1:163748"
/translation="AllaLyNSTRDRVAGESAETEPEPEADYYAKEVTRVLMVEYGNK
IYDKMKSSSHSIYMFRINTSELREAYPEPVLLSRADVRLLFKLKVEGCHVELYGKYSNN
SWYLSNRLLAPSDSPEMLESPVTGVYVRQWLTRFREIEGFRLSAHCSCOSKDWTQVD
INGFSSGRRGDLATTHGMNREPLLLMATPLERAQHLHSSRHRRALDFNYCFSSTEKNC
CVRQLXIDFRKDLGWKWIHEPKGYHANFCLGPCPXIWSLDTQYSKVLALYNQHNPGAS
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Bovine fibropapilloma, CDNA to mRNA, (library of Okayama and Berg).
Bos taurus
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
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Van Obberghen-Schilling, E., Kondaiah, P., Ludwig, R.L., Sporn, M.B.
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Bovine transforming growth factor-beta-1 (TGF beta-1) mRNA, 3'
M36271
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                                         DB 10; Length 862;
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                                         Score 204.6; DB 10;
Pred. No. 3.5e-46;
0; Mismatches 84;
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    /organism="Bos taurus"

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Matches 255; Conservative
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KLKVEQHVELYQKYSNNSWRYLSNRLLAPSDSPEMLSFDVTGVVRQNLTHREEIEGFR
LSAHCSCDSKDWTLQVDINGFSSGRRODLATIHGMNRPFLLAMATPLERAQHLHSRH
RRALDTNYCFSSTEKNCCVRQLYIDFRKDLGWKWIHPPKGYHANFCLGPCPYTWSLDT
QYSKVLALYNQHNPGASAAPCCVPQALEPLPIVYYVGRKVVEQLSNMIVRSCKCS"
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GIEAIRGOILSKLRLASPPSQGDVPPGPLPEAILALYNSTRDRVAGESAETEPEPEAD
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1 (bases 1 to 1173)
Woodall,C.J., McLaren,L.J. and Watt,N.J.
Sequence and chromosomal localisation of the gene encoding ovine latent transforming growth factor-beta 1
Gene 150 (2), 371-373 (1994)
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                      Gaps
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/protein_id="CAA54242.1"
/db_xref="GI:496649"
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378 c 336 g 214 t
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O.aries mRNA for transforming growth factor-beta I.
776916 7776916 G1:496648
TGF-beta 1; transforming growth factor-beta 1.
                   Indels
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Pred. No. 3.4e-46;
0; Mismatches 84
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/organism="Ovis aries"
/db_xref="taxon:9940"
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ORIGIN

Length 1117;

DB 7;

60.4%; Score 204.6;

Query Match

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YYAKEVTRVLMVENTNKIYEKVKKSPHSIYMLFNTSELREAVPEPVLLSRAELRLLRL
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LSAHCSCDSKDNTLQVDINGFSSSRRGDLATIHGMNRPFLLLMATPLERAQHLHSSRQ
RRALDTNYCFSSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /translation="MPPSGLRLLPLLLPLLRLLVLTPGRPAAGLSTCKTIDMELVKRK
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1 (bases I to 1369)
Manning, A.M., Auchampach, J.A., Drong, R.F. and Slightom, J.L.
Cloning of a canine cDNA homologous to human transforming growth factor-beta 1 (TGFbeta1)
                                                                                                                                                                                                                                                                                                                    DOGTGFBIA 1369 bp mRNA 30-OCT-1994 Canine transforming growth factor-beta 1 (TGFB1) mRNA, complete
                                                                                                                                                                                                                                                                          955 GCCAATITCIGCCIGGGCCCIGICCCIACAICIGGAGCCIGGACACACAGTACAGCAAG 1014
                                                                                                                                      tacattgacttccgacaggatctgggctggaagtgggtccatgaacctaagggctactat 120
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                                                                                             Gaps
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Canis familiaris adult jugular vein endothelial cDNA to mRNA
Canis familiaris
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                    Length 1173;
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/function="ant1-inflammatory agent"
/function="ant1-inflammatory agent"
/product="transforming growth factor-beta 1"
/protein_id="Ab51458.1"
/db_xrefe="GI:516072"
                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Canis familiaris"
/db_xref="taxon:9615"
/cell_type="LPS-activated"
/dev_stage="adult"
/tissue_type="jugular vein endothelial"
                                                84;
                                                                                                                                                                                                                                                                                                                                                                                             DB 7;
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                  Score 204.6; DB 7
Pred. No. 3.3e-46;
0; Mismatches 84
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58. .1230
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/gene="TGFB1"
                    60.48;
75.28;
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L34956.1 GI:516071
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                                                 Conservative
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                                Similarity
                                                255;
                    Query Match
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QYSKVLALYNOHNPGASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS"
1039. .1227
/gene="TGFB1"
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Purchio,A.F., Gentry,L., Twardzik,D. and Brunner,A.M.
Cloning and expression of simian transforming growth factor-beta
Patent: EP 0373994-A1 2 20-JUN-1990;
                                                                                                                                                                                                                                                                                           1131
                                                                                                                                                                                                                                                                                                                                                                                        1012 GCTAACTTCTGCCTGGGGCCCTGCCCTACATTTGGAGCCTGGACACGCAGTACAGCAAG 1071
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                                                                                                                                                                                                                                                            892 GCCCTGGACACCAACTACTGCTTCAGCTCCACGGAGAAGAACTGCTGCGTCCGGCAGCTC
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Pred. No. 3.2e-46;
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Pred. No. 3.3e-46;
0; Mismatches 84;
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                                              /product="transforming growth
1231, .1369
/gene="TGFB1"
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Sequence 2 from Patent EP 0373994
108268
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542 c 444 q
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Best Local Similarity 75.2%;
Matches 255; Conservative
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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAL Plate: 6 Row: e Column: 11.

Location/Qualifiers
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RIEAIRGQILSKLRLASPPSQGEVPPGPLPEAVLALYNSTRDRVAGESAEPEPEPEAD
                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens, Similar to transforming growth factor, beta 1, clone enterty, mRNA, complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield, Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin, Letticia Haiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saedi, Jacqueline Schein, Duane Smallus, Michael Smith, Lorraine Spence, Jaff Stott, George Thorne, Miranda Tsai, Natasja van den Bosch, Jill Vardy, George Yang, Scott Zuyderduyn, Marco Marra.
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/protein_id="AAH00125.1"
/db_xreff="GI:12652749"
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (03-NOV-2000) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics.Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
1336 CAGGCGCTGGAGCCACTGCCCATCGTGTACGTGGGCCCCAAGCCCAAGGTGGAGCAG 1395
                                                                   gtgctgggactgtacaacactctgaaccctgaagcatctgcctcgccttgctgcgtgccc
                                                                                                                                                       241 caggacctggagccctgaccatcctgtactatgttgggaggacccccaaagtggagcag
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CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
MA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
info@bcgsc.bc.ca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone="MGC:3119 IMAGE:3351664"
/tissue_type="Epp" retinoblastoma"
/clone_lib="NHH_MGC_16"
/lab_host="DH10B-R"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NIH-MGC Project URL: http://mgc.nci.nih.gov
Conteact: Robert Strausberg, Ph.D.
TTP: (301) 496-1550
Email: Robert_Strausberg@nih.gov
                                                                                                                                                                                                                                                                    301 ctctccaacatggtggtgaagtcttgtaaatgtagctga 339
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/db_xref="taxon:9606"
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BC000125.1 GI:12652748
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Strausberg, R.
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KALVEQHVELYQKYSNNSMRYLSNELLAPSNSPEMLSFDYTGYVRQMLSRGGEIEGFR
LSAHCSCÖSKDNTLQVDINGFTTGRRGDLATHGMNRPFLLLMATPLERAQHLQSRH
RRALDTNYCFSSTERNGCYRQLATIDFRKDLGMWHIHPEKGYBANFCLGPCPYTWSLDT
QYSKVLALIYNQHNPGASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIYRSCKCS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /proteIn_id="AaA35369.1"
/db_xref="G1:176538".
/translation="WPPSGGRILPLILPLIMILIVLIPSRPAAGLSTCKTIDMELVKRK
RIETIRGQILSKLRLASPPSQGEVPPGPLPEAVLALYNSTRDRVAGESAEPEPEAD
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                                                                                                                                                                                                                                                                                                                                                                                                                Simian transforming growth factor-beta (TGF) mRNA, complete cds. M16658 M1658.1 GI:176552 growth factor-beta. African green monkey cells (cell line BSC-40), cDNA to mRNA, clone pTGF-beta-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cercopithecus aethiops
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Cercopithecus.
1 (bases 1 to 1561)
Sharples,K., Plowman,G.D., Rose,T.M., Twardzik,D.R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1. .1561

/db_xref="taxon:9534"

262. .1095

/note="transforming growth factor-beta signal peptide"

262. .1434

/note="transforming growth factor-beta precursor"
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DNA 6, 239-244 (1987)
                                                                                                                                                       241 caggacctggagcccttgaccatcctgtactatgttgggaggacccccaaagtggagcag
                                                                 gtgctgggactgtacaacactctgaaccctgaagcatctgcctcgccttgctgcgtgccc
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/note="transforming growth factor-beta"
/note="46 q 267 t
                                                                                                                                                                                                                                                                      301 ctctccaacatggtggtgaagtcttgtaaatgtagctga 339
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1. .1561
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YYAKEVTRVLMVETHNEIYDKFKQSTHSIYMFNTSELREAVDEPVLLSRAELRLLRL
KLKVEQHVELYQKYSNNSWRYLSNRLLAPSDSPEWLSFDVTGVVRQWLSRGEIEGFR
LSAHCSCOSRDNTLQVDINGFTTGRRGDLATTHGWNRPFLLLMATPLERRAGHLOSSRH
RRALDTNYCDSSTEKNCYRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDT
QYSKVLARYQHNPGAPPCCVPQLYIDFRDLGWKWIHEPKGYHANFCLGPCPYIWSLDT
QYSKVLARYQHNPGAPPCVPQLYBDLYYYYGRKPKVEQLSNMIVRSCKCS"
648 c 493 q 298 L
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                                                                                                                                                                                                                                                                                                                                                           1341 TACATTGACTTCCGCAAGGACCTCGGCTGGAAGTGGATCCACGAGGCCCAAGGGCTACCAT 1400
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
                                                                                                                                                                                                                                DB 91; Length 1780;
                                                                                                                                                                                                                              Score 204.6; DB 91; Length
Pred. No. 3.2e-46;
0; Mismatches 84; Indels
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Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
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Strausberg, R.
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/translation="MPPSGLRLLLLLPLLMLLVLTPGRPAAGLSTCKTIDMELVKRK
RIEAIRGQILGKLRLASPPSGEVPPGPLPBAYLALVNSTRDRVAGESAEPBFBEAD
YYAKEVTRVLAVETHNEIVDKFNGSTHSIYMFPNTSELREAVPBPVLLSRAELRLLRL
KLKVEDHVELYQVSTNNSWRTLSNRLAPSDSPEWLSPDVTGVWGWLSRGETEGFR
LSAHCSCDSRDNTLQVDINGFTTGRRGDLATIHGMNRPFLLLMATPLERAQHLQSSRH
RRADTNYRCFSSTEKNCYRQLYIDFREDLGWWIHBFRGYHNRCLGBCPYTWSLDY
RYSKYLALYNQHNFGASAAPCCVPQLIDFREDLEPLPIVYYVGRKFWVBQLSNMIVRSCKCS"
648 C 298 t
                                                      Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAL Plate: 6 Row: e Column: 10.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                        /product="Similar to transforming growth factor, beta 1" /protein_id="AAH01180.1" /db_xref="G1:12654683"
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1821)
Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy,
George Yang, Scott Zuyderduyn, Marco Marra.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1401 GCCAACTTCTGCCTCGGGCCCTGCCCCTACATTTGGAGCCTGGACACGCAGTACAGCAAG 1460
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                                                                                                                                                                                                                        /tissue_type="Eye, retinoblastoma"
/clone_lib="NIH_MGC_16"
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/db_xref="taxon:9606"
/clone="MGC:2323 IMAGE:3356605"
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DNA encoding human prepro TGF-betal.
E03028
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                                                                                                                                                                                                                                                              /lab_host="DH10B-R"
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75.2%;
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JP 1991180192-A/1.
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/coon_start=1
/transl_table=11
/product="prefgF-beta1"
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/db_xref="G1:412941"
/db_xref="
                                                                                                                                                       NUCLEIC ACID ENCODING TGF- beta 3 AND ITS USE
                                                                                                                                                                                                                                                 /organism="synthetic construct"
/db_xref="taxon:32630"
                                                                                                                                                                              Patent: WO 8912101-A 4 14-DEC-1989;
Location/Qualifiers
                                         synthetic construct.
synthetic construct
artificial sequence.
1 (bases 1 to 2537)
                                                                                                                                                                                                                                                                                             .2014
A06669.1 GI:412940
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Matches 25
                                         SOURCE
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                                                                                                             REFERENCE
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C12P21/00,C07K13/00,C12N5/10,C12N15/18//C12Q1/68,(C12P21/00,
C12R1:91),
(C12N15/18,C12R1:91);
strandedness: Double;
topology: Linear;
hypothetical: No;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1466 GCCAACTTCTGCCTCGGGCCCTGCCTACATTTGGAGCCTGGACACGCAGTACAGCAAG 1525
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                       GENETIC RECOMBINATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FI
                                                                                                                                                    07-DEC-1989 JP 1989318243
OHASHI HIDEYA, ISHII YASUYUKI, MIYATA YOSHINORI, PI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 10; Length 1821;

    .510
    .1683
    /product='human prepro TGF-betal'

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    598. .1680
/note='human pro TGF-betal'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1345. .1680
/product='human TGF-betal'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  301 ctctccaacatggtggtgaagtcttgtaaatgtagctga 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                PRODUCTION OF HUMAN PRO-TGF-BETAL BY GI
Patent: JP 1991180192-A 1 06-AUG-1991;
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*source: clone=pVC19-TGF;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1. .1821
/organism="Homo sapiens"
/db_xref="taxon:9606"
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Location/Qualifiers
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                                                                                     Homo sapiens (human)
JP 1991180192-A/1
06-AUG-1991
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ilarity 75.2%;
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PC C12R1;91
PC C12R1;91
PC C12R1;91
PC C12R1;91
PC C12R1;91
PC Apported
CC Apported
CC Asource:
FH Key
FH Key
FH CD
FH FT CD
FH CA
Sig_Peptide
FI mat_pepti
FT mat_pepti
FT 3'UTR
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Matches 255;
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A06669
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Derynck, R., Jarrett, J.A., Chen, E.Y., Eaton, D.H., Bell, J.R., Assoian, R.K., Roberts, A.B., Sporn, M.B. and Goeddel, D.V.
                                                                                                                                                                                                                                                             1856 Greergecerreraceacearaaceeggecerregeggecerecergerecregegg 1915
                                                                                                                                                                         61 tacattgacttccgacaggatctgggctggaagtgggtccatgaacctaagggctactat 120
                                                                                    1 gotttggacaccaattactgcttccgcaacttggaggagaactgctgtgtgcgcccctc 60
                                                                                                                                                                                                                                                                                                                                                    HSTGFB1 2745 bp mRNA PRI 27-MAR-1:
Human mRNA for transforming growth factor-beta (TGF-beta).
X02812 J05114
X02812.1 GI:37092
                                              ;
60.4%; Score 204.6; DB 9; Length 2537; 75.2%; Pred. No. 3e-46; 1ive 0; Mismatches 84; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  signal peptide; transforming growth factor-beta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CTGTCCAACATGATCGTGCGCTCCTGCAAGTGCAGCTGA 2014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ctctccaacatggtggtgaagtcttgtaaatgtagctga 339
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Synthetic mRNA for preTGF-Betal. A06669

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ACCESSION
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ORIGIN
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AUTHORS
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LKLKVEQHVELYQKYSNNSWRYLSNRLLAPSDSPEMLSFDVTGVVROMLSRGGEIEGF
RLSAHCSCDSRDNTLOVDINGFTTGRRGDLATIHGMNRPFLLLMATPLERAQHLQSSR
                                                                                                                                                                                                                                                                                                           HRRALDTHYCFSSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLD
TQYSKVLALYNQHNPGASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS"
                                                                                                                                                                                                                                                        RIEAIRGQILSKLRLASPPSQGEVPPGPLPEAVLALYNSTRDRVAGESAEPEPEAD
                                                                                                                                                                                                                             /db_xref="SWISS-PROT:P01137"
/translation="MPPSGLRLLPLLPLLWLLVLTPGPPAAGLSTCKTIDMELVKRK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
Human transforming growth factor-beta complementary DNA sequence and expression in normal and transformed cells
Nature 316 (6030), 701-705 (1985)
85296301.
The sequence downstream from the translational stop codon (2015-2017) was taken from a genomic clone.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tacattgacttccgacaggatctgggctggaagtgggtccatgaacctaagggctactat 120
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Notes pot. core sequence of signal peptide (aa -272 -257)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 2745;
                                                                                                                                                                                                                                                                                                                                                                                        /note="pot. altern. translation start site"
1035. .1043
/note="put. glycosylation site"
1247. .1255
/note="put. glycosylation site"
1370. .1378
/note="put. glycosylation site"
/note="put. glycosylation site"
                                                                                                                                     37. .113
/note="pot. hairpin loops-forming region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    84; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'product="mature TGF-beta (aa 1-112)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="put. polyadenylation signal"
2539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 204.6; DB
Pred. No. 3e-46;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2097. .2103 --- reyton"
/note="pATA-box-like region"
2517. .2522
                                                                                                                                                            842. 2017
/note="TGF-beta precursor"
                                                                                                                                                                                                    /protein_id="CAA26580.1"
/db_xref="GI:37093"
                                                                                                        /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2018. 2096
/note="GC-rich region"
2097. .2103
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938 c 801 g 4
                                                                                                                                                                                         /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60.4%;
75.2%;
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1 (bases 1 to 1560)
Purchlo, A.F., Gentry, L. and Twardzik, D.
Cloning and expression of simian transforming growth factor-SS1
Patent: EP 0297885-42 2 07-DEC-1988;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1274
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Purchlo.A.F., Gentry, L. and Twardzik, D.
Cloning and expression of simian transforming growth factor-SS1
Patent: EP 0293785-A2 3 07-DEC-1988;
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                                                                                                                Sequence 2 from Patent EP 0293785.
106216
106216.1 GI:590649
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547 c 442 g
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/organism="unknown"
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74.98;
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Unclassified.
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Pred. No. 9.3e-46;
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20-MAR-1986 JP 1986064661
22-MAR-1985 US 85 7151
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                                                                                                                  /gene="TGF-beta 1"
/product="putative"
1155. :1173
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/gene="TGF-beta 1"
                                                                                1..87
/gene="TGF-beta 1"
88..1170
                                                                                                                                                                                /note="3'primer"
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                                                                                                                                                                                                                                                  59.9%;
ilarity 74.9%;
Conservative
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JP 1986219395-A/1.
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Homo sapiens
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Best Local Similarity
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                                                                                 sig_peptide
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/protein_id="CAA67801.1"
/db_xref="fg1:25984101"
/db_xref="SWISS-PROT:019011"
/translation="MPPSGIRILPLIALILPLIMILVLTPGRPAAGISTCKTIDMELVKRK
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Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 (bases 1 to 1173)
Penha-Goncalves, M.N., Onions, D.E. and Nicolson, L.
Cloning and sequencing of equine transforming growth factor-beta
(TGF beta-1) cDNA
                                                                                                                           1344 CAGGCGCTGGAGCCGCTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAG
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                                                                                    Gaps
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Submitted (18-JUL-1996) M.N. Penha-Goncalves, University of
Glasgow, Veterinary Pathology Department, Veterinary School,
Bearsden Road, Glasgow G61 1QH Scotland, UK
Location/Qualifiers
                                                                                                                                                                                                                                                                               gtgctgggactgtacaacactctgaaccctgaagcatctgcctcgccttgctgcgtgccc
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                                                       Length 1569
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E.caballus mRNA for transforming growth factor beta
 others
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/organism="Equus caballus"
/db_xref="taxon:9796"
/tissue_type="lymph node"
/tissue_type="spleen"
/tissue_type="spleen"
/note="PBMC, ConA and LPS stimulated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                X99438
X99438.1 GI:2598418
TGF-beta 1; transforming growth factor-beta 1.
                                                       DB 10;
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                                                      Score 203.6; DB 1
Pred. No. 6.1e-46;
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                                                                                 0; Mismatches
 265
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98185507
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1. .1173
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 442
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                                                      60.1%;
74.9%;
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Penha-Goncalves, M.N.
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295
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VERSION
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TITLE
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KLSVEQHVELYQKYSNNSWRYLSNRLLTPSDSPEWLSFDVTGVVRQWLSQGGAMEGFR
LSAHGSCOSTSCROWTLRVGITNGFSSSRROCHAITORNRPFLLAATPLEAATPLERAQUHISSRH
RRALDPINYCESSTERNOCVRQLYIDRFKDLGRKWHIEPEKGYRANFCLGPCPYTWSLD7
QYSKYLALYNQHNPGASAAPCCVPQVLEPLPIVYYVGRKPKVEQLSNMIVRSCKCS" ; 0 F1 KIKU MAIKERU ANDORE DERINKU, DEBITSUDO BANNOOMAN GETSUDERU PC C12P21/00,C12N1/00,C12N5/00,C12N15/00//C12Q1/68,(C12P21/00, PC C12R1:91), (C12N1/00,C12R1:19),(C12N5/00,C12R1:91),(C12N15/00,C12R1:91); strandedness: Double; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutherita; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 2527)
Riku,M.A.D.D. and Debitsudo,B.G.
Riku,M.A.D.D. and Debitsudo,B.G.
PUCLEIC ACID CODED WITH TGF-BETA AND ITS USE
Patent: JP 1986219395-A 1 29-SEP-1986; 1014 240 121 gecaacttetgeteaggecettgeceatacetecgeagtgeagacacaaccacageacg 180 241 caggacctggagccctgaccatcctgtactatgttgggaggacccccaaagtggagcag 300 61 tacatigacticcgacaggatctgggctggaagtgggtccatgaacctaagggctactat 120 Gaps 1 gctttggacaccaattactgcttccgcaacttggaggagaactgctgtgtgcgcccctc 60 29-SEP-1997 181 gtgctgggactgtacaacactctgaaccctgaagcatctgcctcgccttgctgcgtgccc ; 0 Length 1173; 85; Indels

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Gaps

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FEATURES

BASE COUNT

ORIGIN

Matches

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241

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/brotein_id="G1:535760"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 336)
McMaster,G.K., Cox,D., Cerletti,N. and Kuhla,J.
Movel hybrid transforming growth factors
Patent: EP 0542679-A 4 19-MAY-1993;
CIBA-GEIGY AG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25-JAN-1995
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                                            /product="transforming growth factor-beta 1" <1. .>334 /codon_start=3
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Pred. No. 1.2e-45;
...matches 82; Indels
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Pred. No. 2.7e-45;
0; Mismatches 84;
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/tissue_type="dorsal skin"
<1. .334
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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Matches 252; Conservative
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VERSION
KEYWORDS
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Caprinae; Ovis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 334)
Sutton, R., Ward, W.G., Raphael, K.A. and Cam, G.R.
Growth factor expression in skin during wool follicle development
Unpublished (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                           1796 GCCAACTTCTGCCTCGGGCCCTGCCCTACATTTGGAGCCTGGACACGCAGTACAGCAAG 1855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1916 CAGGCGCTGGAGCCGCTGCCCATCGTGTACTACGTGGCCCGCAAGCTCGAGGAG 1975
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gtgctgggactgtacaacactctgaacctgaagcatctgcctcgcttgctggtgcc 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  caggacctggagccctgaccatcctgtactatgttggaggacccccaaagtggagcag 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SHPGFB1W 334 bp mRNA MAM 11-SEP-1994
Ovis aries transforming growth factor-beta 1 mRNA, partial cds
L36038
                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                     Key
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 topology: Linear;
hypothetical: No;
anti-sense: No;
arsource: tissue_type=placenta and glyoblastoma; FH
Location/Qualifiers
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0
                                                                                                                                                                                                                                                                                                                                                                             Length 2527;
                                                                                                                                                                                                                                                                                                                                                                                                           85; Indels
                                                                                                842. .2014
/product='pre TGF-beta'
1676. .2011
/product='TGF-beta'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 10;
                                                                                                                                                                                                                                                                                                                                                                           tch 59.9%; Score 203; DB 10; al Similarity 74.9%; Pred. No. 8.4e-46; 254; Conservative 0; Mismatches 85
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2015. . 2537
37. .113
2015. . 2100
2514. . 2519.
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/organism="Homo sapiens"
/db_xref="taxon:9606"
888 c 735 g 43
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/db_xref="taxon:9940"
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Location/Qualifiers
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stem_loop
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DEFINITION ACCESSION VERSION

SHPGFB1W

1976

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ORGANISM

KEYWORDS

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FEATURES

TITLE JOURNAL

REFERENCE

AUTHORS

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Gaps

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Submission
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Medicine, Laboratory of Molecular Carcinogenesis, Rm 122,
188Longwood Avenue, Boston, MA 02115, USA
2 (bases 1 to 469)
Wongy, D.T., Donofff, R.B., Yang, J., Song, B.Z., Matossian, K.,
Nagura, N., Elovic, A., McBride, J., Gallagher, G., Todd, R. et.al.
Sequential expression of transforming growth factors alpha and beta
1 by eosinophils during cutaneous wound healing in the hamster
93304479
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DLGWKWHPEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNPGASAGPCCVPQALE
PLPITYYVGRKPKVEQLSNMIVRSYRCS"
78. 413
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
Mesocricetus.
                                                                                                                                                                                                                      240
                                                                                         caggacctggagccctgaccatcctgtactatgttgggaggacccccaaagtggagcag 300
                                                                                                                                                                                                                                                                                                              241 CAAGATTTAGAACCTCTAACCATTCTCTACTACATTGGCAAAACACCCAAGATTGAACAG 300
                                                                        tacattgacttccgacaggatctgggctggaagtgggtccatgaacctaagggctactat 120
                                                                                                                                               gecaacttetgeteaggecettgeecataceteegeagtgeagacacaacecacageaeg 180
                                     9
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gctttggacaccaattactgcttccgcaacttggaggagaactgctgtgtgcgcccctc
                    gtgctgggactgtacaacactctgaaccctgaagcatctgcctcgccttgctgcggtgccc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MATGFB1 469 bp mRNA ROD 02-
M.auratus mRNA for transforming growth factor beta-1.
X60296
X60296.1 GI:396177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /strain="LVG (Syr)"
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/cell_line="HCPC-1"
/cell_line="HCPC-1"
/clone_lib="oligodt primer-extended cDNA"

    .469
    /organism="Mesocricetus auratus"

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golden hamster.
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/note="primer JY-2"
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/translation="MPPSGLRLLPLLLPLLVLTPGRPAAGLSTCKTIDMELVKRK
RIEAIRGQILSKLRLASPPSQGEVPPGPLPEAVLALYNSTRAQVAGESAETEPEPEAD
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Nixon,A.J.; Brower-Toland,B.T. and Sandell,L.J.
Molecular cloning of equine transforming growth factor beta 1 reveals a divergent nucleotide structure that encodes a novel bioactive peptide among mammalian species
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Nixon, A.J., Brower-Toland, B.T. and Sandell, L.J.
Direct Submission
Submitted (05-AUG-199) Clinical Sciences, Cornell University,
O. Box 25, Ithaca, NY 14853, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                       240
                                                                                                                                                                     tacattgacttccgacaggatctgggctggaagtgggtccatgaacctaagggctactat 120
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Equus caballus transforming growth factor beta 1 (TGFb1) mRNA,
                                                                                                                                        Gaps
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0
                                                                                                          DB 94; Length 469;
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/db_xref="G1:5733114"
growth factor-beta 1"
                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 59.4%; Score 201.4; DB 9
Best Local Similarity 74.6%; Pred. No. 2.9e-45;
Matches 253; Conservative 0; Mismatches 86
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/db_xref="taxon:9796"
                                               82
   /product="transforming
450. .469
/note="primer JY-3"
a 167 c 133 g
                            JY-3"
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AF175709
AF175709.1 GI:5733113
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                    misc_feature
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AUTHORS
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KEYWORDS
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LSAHCPCDSKDNTLRVGINGFSSRRGDLATIDGMNRPFLLLMATPLERAQQLHSSRH
RRALDTWYCSSSTERNCVRQLYIDFREDLGNKWIHBFKGYHANFCLGFCPYINSLDT
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395 c 31 9 20 1
YYAKEVTRVLMVEKENEI YKTVETGSHSI YMFFNASELRAAVPDPMLLSRAELRLLRL
KLSVEQHVELYQKYSNNSWRYLSNRLLTPSDSPEWLSFDVTGVVRQMLSQGGAMEGLR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ROD 24-JUL-2000
precursor (TGF-beta2) mRNA,
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleost
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Koishi,K., Dalzell,K.G. and McLennan,I.S.
The expression and structure of TGF-beta2 transcripts in
                                                                                                                                                            Score 201.4; DB 7; Length 1187;
Pred. No. 2.6e-45;
0; Mismatches 86; Indels 0;
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20461836
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Koishi,K., Dalzell,K.G.B. and McLennan,I.S.
Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /strain="Wistar"
/db_xref="taxon:10116"
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1. .2796
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308. .1552
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                                                                                                                                                                59.4%;
74.6%;
                                                                                                                                                                                                    Matches 253; Conservative
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IHEPKGYNANFCAGACPYLWSSDJQHTKVLSLYNTINPEASASPCCVSQDLEPITILY
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sta 2 long form precursor (TGF-beta2) mRNA,
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleost
Mammalia; Eutheria; Rodentla; Sciurognathi; Muridae; Murinae;
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Koishi,K., Dalzell,K.G. and McLennan,I.S.
The expression and structure of TGF-beta2 transcripts in
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20461836
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Pred. No. 2.3e-45;
0; Mismatches 86;
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2077. .2082
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                                                                                                                                                                                                                                               /note="putative"
2752. .2757
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Koishi,K., Dalzell,K.G.B. and McLennan,I.S.
Direct Submission
Submitted (18-MAY-1999) Anatomy & Structural Biology, University of Octao, Dunedin PO Box 913, New Zealand Octao, Dunedin PO Box 913, New Zealand Location/Qualifiers
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SLYNTINPEASASPCCVSQDLEPLTILLYYIGNTPKIEQLSNMIVKSCKCS"
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Pred. No. 2.3e-45;
0; Mismatches 86;
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308. .1636
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Direct Submission
Submitted (18-MAR-1999) Laboratory of Comparative Carcinogenesis,
National Cancer Institute, FCRDC, Bldg.538, Room 206, Frederick, MD
21702, USA
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VYKIDMPSHFPSENAIPPTFYRPYFRIVRFDVSTMEKNASNLVKAEFRVFRLQNPKAR
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GFKISLHCYCCTFIPSNYIIPNKGSELEARRAGIDGYSTASGODKTIKSTRKKSSG
GFKIELHCLESY FLESNYIIPNKGSELEARRAGIDGYSTATA
THEPKGYNANFCAGACPYLWSSDTQHTKVLSLYNTINPEASASPCCVSQDLEPLTILY
                                                                                                                                                                                            Eukaryota; Métazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="transforming growth factor beta 2 precursor"
/protein_id="AAD24484.1"
/db_xref="G1:4580715"
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Rattus norvegicus transforming growth factor beta 2 precursor, nRNA, complete cds.
AF135598
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                                                                                                                                                                                                                                                                                                                                                                                         2 (bases 1 to 1255)
Plisov,S.Y., Ivanov,S.V., Plisova,T.M., Lerman,M. and
Perantoni,A.O.
                                                                                                                                                                                                                                                                          1 (bases 1 to 1255)
Plisov, S.Y., Ivanov, S.V., Plisova, T.M., Lerman, M. and
Perantoni, A.O.

    1255
    /organism="Rattus norvegicus"
/db_xref="taxon:10116"

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                                                                                     AF135598.1 GI:4580714
                                                                                                                                             Norway rat.
Rattus norvegicus
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Query Match
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/product="TGE-beta2 protein"
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/db_xref="STREMEL:Q9R2B8"
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LSKLKITSPPEDYPEPEDYPFRIVENDSTMERNASNLIVAERERVERGNER
VYKIDMPSHPPERENAIPPFRIVENPSTRUKENSANLIVAERERVERGNER
VARDRIELYQUILKSRDLIZSPTQNYIDSKVVKTNAEGEWLISFDYDDAVHEWLHHKDRNL
GFKISLHCPCCTFIPSNNYIIPNKSQELEARRAGIDGTSTYASGDQKTTKSTRKKSSG
KTPHILLAMLLPSYRLESQOSSRRRKAALDAAYCFRNVQHNCCLRPLYIDFKRDLGWKW
IHEPKGYNANFCAGACPYLMSSDTQHTKVLSLYNTINPEASASPCCVSQDLEPLTILLY
YIGNTPKIEDLSNMTVRSCKCS"
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Konrad,L., Albrecht,M., Renneberg,H. and Aumuller,G.
Transforming growth factor-beta2 mediates mesenchymal-epithelial interactions of testicular somatic cells
Endocrinology 141 (10), 3679-3686 (2000)
                                                                                                                                                                                                                                                                                                 2 (bases 1 to 1274)
Konrad,L.
Birect Submission
Submitted (02-FEB-1999) Konrad L., Anatomy and Cell Biology,
Philipps University, Robert-Koch-Str. 6, 35033 Marburg, GERMANY
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 gccaacttctgctcaggcccttgcccatacctccgcagtgcagacacaacccacagcacg 180
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/cell_type="peritubular myoid primary cells"
16. 1260
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Pred. No. 7e-45;
0; Mismatches 87; Indels
                 RNO132718 1274 bp mRNA RATTUS norvegicus mRNA for TGF-beta2 protein. AJ132718
                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Rattus norvegicus"
                                                                            AJ132718.1 GI:4753895
tgf-beta2 gene; TGF-beta2 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:10116"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="tgf-beta2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="tgf-beta2"
16. .1260
                                                                                                                                                                                                                                                                                                                                                                                                                                        /strain="Wistar"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /codon_start=1
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74.3%;
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Best Local Similarity 74.3
Matches 252; Conservative
                                                                                                               Norway rat.
Rattus norvegicus
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria: Rodentia; Sciurognathi; Muridae; Murinae; Mus. I (bases 1 to 4267)
Miller, D.A., Lee, A., Pelton, R.W., Chen, E.Y., Moses, H.L. and Derynck, R.
1096 GCCTGGACACCAACTACTGCTTCAGAAATGTGCAGGATAATTGCTGCCTACGTCCGCTT 1155
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                                                                                                                                                                                                                                                                                                                  1 (bases 1 to 1561)
Purchio,A.F. and Madisen,L.
TGF - beta 1 / beta 2 : a novel chimeric transforming growth factor-beta
Patent: EP 0374044-A2 3 20-JUN-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14-JUN-1991
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Mouse mRNA for transforming growth factor-beta2.
X57413.
X57413.1 GI:54772
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                                                                     301 ctctccaacatggtggtgaagtcttgtaaatgtagctga 339
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Pred. No. 1.5e-43;
                                                  ctctccaacatggtggtgaagtcttgtaaatgtagctga
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                                                                                                                                                                          108275 1561 bp
Sequence 3 from Patent EP
108275
108275.1 GI:589015
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Best Local Similarity 73.5%;
Matches 249; Conservative
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                                                                                                                                                                                                                                                                                                          Unclassified.
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1547 TTGTCCAACATGATCGTGCGCTCCTGCAAGTGCAGCTGA 1585
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72.9%;
                                   Mammalia; Eutheria;
                     Eukaryota; Metazoa;
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Matches 247; Conservative
 Rattus norvegicus
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LSKLKLTSPPEDYPEBDEVPPEVISIYNSTRDLLQEKASRRAAACERERSEQEYYAKE
VYKIDMPSHLPSENAIPPTFYRPYFRIVRFDVSTMEKNASNLVKAEFRVFRLQNPKAR
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KEYISHLGFOCCTFVPENNYIIPRNESELBARRAGIDGYSTAASGODGYTRYRTSTRKKTSG
KTPHILLIMILPSYRESQOSSRRKRALDAAYCFRNYODNCCLRPLYIDFKRDLGWW
IHEPKGYNANFCAGACPYLWSSDTQHTKVLSLYNTINPEASASPCCVSQDLEPLTILY
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                                                                                                                                                                                                                                                                            /product="transforming growth factor-beta2 precurser"
/protein_id="CAA40672.1"
/db_xref="G1:54773"
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growth factor; TGF-beta 1; transforming growth factor-beta 1.
Norway rat.
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Murine transforming growth factor-beta 2 cDNA sequence and
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Rat mRNA for transforming growth factor-beta 1.
X52498
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Pred. No. 3.5e-43;
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                   expression in adult tissues and embryos Mol. Endocrinol. 3 (7), 1108-1114 (1989) 90014832
                                                                                                                                                                                                                                                                                                                                   /db_xref="SWISS-PROT:P27090"
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                                                                                                    /organism="Mus musculus
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YIGNTPKIEQLSNMIVKSCKCS"
                                                                                                                                        /dev_stage="embryonic"
/cell_type="carcinoma"
/cell_line="PCC3"
                                                                     Location/Qualifiers
                                                                                                                                                                                          1218. .2462
/gene="TGF-beta2"
1218. .2462
/gene="TGF-beta2"
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/gene="TGF-beta2"
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Best Local Similarity 73.2%;
Matches 248; Conservative (
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/translation="MPPSGIRLLPLPLPMLIVLTPCRPAACLSTCKTIDMELVKRK RIEATRQILSKLRLASPPSGGEVPPCPLPEAVLALYNSTRDRVAGESADPEPEAD YYAKEVTRVLMVDRNNAIYDKTKDITHSIYMFFNTSDIREAVPEPPLLSRAELRLQRF KSTVEOHVELYQKYSNNSWRYLGNRLLTPTDTPEWLSFDVTGVVRQWLNQGDGIQGFR SPAGSCDSKDNVLHYBLING 15PKRKOLGYT HIDMRPPLLLMATPLEARQHLHSSRH FRALDTNYCFSSTERNCVRQLY IDFRKDLGWRWI HEPKGYHANFCLGPCPY TYSLLDT QYSKVLALI'NOHNPGASASPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS" ö Chordata; Craniata; Vertebrata; Euteleostomi; Rodentia; Sciurognathi; Muridae; Murinae; 1 (bases 1 to 1585) Su Wen,0. Direct Submission Submitted (01-MAR-1990) Su Wen Q., National Cancer Institute NIH, Bldg 41 Room C629, Laboratory of Chemoprevention, NCI Bethesda MD 1427 GTCCTTGCCCTCTACAACCAACAACCGGGTGCTTCCGCATCACCGTGCTGCGTGCTGCCG 1486 1487 CAGGCTTTGGAGCCACTGCCCATCGTCTACTACGTGGGTCGCAAGCCCAAGGTGGAGCAG 1546 tacattgacttccgacaggatctgggctggaagtgggtccatgaacctaagggctactat 120 Gaps 1 gctttggacaccaattactgcttccgcaacttggaggagaactgctgtgtgcgcccctc 60 2 (bases 1 to 1585) Qian, S.W., Kondaiah, P., Roberts, A.B. and Sporn, M.B. cDNA cloning by PCR of rat transforming growth factor beta-1 Nucleic Acids Res. 18 (10), 3059 (1990) 121 gocaacttctgctcaggcccttgcccatacctccgcagtgcagacacaacccacagcacg gtgctgggactgtacaacactctgaaccctgaagcatctgcctcgccttgctgcgtgccc caggacctgagccctgaccatctgtactatgttgggaggaccccaaagtggagcag Length 1585; ö /1247. .1582 /product="mature TGF-beta 1 (AA 255 to 367)" /product="mature TGF-beta 1 (AA 255 to 367)" to 367)" ..1e-42; nes 92; Indels /product="signal peptide (AA -23 to -1)" /note="pro-TGF-beta 1 (AA 1 to 367)" DB 95; -23 (A /organism="Rattus norvegicus" /protein\_id="CAA36741.1" /db\_xref="GI:57342" /db\_xref="SWISS-PROT:P17246" Score 191.8; I Pred. No. 1.1e-0; Mismatches 413. .1585 /note="prepro-TGF-beta 1 /strain="Sprague Dawley" /db\_xref="taxon:10116" /dev\_stage="adult" /tissue\_type="heart" 413. .481

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mat_peptide
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SAHGSCDSKDNKLHYEING 15 PKRKOCHGT HIDMIRPPLLJAATPLERAQHLHSRH
RRALDTNYGFSSTERNCVRQLY IDFRKDLGRWH HEPKGYRHNFCLGPCPY TWSLLDT
QYSKVLALYNOHNPGASASPCCVPQALEPLPIVYYVGRKPKVEQLSNMIYRSCKCS*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         RIEAIRGQILSKLRLASPPSQGEVPPGPLPEAVLALYNSTRDRVAGESADPEPEAD
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                                                                                                                     Mouse monocytic cell, cDNA to mRNA.

Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                       MUSTGFRNA 1579 bp mRNA ROD 27-APR-1993
Mouse transforming growth factor beta mRNA (TGF-beta), complete
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 190.2; DB 94; Length 1579;
Pred. No. 3.1e-42;
0; Mismatches 93; Indels 0;
                                                                                                                                                                                                        Derynck, R., Jarrett, J.A., Chen, E.Y. and Goeddel, D.V. The murine transforming growth factor-beta precursor J. Biol. Chem. 261, 4377-4379 (1986)
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                                                                                                                                                                                                                                                                                                                                                                            /note="TGF-beta precursor"
                                                                                                                                                                                                                                                                                                  /organism="Mus musculus"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                               /note="TGF-beta mRNA"
                                                                                                                                                                                                                                                                      Location/Qualifiers
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Best Local Similarity 72.6%;
Matches 246; Conservative 0
                                                                                              M13177.1 GI:201952
growth factor.
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KSSVEQHVELYQKYSNNSWRYLGNRLLTPTDTPEWLSFDVTGVVRQWLNQGDG1QGFR
RSAHGSCDSKDNKLHYDLTGPRKROCHGTJHDMRPPLLJAATPLFRAQHHISSRH
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YYAKEVTRVLMYDRNNAIYEKTKDISHSIYMFFNTSDIREAVPEPPLLSRAELRLQRL
                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 2094)
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                                                                                                                                                                                                                                                                           Poirot, L., Bendist, C. and Mathis, D.
Transforming growth factor-beta 1 sequence and expression:
difference between NOD/Lt and C57B1/6 mouse strains
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/gene="TGF beta 1"
/product="transforming growth factor-beta
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AJ009862.1 GI:3688423
AJ009862.1 GI:3688423
TGF beta 1 gene; transforming growth factor-beta
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0; Mismatches
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1. .2094
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868. .2040
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                                                                                                                                                                     Poirot, L.
Direct Submission
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                                                                                        Mus musculus
                                                                house mouse.
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01-OCT-1998

MMU009862 2094 bp mRNA ROD 01-OCT Mus musculus mRNA for transforming growth factor-beta 1.

LOCUS DEFINITION

349 CCAACATGAT 358

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Scarozza, A.M., Ramsingh, A.I., Wicher, V. and Wicher, K.
Spontaneous cytokine gene expression in normal guinea pig blood and
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Mammalia; Eutheria, Rodentia, Hystricognathi, Caviidae, Cavia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Scarozza, A.M., Ramsingh, A.I., Wicher, V. and Wicher, K. Direct Submission
Submitted (05-OCT-1998) New York State Dept of Health, David Axelrod Institute, Wadsworth Center for Laboratories & Research, 120 New Scotland Ave, Albany, NY 12208, USA
Location/Qualifiers
1. 358
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                245 acctggagcccctgaccatcctgtactatgttgggaggacccccaaagtggagcagctct 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CGTTGGAGCCACTGCCCATCGTGTACTACGTGGGCCGCAAAGCCAAGGTGGAGCAGCTCT 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                       09-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tgggactgtacaacactctgaaccctgaagcatctgcctcgccttgctgcgtgccccagg
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                                                                    AF097509 358 bp DNA ROD 09-DI
Cavia porcellus interleukin TGF beta gene, partial cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 186.8; DB 94; Length
Pred. No. 3.3e-41;
0; Mismatches 77; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Cavia porcellus"
/db_xref="taxon:10141"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   with Treponema pallidum
Immunology 95 (2), 242-247 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cytokine 10 (11), 851-859 (1998)
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120 c 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          <1. .>358
/codon_start=3
                                                                                                                                                                AF097509.1 GI:3983112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         55.1%;
75.2%;
                                                                                                                                                                                                                                     domestic guinea pig.
Cavia porcellus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (bases 1 to 358)
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Matches 233; Conservative
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                                                                                               DEFINITION
ACCESSION
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TITLE
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REFERENCE
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TITLE
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REFERENCE
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JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AUTHORS
RESULT 7
AF097509
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                                                                                                                                                                    VERSION
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/translation="HYCVLSAPLLLHUYTVALSLSTCSTLDMDQFWRKRIEAIRGQIL
SKIKLTSPPEDYPPEEVPPEVISIYNSTRDLLQEKASRRAAGERERSDEEYYAKEV
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FKISLHCPCCTFVPSNNYIIPNKSEELEARFAGIDGTSTYTSGDQKTIKSTRKKNSGK
TPHLILMLLPSYGLESQOSNRRKRALDAAYCFRNVQDNCCLRPLYIDFKRDLGWKWI
HEPRGYNANFCAGACPYLWSSDTQHSRVLSLYNTINPEASASPCCVSQDLEPLTILYY
1GKTPKIEQLSNMIVKSCKCSKTKLAAFARLYHSHSNLGSET"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ó
                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
1 (bases 1 to 1427)
                                                                                                                                                                                                                                                Cloning and expression of porcine transforming growth factor beta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1084 GITCICAGCITATATAACACCATAAACCCAGAAGCITCIGCITCCCCTTGCTGCGGGTGTCC 1143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tacattgacttccgacaggatctgggctggaagtgggtccatgaacctaagggctactat 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                     PIGTGFB2A 1427 bp mRNA MAM 16-JUL-1996
Sus scrofa transforming growth factor beta 2 mRNA, 3' end.
L08375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 gctttggacaccaattactgcttccgcaacttggaggagaagtgctgtgtgcgcccctc 60
                                                                                                         transforming growth factor beta 2.
Sus scrofa (strain crossbreed) male adult Lung cDNA to mRNA.
Sus scrofa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gtgctgggactgtacaacactctgaaccctgaagcatctgcctcgccttgctgcgtgccc
                                                                                                                                                                                                                                                                    in immune cells
Unpublished (1993)
On Jul 16, 1996 this sequence version replaced gi:164688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 185.6; DB 7; Length 1427;
Pred. No. 5.8e-41;
0; Mismatches 94; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="transforming growth factor beta 2"
395 c 336 q 307 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="transforming growth factor beta
/protein_id="AAB03850.1"
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                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="taxon:9823"
/cell_type="alveolar macrophage cells"
/dev_stage="adult"
/sex="male"
                                                                                                                                                                                                                                                                                                                                              1. .1427
/organism="Sus scrofa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue_type="Lung"
<1. .1305
/note="precursor"
                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                    /strain="crossbreed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 54.7%;
Best Local Similarity 72.0%;
Matches 242; Conservative
                                                                                               L08375.1 GI:1421492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           389
                                                                                                                                                                                                                             Zhou, Y.
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                                                                                                                                                                                                                                                                                                                                                source
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RESULT 71
PIGTGFB2A
                                                        DEFINITION
                                                                                                                                                      ORGANISM
                                                                                                                                                                                                                               AUTHORS
TITLE
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                                                                          ACCESSION
                                                                                                               KEYWORDS
                                                                                                                                                                                                               REFERENCE
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                                                                                               VERSION
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tqfb3n.rge

δ g SOURCE

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/translation="MHYCVLSAFLILHLVTVALSLSTCSTLDMDQFMRKRIEAIRGOI
LSKLKITSPPEDAPEDSPPEDVPPENTSTROLLOGERARRAAACERERSDEETYAKE
USKIDMPPFPPEDAPEPPEPPRPY TRYTVRTPOLDGFASRAAACERERSDEETYAKE
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HERPKGYNANFCAGACPYLMSSDTOHSRVLSLYNTINPEASASPCCVSQDLEPITILY
                                                                                                                                                                                                                                         Amino acid sequence of the BSC-1 cell growth inhibitor (polyergin) deduced from the nucleotide sequence of the cDNA Proc. Natl. Acad. Sci. U.S.A. 85, 79-82 (1988) 88124824
                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1106 GCTTTGGATGCGGCCTATTGCTTTAGAAATGTGCAGGATAATTGCTGCCTACGTCCGCTT 1165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1346 CAAGACTTAGAACCTCTAACCATTCTCTACTACATTGGCAAAACACCCAAGATTGAACAG 1405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCUS CCU66874 1083 bp mRNA VRT 14-JUL-1997
DEFINITION Cyprinus carpio transforming growth factor-beta 2 mRNA, partial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                241 caggacctggagcccctgaccatcctgtactatgttgggaggaccccaaagtggagcag 300
                                                                                         Cercopithecinae; Cercopithecus.
1 (bases 1 to 1585)
Hanks,S., Armour,R., Baldwin,J.H., Maldonado,F., Spiess,J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1166 TACATTGATTCAAGAGGGATCTAGGGTGGAAATGGATACACGAACCCAAAGGATACAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  getttggacaccaattactgcttccgcaacttggaggagaactgctgtgtgcgcccctc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tacattgacttccgacaggatctgggctggaagtgggtccatgaacctaagggctactat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gecaacttetgeteaggecettgeceatacetecgeagtgeagacaeaaceaageaeg
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polyergin; transforming growth factor-beta 2.
African green monkey kidney epithelium, cDNA to mRNA.
Cercopithecus aethiops
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 183.8; DB 89; Length
Pred. No. 1.8e-40;
0; Mismatches 97; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         301 ctctccaacatggtggtgaagtcttgtaaatgtagctga 339
                                                                                                                                                                                                                                                                                                                                                                                                            /note="polyergin precursor"
                                                                                                                                                                                                                                                                                                                  /organism="Cercopithecus
                                                                                                                                                                                                                                                                                                                                                                                                                                              /protein_id="AAA35358.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YIGKTPKIEQLSNMIVKSCKCS"
                                                                                                                                                                                                                                                                                                                                                                        /note="polyergin mRNA"
                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:9534"
<1. .>1585
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1106. .1441
/note="polyergin"
                                                                                                                                                                                                                                                                                                                                                                                                                             /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 54.2%;
Best Local Similarity 71.4%;
Matches 242; Conservative
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                                                                                                                                                                                                                                                                                                1. .1585
                                                                                                                                                   Holley, R.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unreported.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    487
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0
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1 (bases 1 to 477)

Mulheron, G.W., Mulheron, J.G., Danielpour, D. and Schomberg, D.W.
Porcine granulosa cells do not express transforming growth factor-beta 2 (TGF-beta 2) messenger ribonucleic acid: molecular basis for their inability to produce TGF-beta activity comparable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gocaacttotgotcaggocottgocoatacotocgoagtgoagacacaaccacagcacg 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="Transforming Growth Factor-beta 2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 477;
                                                                                                                                    S. scrofa mRNA for transforming growth factor beta X70142 S48994 X70142.1 GI:312949
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                                                                                                                                                                                X70142.1 GI:312949
TGF-beta 2; transforming growth factor-beta2
                                                                                                                                                                                                                                                                                                                                                                                                                                                             1. .477 '-
/organism="Sus scrofa"
/db_xref="taxon:9823"
/cell_type="1-3mm size follicles"
<1. .>477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 184; DB 7;
Pred. No. 1.9e-40;
to that of rat granulosa cells
Endocrinology 131 (6), 2609-2614 (1992)
93076683
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71.7%;
                                                                                                                                477 bp
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124 C
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Length 1585;

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ORGANISM

REFERENCE AUTHORS

TITLE

TITLE JOURNAL AUTHORS MEDLINE REFERENCE JOURNAL

FEATURES

ACCESSION VERSION KEYWORDS

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7. 339 / Advanism="synthetic construct" / Advaref="taxon:32630" 1. 339 / Note="Protein sequence is in conflict with the conceptual
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /translation="aldaaycfrnvqdncclrplyidfkrdlgwkwihepkgynanfc
agacpylwssdyqysrvlslynfinpeasaspccvsqdleplfilxyigktprieqls
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 339)
                                                                                                                             synthetic construct
artificial sequence.
1 (bases 1 to 339)
Cerletti,N., mcMaster,G.K., Cox,D., Schmitz,A. and Meyhack,B.
Process for the production of biologically active protein (e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tacattgacttccgacaggatctgggctggaagtgggtccatgaacctaagggctactat 120
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sapiens TGF-beta 2 peptide seq ID No:2
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Pred. No. 6.2e-40;
0; Mismatches 98
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                                                                                                                                                                                                                                                                                      Patent: EP 0433225-A 3 19-JUN-1991;
CIBA-GEIGY AG
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/transl_table=11
/product="TGF-beta 2"
/protein_id="CAA01386.1"
/db_xref="GI:4529904"
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al Similarity 71.1%;
241; Conservative
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                                                   GI:513239
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ACERQRYTGERYAKEVHKIDMQPPPPAENYIPKHYNPYERRLREDYSSMEKNASNL
VKAELRIFRLQNPKRARVSEQRIELYQILGHKDLPTSPTQRYIDSKVVRTRTEGEWLSFD
VTEAVSEWLLHRDRNGFKISLHCPCCTFVPSNNYIIPNKSEELEARFAGIDDSFVHG
GDLKMFKKRRHSGQSPHLLLMLLPSYRLESQHKSHRQKRALDAAFCFRNVQDNCCLRS
LYIDFKKDLGWKWHIRERKGYRANFCGAACPYIWSADTQHSNILGLYWTINPEASASPC
CVSQDLEDFYILYYIGKTPRIGGLSNM
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                                                                                                                                                                                                                                                                                                                                                                                            2 (bases 1 to 1083)
Sumathy, K., Desai, K.V. and Kondaiah, P.
Direct Submission
Submitted (14-AUG-1996) Center for Reproductive Biology and
Molecular Endocrinology, Indian Institute of Science, Bangalore,
Karnataka 560 012, India
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/protein_id="AAB62983.1"
/db_xref="GI:1519489"
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Pred. No. 4.6e-40;
0; Mismatches 81;
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/db_xref="taxon:7962"
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1. .1083
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/protein_id="CAA03114.1"
/brotein_id="C12302322"
/da_xxef="G1:2302322"
/translation="ALDAAYCFRNYQDNCCLRPLYIDFRRDLGWKWIHEPKGYNANFC
AGACPYLWSSDTQHSRVLSLYNTINPEASASPCCVSQDLEPLTLYYIGKTPKIEQLS
NMIVKSCKCS"
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1 .336
/note="Protein sequence is in conflict with the conceptual
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                                                                                                                                               Length 339;
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McMaster,G.K., Cox,D., Cerletti,N. and Kuhla,J.
Novel hybrid transforming growth factors
tent: EP 0542679-A 2 19-MAY-1993;
CIBA-GEIGY AG
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                                                                                                                                            Query Match 53.7%; Score 182.2; DB 9; Best Local Similarity 71.1%; Pred. No. 6.2e-40; Matches 241; Conservative 0; Mismatches 98;
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Other publication AU 3109595 960222.
Location/Qualifiers
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CIBA GEIGY AG (CH)
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                                                          1. .339
/organism="Homo sapiens"
/db_xref="taxon:9606"
a 77 c 70 g 94

    .339
    /organism="unidentified"

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Sequence 3 from Patent W09603432.
A48551
A48551.1 GI:2302321
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Cerletti, N.
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//ab.xref="01:2300.336"
//translation="ALDAAVCERNYODNCCLRPLYIDFKRDLGWKWIHEPKGYNANFC
AGACPYLWSSDTQHSRVLSLYNTINPEASASPCCVSQDLEPLTILYYIGKTPKIEQLS
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Cerletti,N.
NEW PROCESS FOR THE PRODUCTION OF BIOLOGICALLY ACTIVE PROTEIN
PATENT: WO 9663433.A 3 08-FEB-1996;
CIBA GEIGY AG (CH)
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Score 182.2; DB 9;
Pred. No. 6.2e-40;
0; Mismatches 98;
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Pred. No. 6.2e-40;
0; Mismatches 98
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/product="HUMAN TGF-BETA2"
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Sequence 3 from Patent WO9603433.
A48565
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illarity 71.1%;
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Best Local Similarity 71.1
Matches 241; Conservative
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Best Local Similarity
Matches 241; Conserv
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artificial sequence.
1 (bases 1 to 342)
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Unclassified.
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I (bases 1 to 339)
Hall,F.L., Nimni,M.E., Tuan,T., Wu,L. and Cheung,D.T.
Hatl,F.L., Nimni,M.E., Tuan,T., Wu,L. and cheung,D.T.
transforming growth factor-.beta. having a collagen binding site
patent: US 5800811-A 31 01-SEP-1998;
Location/Qualifiers
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                          TACATTGATTTCAAGAGGGATCTAGGGTGGAAATGGATACACGAACCCAAAGGGTACAAT 120
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                                                                             GTCCTGAGCTTATATATACCATAAATCCAGAAGCATCTGCTTCTCCTTGCTGCGTGTCC
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1 (bases 1 to 339)
Cerletti,N., McMaster,G.Kent, Cox,D., Schmitz,A. and Meyhack,B.
Process for refolding recombinantly produced TGF-.beta.-like
proteins
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   07-0CT-1997
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                                                                                                                                                                                                                                                                                                                                                                           1 gotttggacaccaattactgcttccgcaacttggaggagaactgctgtgtgcgcccctc
                                                                                                                                                                                                                                                                                                              Length 339;
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   PAT
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Pred. No. 6.2
                                                                                                                                                                                                                                                                                                                                             0; Mismatches
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                                                                                                                                                                                    Patent: US 5650494-A 2 22-JUL-1997;
Location/Qualifiers
1. .339
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                 5650494
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/organism="synthetic or/db_xref="taxon:32630"
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Sequence 2 from patent US 56
156855
156855.1 GI:2477268
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77 c 70 g
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/gene="G-TsF"
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/product="q1ioblastoma-derived T-cell suppressor factor"
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De Martin, R., Fontana, A., Hofer, E., Hofer-Warbinek, R. and Wrann, M. Production and use of a novel T-cell suppressor factor Patent: EP 026861-A 6 25-MAY-1988;
SANDOZ AG; SANDOZ-PATENT-GMBH; SANDOZ-ERFINDUNGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Pred. No. 6.1e-40;
0; Mismatches 98
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/db_xref="taxon:9606"
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71.1%;
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LSKLKLTSPPEDYPEEVPPEVISIYNSTRDLLQEKASRRAAACERERSDEEYYAKE
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GFKISLHCPCCTFVPSNNYIIPNKSEELEARFAGIDGTSTYTSGDQKTIKSFTKKNSG
KTPHLLLMLLPSYRLESQQTNRRKKRALDAAYCFRNVQDNCCLRPLYIDFKRDLGWKW
IHEPRGYNANFCAGACPYLMSSDTQHSRVLSLYNIINPEASASPCCVSQDLEPLTILY
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386 c 354 g 432 t
tacattgacttccgacaggatctgggctggaagtgggtccatgaacctaagggctactat 120
                                                                                                                   124 GCCAACTTCTGTGCTGGAGCATGCCCGTATTTATGGAGTTCAGACACTCAGCACAGCAGG 183
                                                                                                                                                                                                 244 CAAGATTTAGAACCTCTAACCATTCTCTACTACATTGGCAAAACACCCAAGATTGAACAG 303
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                                                TACATTGATTTCAAGAGGGATCTAGGGTGGAAATGGATACACGAACCCAAAGGGTACAAT
                                                                                                 gccaacttctgctcaggcccttgcccatacctccgcagtgcagacacaacccacaggacg
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/organism="synthetic construct"
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1088, 1422
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synthetic construct
artificial sequence.
1 (bases 1 to 1695)
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Matches 241; Conservative
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/COGGUESCATION
/COGGUESCATION
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//FOCCHALL 1354 g 432 t
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                                        HSGTSF 1695 bp mRNA PRI 27-MAR-1995
Human mRNA for glioblastoma-derived T-cell suppressor factor G-TsF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Complementary DNA for human glioblastoma-derived T cell suppressor factor, a novel member of the transforming growth factor-beta gene
                                                                                                                                                                                           Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1695)
Hofer, E.
Direct Submission
                                                                                                                                                                                                                                                                                                                 Submitted (02-NoV-1987) Hofer, E., Sandoz AG, Department for Biotechnology, Preclinical Research, Bullding 386/328, Sandoz AG, CH-4002 Basel
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de Martin,R., Haendler,B., Hofer-Warbinek,R., Gaugitsch,H.,
Wrann,M., Schlusener,H., Selfert,J.M., Bodmer,S., Fontana,A. and
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1. .1695
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/clone="lambda SUP25, lambda SUP40, lambda SUP42"
/note="griff precursor"
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T-cell suppressor factor; transforming growth factor-beta2.
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                                                                                      transforming growth factor-beta2, TGF-beta2)
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tacattgacttccgacaggatctgggctggaagtgggtccatgaacctaagggctactat 120
                                                                                                                                                                                                                                                                                                                                                                                    /note="TGB-beta-2 mRNA"
                                                                                                                                                                                                                                                                                             /db_xref="taxon:9606"
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599 c 512 g
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Webb,N.R., Madisen,L., Rose,T.M. and Purchio,A.F.
Structural and sequence analysis of TGF-beta 2 cDNA clones protective different precursor proteins produced by alternative mRNA Gaps 1 (bases 1 to 2570)
Madisen,L., Webb,N.R., Rose,T.M., Marquardt,H., Ikeda,T.,
Twardzik,D., Seyedin,S. and Purchio,A.F.
Transforming growth factor beta 2: cDNA cloning and sequence SLYNTINPEASASPCCVSQDLEPLTLLYYIGKTPKIEQLSNMIVKSCKCS" /note="transforming growth factor-beta-2 precursor" Score 182.2; DB 97; Length 2570; Pred. No. 4.7e-40; 0; Mismatches 98; Indels 0; 1458. 1793 /note="transforming growth factor-beta-2" son 513 q 687 t /clone=" lambda-PC21" /tissue\_type="tamoxifen-treated /map="19q13.1-q13" /protein\_id="AAA50404.1" /db\_xref="GI:339550" .2570
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MCMaster.G.K., COx.D., Cerletti,N. and Kuhla,J.

Novel hybrid transforming growth factors

Patent: EP 042679-A 6 19-MAY-1993;

CIBA-GEIGY AG
                                                                                                                                                                                                                                              A23756 336 bp mRNA PAT TGF-beta2(44/45)beta1 hybrid coding region.
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/db_xref="taxon:9606"
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VYKIDMLPYYTSENVI PPSYTTPYFRIVREDVSSMERNASNIVKAEFERYFRLMYTKAR
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EVELSLCPCTFI PSNNY I IPNKSEELETFRAGIDDAYMYAGGDSK KRYTGRE
TPHLLMLLPSYRLESQQSSRRKKRALDAAYCFRNVQDNCCLRPLY IDPKKDLGWKWI
HEPKGYNANFCAGACPYLMSSDTQHSRVLSLYNTINPEASASPCCVSQDLDSLTILYY XLTGPB2 2724 bp mRNA VRT 08-NOV-1993 Xenopus laevis TGF-beta2 mRNA for transforming growth factor-beta2. X51817 /db\_xref="SWISS-PROT:P17247"
/translation="MMYYVLFTFLTLDLAPVALSLSTCSALDMDQFMRKRIEAIRGQI conceptual Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopodinae; Xenopus. Direct Submission Submitted (07-FEB-1990) Rebbert M.L., Laboratory of Molecular Genetics, National Institute of Child, Health and Human Development, Bldg 6 Rm 324, Bethesda MD 20892, U S A sequence revised by [3] Submitted (08-NOV-1993) Rebbert M.L., Laboratory of Molecular Genetics, National Institute of Child, Health and Human Development, Bldg 6 Rm 324, Bethesda MD 20892, U S A On Nov 9, 1993 this sequence version replaced gi:65136. Data kindly reviewed (16-Aug-1990) by Rebbert .M.L. Location/Qualifiers conflict with the Rebbert, M.L., Bhatia-Dey, N. and Dawid, I.B.
The sequence of TGF-beta 2 from Xenopus laevis
Nucleic Acids Res. 18 (8), 2185 (1990)
Mc16578 X51817.1 GI:414789 growth factor; transforming growth factor. African clawed frog. Xenopus laevis ü /product="prepro-polypeptide" /protein\_id="CAA36116.1" /db\_xref="GI:65137" 1. .2724 /organism="Xenopus laevis" /db\_xref="taxon:8355" /cell\_line="XTC cells" /clone\_lib="lambda\_ZAP" 79. .1320 /db\_xref="SWISS-PROT:P17247" /product="signal peptide" 136. 1317 /note="Protein sequence is /product="mature TGF-beta2" 527 c 543 g 788 t /product="pro-TGF-beta2" /protein\_id="CAA36117.1" /db\_xref="G1:1334690" IGNKPKIEQLSNMIVKSCKCS" /codon\_start=1 /codon\_start=1 translation" (bases 1 to 2724) (bases 1 to 2724) (bases 1 to 2724) Direct Submission Rebbert, M.L. Rebbert, M.L. ď 866 BASE COUNT ORIGIN

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /translation="TFLLLHLVPVALSLSTCSTLDMDQFMRKRIEAIRGQILSKLKLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 (bases 1 to 1197)
Ramesh,G., Kondaiah,P. and Seshagiri,P.B.
Differential expression and selective localization of transforming growth factor beta isoforms in the hamster uterus during estrous
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Sciurognathi; Muridae; Cricetinae;
                                                                                                                                                                                           982 GCTCTCGATGCCGCCTACTGCTTTAGGAACGTCCAGGACAATTGCTGTCTACGTCCCTTA 1041
                                                                                                                                                                    61 tacattgacttccgacaggatctgggctggaagtgggtccatgaacctaagggctactat 120
                                                                                                                                                                                                                                        121 gecaactictgeteaggeeettgeecataceteegeagtgeagacacaaceacageacg 180
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                                                                      Gaps
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Ramesh, G., Kondalah, P. and Seshagiri, P.B.
Direct Submission
Submitted (15-AUG-2000) Molecular Reproduction, Development
Genetics, Indian Institute of science, Bangalore, Karnataka
                                                                                                                                                                                                                                                                                                           181 gtgctgggactgtacaacactctgaaccctgaagcatctgcctcgccttgctgcgtgccc
                                                                                                                                                                                                                                                                                                                                                                                241 caggacctggagccctgaccatcctgtactatgttgggaggacccccaaagtggagcag
                                                                    0;
                              Length 2724;
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/protein_id="AAG02247.1"
/db_xref="GI:9965486"
                            Score 179; DB 8; Length 27
Pred. No. 3.6e-39;
0; Mismatches 100; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          301 ctctccaacatggtggtgaagtcttgtaaatgtagctga 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Mesocricetus auratus"
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Mammalia; Eutheria; Rodentia;
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                              52.8%;
70.5%;
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                                                               Matches 239; Conservative
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Burt,D.W. and Jakowlew,S.B.
Correction: a new interpretation of a chicken transforming growth factor-beta 4 complementary DNA
MOL. Endocrinol. 6 (6), 989-992 (1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 (bases 1 to 1256)
Jakowlew, S.B., Dillard, P.J., Sporn, M.B. and Roberts, A.B.
Complementary deoxyribonucleic acid cloning of a messenger
ribonucleic acid encoding transforming growth factor beta 4 from
                                                                                                                                                                                                                                                                      61 tacattgacttccgacaggatctgggctggaagtgggtccatgaacctaagggctactat 120
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                                                                                                                                                                                   Gaps
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Chicken transforming growth factor beta 4 (TGF-beta 4) mRNA,
partial cds.
                                                                                                                                                             gctttggacaccaattactgcttccgcaacttggaggagaactgctgtgtgcgcccctc
                                                                                                                                                                                                                                                                                                                              181 gigciggacigiacaacacicigaacccigaagcaicigccicgccitgcigcgigcc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                caggacctggagccctgaccatcctgtactatgttgggaggaccccaaagtggagcag
                                                                            Length 1197;
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Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
                                                                                                                     86; Indels
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                                                                            DB 94;
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                                                                                                  .5e-38;
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/db_xref="taxon:9031"
/dev_stage="embryo"
/clone="pTGFB-ChX63"
/tissue_type="chondrocyte"
<1. .1256
                                                                            Score 174.4;
Pred. No. 7.5e
0; Mismatches
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growth factor; transforming
Chicken cDNA to mRNA.
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/organism="Gallus
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                                                                            51.4%;
72.4%;
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/product-"transforming growth factor beta"

protein_1d="AAD45726.1"

/db_xref="G1:616327"

/translation="CFSSTEKNCCVRQLYRDFRKDLGWKWIHEPKGYHANFCLGPCPY

    .18
/note="phosphorylated by casein kinase II; phosphorylation

                                                                                                                                                                                                                                                                                          13. .21
/note="phosphorylated by protein kinase C; phosphorylation
                                                                                                                                                                                                            IWSLHTQYSKVLALYNQHNPGASASPCCVPQALEPLPIVYYVGRKPKVEQLSNMFVR"
                                                                                                                                                                                                                                                                                                                                                                         /note="phosphorylated by tyrosine kinase; phosphorylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AF169347 278 bp mRNA ROD 15-AUG-1999
Cavia porcellus transforming growth factor-beta mRNA, partial cds.
AF169347
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
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Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     241 CCCATCGTCTACGTGGGCCGCAAGCCCAAGGTGGAGCAGTTGTCCAACATGTTCGTG 300
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Morishima,Y., Uchida,Y., Nomura,A., Ishii,Y., Sakamoto,T. and Sekizawa,K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 (bases 1 to 278)
Morishima,Y., Uchida,Y., Nomura,A., Ishii,Y., Sakamoto,T. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19 tgcttccgcaacttggaggagaactgctgtgtgcgccccctctacattgacttccgacag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 302;
                                                                                                                                                                                                                                                                                                                                                                                                               /note="Region: TGF-beta family signature"
256. .267
/organism="Meriones unguiculatus"
/db_xref="taxon:10047"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; DB 94;
4.1e-37;
                                                      /tissue_type="renal lymph node"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 172; DB Pred. No. 4.1e-0; Mismatches
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g
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/note="amidation s
                                                                                               /note="TGF-beta"
                                                                                                                 /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       50.78;
                                    /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                domestic guinea pig.
                                                                                                                                                                                                                                                                                                                                                                                                           .126
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AF169347
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SOURCE
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                                                      /product-"transforming growth factor beta 4 precursor"
protein_id="AAB05637.1"
/db_xref="GI:1262438"
/translation-"ALSTCQRLDLEAAKKRIEAVRGQILSKLRLTAPPPASETPPRP
                                                                                                                               LEDDVARALYNSTOELLKORARIRPPPOGPDEYWAKELERIPMETTWDGAMEHWOPQSH
SIFFYFNYSTREGRPTLLHRAELBWLROKAADSAGTEORLELYOGYGNNSWRYLH
GRSYRATADDEWLSFDVFDAVHQWLSGSELLGVFKLSVHCFCFEMGFGHAEEMRISIEG
FEQQRGDMGSTAKKHRVPYYLAMALPAERANELHSARRRDLDTDYCFGFGFDFEKNC
CVRPLYIDFRKDLQWKWIHEPKGYMANFCMGPCPYIWSADTQYTKVLALYNOHNPGAS
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Meriones unguiculatus transforming growth factor beta mRNA, partial
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Sciurognathi; Muridae; Gerbillinae;
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Rao, U.R. and Klei, T.R.
Direct Submission
Submitted (21-JUN-1999) Microbiology and Parasitology, School of
Veterinary Medicine, South Stadium Drive, Baton Rouge, LA 70803, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  972 GCGCTGTACAACCAACACAACACCGGGGGCTTCGGCCGCTCCGTGCTGCGTCCCGCAGACC 1031
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gacttecgacaggatetgggetggaagtgggtecatgaacetaagggetactatgecaae 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         911
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ttctgctcaggcccttgcccatacctccgcagtgcagacacaaaccacagcacggtgctg
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                                                                                                                                                                                                                                                                         /product="transforming growth factor beta 4"
450 c 379 q 196 t
                                                                                                                                                                                                                                                                                                                                                                           Length 1256;
                                                                                                                                                                                                                                                                                                                                                                       Score 173; DB 8; Length 12
Pred. No. 1.8e-37;
0; Mismatches 100; Indels
                                                                                                                                                                                                                                   AAPCCVPQTLDPLPIIYYVGRNVRVEQLSNMVVRACKCS"
780. .1121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="TGF-beta 4 mRNA"
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
Meriones.
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1. .302
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70.0%;
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                                                                                                                                                                                                                                                                                              450 c
                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 70.0
Matches 233; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mongolian gerbil.
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                                                                                                                                                                                                                                                       mat_peptide
                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local
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Gaps

240

SOURCE ORGANISM

AUTHORS TITLE

JOURNAL REFERENCE

REFERENCE

AUTHORS TITLE

JOURNAL

LOCUS DEFINITION

ACCESSION VERSION KEYWORDS

RESULT 92

AF161218

247

q

δ g source

FEATURES

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Query Match
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ORIGIN
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                                                     TITLE
JOURNAL
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   REFERENCE
                      AUTHORS
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            Direct Submission
Submitted (16-JUL-1999) Department of Pulmonary Medicine, Institute
of Clinical Medicine, University of Tsukuba, 1-1-1 Tennoudai,
Tsukuba, Ibaraki 305-8575, Japan
                                                                                                                                                                                                                             <1. >>278
/codon_start=1
/product="transforming growth factor-beta"
/product="datab49347.1"
/db_xref="G1:5732936"
/translation="PLDTNVCPSSTERNCCVRQLYIDFRKDLGWKWTHEPKGYHANFC
LGPCPYIWSLDTQYSKVLALYNOHNPGASAAPCCVPQALEPLPIVYYVG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cloning and sequencing hybrid striped bass (Morone saxatilis x M. chrysops) transforming growth factor-beta (TGF-beta), and development of a reverse transcription quantitative competitive polymerase chain reaction (RT-qcpCR) assay to measure TGF-beta mRNA
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes;
Percoidei; Moronidae; Morone.
1 (bases 1 to 1514)
Harmis,C.A., Kennedy-Stoskopf,S., Horne,W.A., Fuller,F.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AF140363 1514 bp mRNA VRT 18-FEB-2000 Morone chrysops x Morone saxatilis transforming growth factor-beta precursor (TGF-beta) mRNA, complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ttgacttccgacaggatctgggctggaagtgggtccatgaacctaagggctactatgcca 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tgggactgtacaacactctgaaccctgaagcatctgcctcgccttgctgcgtgccccagg 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     185 TGGCCCTGTACAACCAGCACAACCCGGCGCTTCGGCGGCGCCTTGCTGTGTGCCGCAGG 244
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tggacaccaattactgcttccgcaacttggaggagaactgctgtgtgcgcccctctaca 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5 TGGACACCAACTATTGCTTCAGCTCCACGGAGAAGAACTGCTGTGTGCGGCAGCTCTACA 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                               Score 170; DB 94; Length 278;
Pred. No. 1.5e-36;
0; Mismatches 65; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                         /db_xref="taxon'10141"
/cell_type="epithelium"
/tissue_type="trachea"
/note="obtained from injured tissue"
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                                                                                                                      /organism="Cavia porcellus"
                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                          77 g
                                                                                                                                          /strain-"Hartley"
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                                                                                                                                                                                                                                                                                                                                                                                                                               tch 50.1%;
al Similarity 76.3%;
209; Conservative
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Sekizawa, K.
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Best Local :
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KEYWORDS
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                                                                                    FEATURES
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/translation="MRIAFLMLVVVYTVGNVSGMSTCKTLDLEMVKKKRIEAIRSQIL
SKLRLPKEPEPDQAGDEEEIPTPLLSLYNSTKEMLKEQQTEVQTDISTEQEEEEYFAK
VLHKFNMTRKNNTDTTKKMFPNISEIRESVGDYRLJSAELANLIKKTTIVDEGNVE
YSGLGEPPFYLASRFITASPTTYTLQDMLKGTDDEQGFQLRLFCECNNVS
AGETIERPSTGSIDFORTWRDMLATTQQPPYILTMSIPQNISSPSTSRKRESTETKD
VCTAQTETCCVRSLYIDFRKDLGWKWIHKPTGYNANYCMGSCTYIMNAENKYSQILAL
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                                                                                                 North
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1055 AATGCTGAAAACAAATATTCTCAGATTTTGGCCTTGTATAAGCATCACAACCCAGGAGCC 1114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  935 GAGACCTGTTGCGTGCGGAGCTTGTACATCGACTTCAGGAAAGATCTGGGATGGAAGTGG 994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                          Submitted (05-APR-1999) MPP, College of Veterinary Medicine, Carolina State University, 4700 Hillsborough St., Raleigh, NC
                                                                                                                                                                                                                                                                                                                                                                                                               /product="transforming growth factor-beta precursor"
/protein_id="AAD46997.1"
/db_xref="GI:5690246"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gagaactgctgtgtgcgcccctctacattgacttccgacaggatctggggctggaagtgg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YKHHNPGASAQPCCVPQALEPLPILYYVGRQHKVEQLSNMIVKSCKCS"
2 (bases 1 to 1514)
Harms,C.A., Kennedy-Stoskopf,S., Horne,W.A., Fuller,F.J.
Tompkins,W.A.F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'note="Region: latency associated peptide (LAP)"
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0
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                                                                                                                                                                                  1. .1514
/organism="Morone chrysops x Morone saxatilis"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tetrabasic cleavage site'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="transforming growth factor-beta"
359 c 378 g 329 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'note="Region: RGD integrin binding site"
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Pred. No. 1.7e-34;
0; Mismatches 88;
                                                                                                                                                                                                                                                                            /tissue_type="anterior kidney"
1. .1514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'note="encodes transforming
                                                                                                                                                                                                                               /db_xref="taxon:45352"
/cell_type="mononuclear"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'note="Region: RKKR
                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                       /gene="TGF-beta"
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/gene="TGF-beta"
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/gene="TGF-beta"
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/gene="TGF-beta"
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71.0%;
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Matches 215; Conservative
                                                                       Direct Submission
                                                                                                                                       27606, USA
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Chen, E. Y.
Chen, E. Y.
Chen, E. Y.
Direct Submission
Submitsed (23-MAR-1989) Chen E. Y., Genentech Inc., 460 Pt. San
Bruno Blvd., San Francisco, CA 94080, USA
2 (bases 1 to 1676)
Derynck, R., Lindquist, P. B., Lee, A., Wen, D., Tamm, J., Graycar, J. L.,
Rhee, L., Mason, A. J., Miller, D. A., Coffey, R. J., Moses, H. L. and
Chen, E. Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhin1; Hominidae; Homo.
1 (bases 1 to 1676)
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                                                            HSTGF37 1676 bp DNA PRI 26-JUN-1997
H.sapiens gene for transforming growth factor-beta 3 (TGF-beta
exon 7.
                                                                                                                                                                                                                                                                                                                                                       X14891.1 GI:37087
growth factor; transforming growth factor; transforming growth
factor-beta 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A new type of transforming growth factor-beta, TGF-beta 3 EMBO J. 7 (12), 3737-3743 (1988) 89091120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
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                                                                                                                                                            1627 TGGTAAGGTCTTGCAACTGCAGCTGA 1652
                                                                                                                                        314 tggtgaagtcttgtaaatgtagctga 339
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1356
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108. .266
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 414 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 47.2
Best Local Similarity 100.
Matches 160; Conservative
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1 (bases 1 to 2754)

Kondalah, P., Sands, M.J., Smith, J.M., Fields, A., Roberts, A.B.,
Sporn, M.B. and Welton, D.A.
Identification of a novel transforming growth factor-beta (TGF-beta 5) mRNA in Xenopus laevis
J. Blol. Chem. 265, 1089-1093 (1990)

90110090

Draft entry and computer-readable sequence for [1] kindly submitted by P.Kondalah, 21-NOV-1989.

1. 2754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QVYRFESITELEDHERFKFRASHVRRNVGMNSLLHARELRNYKKQTDKNMDORMELR
WKYQENGTTHSRYLESKYITPVTDDEWMSFDVTKTVNEWLKRAEENEOFGLOPACKCP
FPOAKDIDIDEPPALSKOIASLSKRWTKPYLMITSWPAERIDTVTSSRKKRCVGOEY
CFGNNGPNCCVKPLYINFRKDLGWKHIHEPKCYEANYCLGNCPYIWSMDTQYSKVLSL
YNQNNPGASISPCCVPDVLEPLPIIYYVGRTAKVEQLSNMVYRSCNCS"
1314. 1649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /protein_id="AAA49968.1"
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                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="transforming growth factor-beta 5 signal peptide"
504. .1652
/note="transforming growth factor-beta (TGF-beta 5)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1447 TAGGAAATIGICCITACATCIGGAGCATGGATACTCAGTACAGCAAGGTGCTATCACTTT 1506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1327 AGTATTGCTTTGGGAACAATGGGCCAAACTGCTGTGTGAAACCTCTTTACATAAATTTTC 1386
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                                                                                                                  XELTGFBS 2754 bp mRNA VRT 28-APR-1993 X.laevis transforming growth factor-beta (TGF-beta 5) mRNA, complete cds.
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                                                                                                                                                                                                                                   transforming growth factor-beta.
X.laevis neurula, cDNA to mRNA, clone XC-beta-4.
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Pred. No. 3e-34;
0; Mismatches 103;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Xenopus laevis"
/db_xref="taxon:8355"
504. .566
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/note="putative"
2737. .2742
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Best Local Similarity 68.4%;
Matches 223; Conservative
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J05180.1 GI:214821
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                                                                                                                                                                                                                                                                             Xenopus laevis
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                                      1235 TAA 1237
337 tga 339
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SOURCE
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                                                                                                                  XELTGFB5
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                                                                                                                                                                                                                                                      Length 1676;
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/tissue_type="liver"
/clone="lambda beta3-24 and beta 3-5"
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                                                                                                                                                                                                                                                   47.2%; Score 160; DB 93;
100.0%; Pred. No. 6.8e-34;
ive 0; Mismatches 0;
                                                                                                                                                                                                 435
                                      108. .266
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108. .1356
/gene="TGF-beta 3"
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repeat_region
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                                                                                                                                                                                                      DJ270M14 192126 bp DNA PRI 14-JUL-1999
Homo sapiens chromosome 14q24.3 clone BAC270M14 transforming growth
factor-beta 3 (TGF-beta 3) gene, complete cds; and unknown genes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (20-NOV-1998) Department of Molecular Biotechnology, Box 357730 University of Washington, Seattle, WA 98195, USA On Jul 14, 1999 this sequence version replaced gi:3928926. Sequence methodology: High Redundant shotgun sequence using plasmid subclones. Interspersed Repeats were identified with RepeatMasker (available from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /translation="VTNLNLATGIINRSSASAPPTLRPIISPSGPTWSTQSDPQAPENHSSSPGSSFI"
                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 192126)
Madan,A., Rowen,L., Qin,S., Dickhoff,R., Shaffer,T., James,R.,
Abbasi,N., Loretz,C., Madan,A., Dors,M., Dahl,T., Hall,J., Lasky,S.
and Hood,L.
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Trpt_family="LINE2"
join(<2488 . 2424,3084. .3093)
Anote="intron-exon boundaries defined in relation to ESTs
in Genbank Accession Numbers AA399388 and A398013"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Complete genomic sequence of human transforming growth factor-beta
167 CCAGGACCTGGAGCCCCTGACCATCCTGTACTAGGAGGAGGACCCCCAAAGTGGAGCA 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     http://ftp.genome.washington.edu/RM/RepeatMasker.html)
Location/Qualifiers
1. 192126
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complement(292. .317)
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complement(689. .713)
/rpt_family="AT_rich"
complement(689. .1277)
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complement (6573, .6654)
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6920, .7214
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complement(2078. .2110)
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                                                                                                                                                                                                                                                                                                 AF107885.2 GI:5468516
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2 (bases 1 to 192126)
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AUTHORS
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complement(27921. .27949)
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complement(28064. .28276)
/rpt_family="MIR"
28990. .29291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /rpt_family="(CA)n"
complement(20378, .205co.
/rpt_famil-
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12845. .13063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           rpt_family="MLT1F"
omplement/1000
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omplement(22222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /rpt_family="MLT1F" complement(23293, .23125) /rpt_family="MLT1F" 
                                                                                                                                                                                                              complement(8985. 9052)
/rpt_family="(TAAA)n"
complement(10200. 10497)
/rpt_family="AluJb"
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10754. .21061
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omplement of the state of
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/rpt_family="LIME3A"
26125. .26157
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complement(26374. .26660)
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26987. .27179
                                                                                                                                                                                                                                                                                                                                                                                     complement(10691, .10758)
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/rpt_family="LIPA8"
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/rpt_family="AT_rich"
.5938. .16174
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19189. 19222
'rpt_family="AT_rich"
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complement(11800. .12
                                       8770. .8813
/rpt_family="(CA)n"
8838. .8939
/rpt_family="L1MB2"
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8091. .18287
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complement(21737...
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/rpt_family="MIR"
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/rpt_family="L1"
18140. .19188
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'rpt_family="MIR"
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17-JUL-1998

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (30-JUL-1996) C.J. Secombes, Univ. of Aberdeen, Dept. of Zoology and Medicine, Therapeutics,, Tillydrone Avenue, Aberdeen AB24 2TZ, UK
On Aug 2, 1996 this sequence version replaced gi:1438515.
                                                                                                                                                                                                                                                                                                                                                                                                                               Oncorpynchus mykiss
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
1 (bases 1 to 1152)
Hardie, L. J., Laing, K. J., Daniels, G. D., Grabowski, P. S.,
Cunningham, C. and Secombes, C. J.
Isolation of the first piscine transforming growth factor B gene: analysis reveals tissue specific expression and a potential regulatory sequence in rainbow trout (Oncorhynchus mykiss)
Db 141767 CCAGGACCTGGAGCCCTGACCATCTTGTACTATGTTGGGAGGACCCCCAAAGTGGGAGCA 141708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (11-JUL-1996) C.J. Secombes, Univ. of Aberdeen, Dept. o
Zoology and Medicine, Therapeutics,, Tillydrone Avenue, Aberdeen
AB24 2TZ, UK
                                                                                                                                                                                                                                                 OMTGFB 1152 bp mRNA VRT
O.mykiss mRNA for transforming growth factor beta.
X99303
                                                                            Location/Qualifiers
1. 1152
1. organism="Oncorhynchus mykiss"
//organism="Oncorhynchus mykiss"
//db_xref="taxon:8022"
/tissue_type="head"
/tissue_type="kidney"
//cell_type="macrophages"
<1. 616
                                                                                                                                                                                                                                                                                                                                                                                       IGF-beta; transforming growth factor beta.
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260. .271
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3 (bases 1 to 1152)
Secombes, C.J.
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2 (bases 1 to 1152)
Secombes, C.J.
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/note="intron-exon boundaries based in relation to EST
GenBank Accession Number AA382660"
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100.0%; Pred. No. 3.6e-34;
ive 0; Mismatches 0; Indels 0;
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/rpt_family="MER64"
complement(41322. 41473)
/rpt_family="MER20"
complement(4326. 45023)
/rpt_family="L1MB5"
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complement(46860. .46969)
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47877. .48017
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complement(40607, .4177-17pt_family="Alusx"
/rpt_family="Alusx"
              /rpt_family="Alusx"
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/rpt_family="Alusg"
complement(39652. .40120)
/rpt_family="L1"
                                                                       complement(30012. .30235)
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                                                                                                                       'rpt_family="MER5A"
complement':
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complement (34792. .34838)
/rpt_family="(GAAA)n"
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37627. .37665
                                                                                                                                                                                      complement(30430. 30493)
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/rpt_family="AluSp"
complement(33014. .33060)
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/rpt_family="AT_rich"
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/protein_id="AAC79729.1"
/db_xref="G1:3928929"
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/rpt_family="POLY_A"
38307. .38560
/rpt_family="L191_5enr
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rpt_family="AluJo"
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rpt_family="Alusq"
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240 ccaggacctggagccctgaccatcctgtactatgttgggaggaccccaaagtggagca 299

/product="transforming growth factor beta" 1114. 1119 1223 c 266 g 342 t

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2 (bases 1 to 379)
Derynck, R., Lindquist, P.B., Lee, A., Wen, D., Tamm, J., Graycar, J.L., Rhee, L., Mason, A.J., Miller, D.A., Coffey, R.J., Moses, H.L. and Chen, E.Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HSTGF36 379 bp DNA PRI 23-FEB-1996
H.sapiens gene for transforming growth factor-beta 3 (TGF-beta 3)
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growth factor; transforming growth factor; transforming growth
factor-beta 3.
                                                                                                                                                                                                                                                                                                                     276 tgggaggacccccaaagtggagcagctctccaacatggtggtgaagtcttgtaaatgtag 335
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                                                                                                                         307 GGAGAGTIGCTGTGTGCGAAAACTTTACATTGACTTCCGTAAGGACCTGGGCTGGAAGTG 366
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                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A new type of transforming growth factor-beta, TGF-beta
EMBO J. 7 (12), 3737-3743 (1988)
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                                          Length 1152;
                                                                     Indels
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/clone="lambda beta3-24 and beta3-5"
107. .260
                                                                    89;
                                          DB 8;
                                         Score 159.6; DB 8
Pred. No. 9.3e-34;
0; Mismatches 89
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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/usedin=X14885:TGF_mRNA
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/label=ex6
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107. .260
                                         47.18;
70.58;
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                                      Query Match 47.1
Best Local Similarity 70.5
Matches 213; Conservative
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/protein_id="BAA36950.1"
/db_xxef="61:412721"
/translation="FSTYVCFSFTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCL
GPCPYTWSLDFGYKVLALYNOHPGASAAPCCVPQALEATAHRVTTLGRKPKVE"
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I (bases 1 to 298)

Inoue, K., Kawabe, Y. and Kodama, T.
Direct Submission
Submitted (18-NOV-1998) to the DDBJ/EMBL/GenBank databases. Kenji Inoue, Research Center for Advanced Science and Technology, University of Tokyo, Molecular Biology and Medicine; 4-6-1, Komaba, Meguro, Tokyo 153-8904, Japan
(E-mail: keinoue-tky@umin.u-tokyo.ac.jp, Tel:81-3-3481-4560,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oryctolagus cuniculus mRNA for transforming growth factor beta-1, partial cds.
                                                                                                                                                                                                                                                                                   acaggatctgggctggaagtgggtccatgaacctaagggctactatgccaacttctgctc 134
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TGF-beta-1; transforming growth factor beta-1.
Oryctolagus cuniculus cDNA to mRNA.
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Inoue-K., Rawabe,Y. and Kodama,T.
Rabbit TGF-beta-1 cDNA,partial
Published Only in DataBase (1999) In press
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Search completed: October 30, 2001, 11:17:46 Job time: 6184 sec

Human TGF-beta-3. Human transforming

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Hybrid TGF-beta 2-cDNA encoding huma Transforming Growt Transforming Growt

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cDNA encoding tran CDNA encoding a ch TGFbetal 5'-UTR-CD Transforming Growt

Human pro-TGF-beta Sequence encoding CDNA encoding huma

Coding sequence of Simian Transformin Simian transformin

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Human TGF-beta 2

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P-PSDB; AAR12404.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19-JUN-1991
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AAQ11995;
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100.0%; Score 339; DB 12; llarity 100.0%; Pred. No. 3.3e-87; Conservative 0; Mismatches 0;

Query Match Best Local Similarity Matches 339; Conserv

Length 339;

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The invention covers hybrid TGF-beta molecules consisting of parts of the human isoforms TGF-betal, TGF-beta2 and TGF-beta3 (see AAQ41599, AAQ41600 and AAQ41601, respectively). The hinge points between parts derived from different parent isoforms are pref. between amino acids 44 and 45, 56 and 57, 79 and 80, 90 and 91, or 22 and 23. The hybrid molecules pronote cell migration, inhibit the growth of A375 melanoma cells, accelerate the healing of partial-thickness burn wounds and full-thickness incisional wounds and increase formation
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                                                                                                                                                                                        tacattgacttccgacaggatctgggctggaagtgggtccatgaacctaagggctactat
                                                                                                   gecaacttctgeteaggeeettgeecataceteegeagtgeagacacaaaceaageacg
                                                                                                                                         gtgctggggactgtacaacactctgaaccctgaagcatctgcctcgccttgctgctgcgtgccc
                                                                                                                                                                                                                                                                                                                                                                                                                                    -beta3; hybrid protein; wound healing; cancer treatment;
repair; growth regulation; ss.
                                                                                                                                                                                                                                         Mature human Transforming Growth Factor-beta3
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                                                                                                                                                                                                                                                                                                                                   BP
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                                                                                                                                                                                                                                                                                                                                AAQ41601 standard; cDNA; 339
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P-PSDB; AAR39640.
                                                                                                                                                                                                                                                                                                                                                                                                                                     hTGF-beta3; hybrid
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WPI; 1996-116999/12
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                                                                                            1 getttggacaccaattactgetteegeaacttggaggagaactgetgtgtgegeeeeete 60
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                                                                         1 gctttggacaccaattactgcttccgcaacttggaggagaactgctgtgtgcgcccctc
                                                                                                                                                       gccaacttctgctcaggcccttgcccatacctccgcagtgcagacacaacccacagcacg
                                                                                                                                                                               gtgctgggactgtacaacactctgaaccctgaagcatctgcctcgccttgctgcgtgccc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Prodn. of dimeric biologically active transforming growth factor by refolding denatured monomer in detergent-free folding buffer contg. specific organic solvent to improve yield
                                                          ö
                                         Length 339;
                                                          Indels
See e.g. AAQ41602-Q41607
               Sequence 339 BP; 74 A; 104 C; 86 G; 75 T; 0 other;
                                         100.0%; Score 339; DB 14;
100.0%; Pred. No. 3.3e-87;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                             Transforming growth factor type beta; TGF-beta 3; protein renaturation; protein folding; ds.
                                                                                                                                                                                                                                                           ctctccaacatggtggtgaagtcttgtaaatgtagctga 339
                                                                                                                                                                                                                                                                                                            BP
                                                                                                                                                                                                                                                                                                            mRNA; 339
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tissue.
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                                                                                                                                                                                                                                                                                                          AAT17234 standard; cDNA to
                                                  Best_Local Similarity 100.
Matches 339; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AG.
                                                                                                                                                                                                                                                                                                                                                            Human TGF-beta 3 cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1996-117000/12.
fibrous granular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GEIGY
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pPLMu yielded plasmid pPLMu.hTGF-beta 3. Non-soluble, monomeric TGF-beta 3 was recovered from E. coli LC 137/pPLMu.hTGF-beta 3 (DSM 5658) transformants. A biologically active, dimeric form of TGF-beta 3 was obtd. by refolding this monomer in detergent-free buffer cong. DMSO and/or DMF. Dimers of TGF-beta 1 (AAR92773) and TGF-beta 2 (AAR92774), and hybrid dimers (see also AAR92775), were
                                                                                                                                                                                                                                                                                                                                                                                                             180
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                                                                                                                                                                                                Length 339;
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                                                                                                                                                                                                                                 Indels
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                                                                                                                                         75 T; 0 other;
                                                                                                                                                                                              Score 339; DB 17;
Pred. No. 3.3e-87;
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/product= human_TGF-beta-3
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                                                                                                                                                                                            100.0%;
                                                                                                                                         Sequence 339 BP; 74 A; 104 C;
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Best Local Similarity 100.
Matches 339; Conservative
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                                                                                                           also produced
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                                                                       Transforming growth factor beta3; TGF-beta3; human; mature protein; acid-stable; heart-stable; homodimer; mitogenesis; cell proliferation; cell growth; wound; oral mucositis; intestinal mucositis; osteoarthritis; bone disease; bone repair; therapy; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                             240
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                                                                                                                                                                                                                                                                                                                                                                                                                                             gtgctgggactgtacaacactctgaaccctgaagcatctgcctcgccttgctgcggtgccc
                  Prodn. of dimeric, biologically active transforming growth factor beta - by refolding denatured monomer in buffer contg. mild detergent and specific organic solvents to improve yields
                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                  100.0%; Score 339; DB 17; Length 339; 100.0%; Pred. No. 3.3e-87; Ative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mature transforming growth factor beta3 coding sequence.
                                                                                                                                                                                                                                                       Sequence 339 BP; 74 A; 104 C; 86 G; 75 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAT80110 standard; cDNA to mRNA; 339 BP.
                                                        Example 1; Page 36-37; 59pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                             Best Local Similarity 100.
Matches 339; Conservative
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 241 caggacctggagccctgaccatcctgtactatgttgggaggacccccaaagtggagcag

ctctccaacatggtggtgaagtcttgtaaatgtagctga 339

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gtgotgggaetgtacaacaetctgaaccetgaagcatctgcctcgccttgctgcggtgccc 

61 tacattgacttccgacaggatctgggctggaagtgggtccatgaacctaagggctactat 120 gocaacttotgeteaggeeettgeecataeeteegeagtgeagacacaacceacageacg 180

1 gctttggacaccaattactgcttccgcaacttggaggagaactgctgtgtgcgcccctc 1 gotttggacaccaattactgcttccgcaacttggaggagaactgctgtgtgcgcccctc

/ Match 100.0%; Score 339; DB 18; Local Similarity 100.0%; Pred. No. 3.3e-87; nes 339; Conservative 0; Mismatches 0;

Matches 339; Conservative

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Query Match

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This sequence represents the coding sequence for human transforming growth factor beta3 (TGF-beta3). TGF-beta3 is one of five distinct homodimeric TGFbeta3 is a acid-stable and heat-stable disulphide linked homodimer. All the TGF-beta's are produced as 390-412 amino acid precursors, which undergo proteolytic cleavage to produce to mature forms which consist of the C-terminal 112 amino acids. Depending upon cell and tissue type, and the presence of other growth factors.

TGF-beta may either stimulate mitogenesis, cell proliferation and growth, or inhibit these processes. Many of the actions of TGF-beta are related to the response of cells or tissues to stress or injury, and to the repair of resultant damage. A crystalline form of TGF-beta3 can be produced by a method of the invention. Crystalline TGF-beta3 is useful in the crystalline TGF-beta3 is useful in the second of the invention. Crystalline TGF-beta3 is useful in the crystalline TGF-beta3 is normally used. The crystalline form is also used for structure determination in rational drug design.

Crystalline TGF-beta3 shows lower tendency than the dissolved protein to adsorb on the walls of vials and is more stable against oxidation.

Variation of the properties, e.g. slze, of the crystals allows control over the rate at which active TGF is released in vivo.
                                                                                                                                                                                                                                                                                                                                                          veta-3 - useful in wound healing, and
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                                                                                                                                                                                                                                                                                                                                                        Crystalline form of transforming growth factor compsns. as slow release form of TGF, e.g. for for structure determn. in rational drug design
                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 1; Page 25-26; 34pp; English
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                                                                                                                                                                                                                                                                                                                      P-PSDB; AAW26173
  Homo sapiens.
                                       WO9705166-A1
                                                                                                                     17-JUL-1996;
                                                                                13-FEB-1997
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Tue Oct 30:12:56:34 2001

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Comprises a purification tag and a TGF active fragment. The present sequence encodes a specifically claimed TGF active fragment. The present sequence encodes a specifically claimed TGF active fragment.

Additionally, the fusion protein may comprise proteinase-sensitive linker sites and binding domain so the protein sequence may contain some or all of the following elements: purification tag:proteinase site: TGF-beta promotes wound healing, and the fusion protein can be used to reduce surgery recovery time and in the preparation of artificial skin. The inclusion of a purification tag facilitates purification of the fusion protein.

The proteinase site is included to permit cleavage and release of the purification tag after purification if desired. The extracellular matrix binding site facilitates delivery of the fusion protein to the desired site of action. Delivery of the TGF-beta to the site to be calculated and reduces the amount of TGF-beta required to be administered to the fusion protein to the concentration of circulating TGF-beta

    useful to

                                                                                                                                                                             TGF active fragment of a TGF-beta fusion protein encoding cDNA.
                                                                                                                                                                                                             growth factor-beta fusion protein; wound healing,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Prepn. of transforming growth factor-beta fusion protein - ureduce surgery recovery time and to prepare artificial skin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 339 BP; 74 A; 104 C; 86 G; 75 T; 0 other;
301 ctctccaacatggtggtgaagtcttgtaaatgtagctga 339
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/function= TGF active fragment
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                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 48; 59pp; English.
                                                                               AAT42773 standard; cDNA; 339
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HALL F L.
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                                                                                                                                                                                                                                                             Homo sapiens
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factor beta-3. Dimeric, biologically active TGF-beta-like protein can be produced by subjecting the denatured monomeric form to refolding conditions. The new monomeric S-sulphonated TGF-beta-like protein is useful for the production of the dimeric, biologically active TGF-beta-like protein, which is useful for the treatment of wounds (surface or internal) and cancer in a mammal, in bone and tissue repair, as a bone marrow protective agent, a mediator of cardioprotection, for the production of an anti-inflammatory or immunosuppressive preparation. Treatment is useful for animals,
                                                                                                                                                                                                                                                  300
                                                                 gccaacttctgctcaggcccttgcccatacctccgcagtgcagacacaacccacagcacg 180
                                                                                                                                              121 gocaacttotgotcaggocottgoccatacotocgoagtgoagacacaaccacagoacg 180
                                                                                                                                                                                                                                                                                 241 caggacctggagcccctgaccatcctgtactatgttgggaggacccccaaagtggagcag 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cDNA encoding the mature form of transforming growth factor-beta-3.
tacattgacttccgacaggatctgggctggaagtgggtccatgaacctaagggctactat
                                                                                                                                                                                 181 gtgctgggactgtacaacactctgaaccctgaagcatctgcctcgccttgctgcgtgccc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Transforming growth factor-beta-3; TGF-beta-like protein; S-sulphonated TGF-beta-like protein; wound treatment; cancer; bone repair; tissue repair; bone marrow protective agent; cardioprotection; anti-inflammatory; immunosuppressive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Producing biologically active dimeric Transforming Growth Factor-beta - by refolding new monomeric Transforming Growth Factor-beta, useful for treatment of wounds and cancer
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Query Match 100.0%; Score 339; DB 18; Best Local Similarity 100.0%; Pred. No. 3.3e-87; Matches 339; Conservative 0; Mismatches 0;

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 sores etc.) is
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    241 caggacctggagcccctgaccatcctgtactatgttgggaggaccccaaagtggagcag 300
    241 caggacctggagcccctgaccatcctgtactatgttgggaggacccccaaagtggagcag 300

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                                                         Gaps
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                                                                                                                           gctttggacaccaattactgcttccgcaacttggaggagaactgctgtgtgcgcccctc
                                                                            cDNA encoding a transforming growth factor beta active fragment.
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                                          Length 339;
and wound treatment (e.g. ulcers, bed
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                     0 other
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                    75
       particularly useful for the elderly
                    Sequence 339 BP; 74 A; 104 C; 86 G;
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                                                       Conservative
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P-PSDB; AAW84209.
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especially humans,
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NIMNI M E.
SHORS E C.
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fragment. The protein can be used in place of a bone morphogenetic active fragment to create the fusion proteins of the invention. When a bone morphogenetic active fragment is used, the fusion proteins are designated bone morphogenetic fusion proteins. The bone morphogenetic fusion proteins. The bone morphogenetic fusion proteins are purification may contain some or all of the following elements: a purification tag, a proteinase site, an ECM/bone binding site, a second proteinase site, and a bone morphogenetic protein active fragment. The bone morphogenetic fusion proteins can be used for enhancing wound
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                                                   present sequence encodes a transforming growth factor beta active
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TGF-alpha; ds;
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64pp; English.
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                                                                                                                                                                                                                                                                                               healing or bone growth.
Page 43;
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20-OCT-1986;
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                                                                                                                                                                                                                                                                                                                              caggacctggagccctgaccatcctgtactatgttgggaggaccccaaagtggagcag 300
                                                                                                                                                                                Gaps
                                                                                                                                                                                              1 gctttggacaccaattactgcttccgcaacttggaggagaactgctgtgtgcgcccctc 60
                                                                                         паγ
                                                                             Gene product may be used to inhibit growth of tumour cells, to treat proliferative type disorders, burns and other wounds, and may also be used as an immune modulator. Detection of proteins and of TGF-alpha can indicate presence of a tumour.

Proteins may be produced from a bacterial or eukaryotic expression
                                                                                                                                                                                                                                                                                                       gtgctgggactgtacaacactctgaaccctgaagcatctgcctcgccttgctgcgtgccc
                             Tissue-derived tumour growth inhibitors - used in diagnosis and treatment of tumours and treatment of proliferative type disorders, burns and wounds
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                                                                                                                                                               Length 609;
                                                                                                                                                                              Indels
                                                                                                                                      Sequence 609 BP; 154 A; 172 C; 158 G; 125 T; 0 other;
                                                                                                                                                             100.0%; Score 339; DB 11; 100.0%; Pred. No. 3.8e-87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       coding sequence
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                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      beta 3
                                                              Disclosure; Fig 29; 81pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                      AAQ20576 standard; cDNA; 2529
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGF-beta 3; homodimer; ss
                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (ONCO-) ONCOGENE SCI INC
       WPI; 1990-262507/35
                                                                                                                                                                     Best Local Similarity
Matches 339; Conser
                P-PSDB; AAR06548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-JUN-1991;
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                                                                                                                                                                                                                                                                                                                                                                                                                                       AA020576;
                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 10
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1403 caggacctggagcccctgaccatcctgtactatgttgggaggaccccaaagtggagcag 1462
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                                                                                                                                                                                                                                                                              This 2529bp full-length TGF-beta3 gene sequence was obtained from three shorter overlapping clones derived from human placental, human umbilical cord and A673 cells cDNA libraries, respectively. The predicted amino acid sequence of the gene encoding TGF-beta3 shows extensive homology to TGF-beta 1 and beta 2. See also AAQ22229 and AAR20622.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 tacattgacttccgacaggatctgggctggaagtgggtccatgaacctaagggctactat 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 gctttggacaccaattactgcttccgcaacttggaggagaactgctgtgtgcgcccctc
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0
                                                                                                                         Transforming growth factor beta 3 proteins, precursors and mutants - obtd. from polypeptide and antibodies, with optimal therapeutic use due to genetic manipulation of coding sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 2529;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2529 BP; 617 A; 670 C; 661 G; 581 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 339; DB 13;
100.0%; Pred. No. 5.5e-87;
iive 0; Mismatches 0;
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Haley JD;
Tendijke P,
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/product= TGF-beta3
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Foulkes JG,
                                                WPI; 1992-041510/05
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Best Local Similarity
Matches 339; Conserv
                                                                           P-PSDB; AAR20621
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          vulnerary;
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                                                                                                                                                                                      (TGF-beta3). The specification describes a composition for regulating trophoblast invasion which comprises an inhibitor of TGF-beta3, TGF-beta family cytokine receptors, hypoxia inducible factor 1 alpha (HF-1 alpha) or oxygen tension. The composition is used in methods of diagnosing, monitoring, preventing or treating conditions requiring regulation of trophoblast invasion, especially preeclempsia in pregnant
                                                                                                                                                                                                                                                                                                                                                     gctttggacaccaattactgcttccgcaacttggaggagaactgctgtgtgcgcccctc 1213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          caggacctggagccctgaccatcctgtactatgttgggaggaccccaaagtggagcag 1453
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                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                             - by, e.g. transforming growth detecting or treating
                                                                                                                                                                               present sequence encodes human transforming growth factor beta
                                                                                                                                                                                                                                                                                                                                                                                                                                                           caggacctggagccctgaccatcctgtactatgttgggaggaccccaaagtggagcag
                                                                                                                                                                                                                                                                                                    0
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Pred. No. 5.5e-87;
0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGF-beta-1; TGF-beta-2; transforming growth factor beta-1;
                                                                                                                                                                                                                                                         Sequence 2574 BP; 629 A; 680 C; 666 G; 599 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ctctccaacatggtggtgaagtcttgtaaatgtagctga 339
                                                                                                                           Regulation of trophoblast invasion factor-beta3 inhibitor, useful for preeclempsia in pregnant women
                                                         HOSPITAL FOR SICK CHILDREN MOUNT SINAI HOSPITAL CORP.
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                                                                                                                                                               English
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                         98WO-CA00180
                                         97US-0039919
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                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.
Matches 339; Conservative
                                                                                                                                                               Disclosure; Fig 1; 59pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAQ56926 standard; cDNA;
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                                                                                    Lye S,
                                                                                                    WPI; 1998-520837/44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human TGF-beta-3
                                                                                                             P-PSDB; AAW80417
                         05-MAR-1998;
                                                                                    Caniggia I,
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       17-SEP-1998
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cDNA sequences were determined for human pre-TGF-beta-1 (AAQ56923), pig TGF-beta-3 (AAQ56925) and the corresponding amino acid sequences were determined (AAR4627-29, respectively). A genomic fragment corresponding to a human TGF-beta-1 exon (AAQ56924) was also isolated and its amino acid sequence determined (AAR46230). The sequences have been used in the construction of vectors for the expression of recombinant TGF-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                encoding transforming growth factor-beta for use in therapeutics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 2157;
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transforming growth factor beta-3; recombinant; wound healing;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 337.4; DB 15;
Pred. No. 1.5e-86;
0; Mismatches 1; 1
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87US-0025423.
89US-0389929.
92US-0845893.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 99.7%;
Matches 338; Conservative
                                                                                                                                                                  85US-0715142
                                                                                                                                                                                                                                                                                                                                   Derynk RMA, Goeddel DV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   diagnostic probes, and
                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleic acid sequences
                                                                                                                                                                                                                                                                                                (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                       WPI; 1994-056343/07.
P-PSDB; AAR46229.
                                                                                                                                                                                                                    13-MAR-1987;
04-AUG-1989;
04-MAR-1992;
                                                       Homo sapiens
                                                                                                                                                                  22-MAR-1985;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            vectors which are replicated in bacteria and expressed in eukaryotic cells. TGF-beta recovered from transformed cells is used in known therapeutic applications. TGF-beta nucleic acids are also useful in diagnosis and identification of TGF-beta clones.
                                                                                                                                                                                                                                                                                                                                                                                                      This nucleotide sequence, hu4, codes for a human partial transforming growth factor-beta 3 (TGF-beta 3) sequence including all of the mature sequence. Clone hu4 was isolated from a human ovarian cDNA library using porcine TGF-beta 3 cDNA (see AAV52934) as probe. The invention relates to the recombinant production of TGF-beta. Biologically active TGF-beta is defined as being capable of inducing EGF-potentiated anchorage independent growth of target cell lines and/or growth inhibition of neoplastic cell lines. Nucleic acids encoding TGF-beta have been isolated and cloned into
                                                                                                                                                                                                                                                                                                                                     הוא פונטטווס transforming growth factor-beta precursor sequence -
useful for analysis to perform manipulations to increase yield of
recombinant production of the protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gctttggacaccaattactgcttccgcaacttggaggagaactgctgtgtgcgcccctc
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                                                          SS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2157 BP; 621 A; 462 C; 492 G; 582 T; 0 other;
                                                          human;
                                                                                                                            aa:Thr)
                                                        Transforming growth factor-beta 3; TGF-beta 3;
                                      Human transforming growth factor-beta 3 cDNA
                                                                                                                           /transl_except= (pos:50..52,
                                                                                               Location/Qualifiers
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89US-0389929.
92US-0845893.
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95US-0454468
                                                                                                                                                                                                                                                                                             Goeddel DV;
                   (first entry)
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Matches 338; Conservative
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/*tag=
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P-PSDB; AAW78787.
                                                                                                                                                                                                                                                                                              Derynck RMA,
                                                                             Homo sapiens
                  21-DEC-1998
                                                                                                                                              US5801231-A.
                                                                                                                                                                                     22-MAR-1985;
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04-MAR-1992
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AAV52935;
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Nucleotide sequence encoding transforming growth factor beta-3 -used as a probe, or to produce TGF beta 3, for inhibition of growth of normal and neoplastic cells, eg A549.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This sequence encodes human transforming growth factor-beta 3 (TGF-beta 3) polypeptide. The nucleic acid sequence encoding this subtype is useful as a probe or to produce TGF-beta 3 for both normal and neoplastic cell growth inhibition.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gtgctgggactgtacaacactctgaaccctgaagcatctgcctcgccttgctgcgtgccc 240
240
                                                                           397
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          cells; growth
1 getttggacaccaattactgcttccgcaacttggaggagaactgctgtgtgcgcccctc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tacattgacttccgacaggatctgggctggaagtgggtccatgaacctaagggctactat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tacattgacttccgacaggatctgggctggaagtgggtccatgaacctaagggctactat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99.5%; Score 337.4; DB 11; Length 2158; 99.7%; Pred. No. 1.5e-86; ive 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        growth factor beta-3 (TGF beta 3); tumour
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2158 BP; 621 A; 462 C; 493 G; 582 T; 0 other;
                                                                                                                                                           339
                                                                                                                                                         301 ctctccaacatggtggtgaagtcttgtaaatgtagctga
                                                                                                                                                                                                  578 ctctccaacatggtggtgaagtcttgtaaatgtagctga
                                                                                                                                                                                                                                                                                                                                                                                                                   cDNA sequence encoding human TGF-beta 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Fig. 4; 61pp; English.
                                                                                                                                                                                                                                                                                                BP.
                                                                                                                                                                                                                                                                                                AAQ02820 standard; DNA; 2158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        88WO-UO01945.
                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       338; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Goeddel DV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1990-007474/01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Transforming
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08-JUN-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      08-JUN-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Dernyck RM,
                                                                                                                                                                                                                                                                                                                                                                            31-MAY-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO8912101-A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              inhibition
                                                                                                                                                                                                                                                                                                                                       AAQ02820;
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                                                                                                                                                                                                                                                           RESULT 14
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RESULT 16
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                This sequence has been compiled from the description of a mutant TGF-beta3 contained in the claims. The sequence coding for the Factor Xa cleavage site may be replaced by one encoding a similar procease recognition site, e.g. for collagenase. The coding sequence may also include a region encoding a hydrophobic transmembrane amino acid sequence. e.g. from c-ebbB2 cDNA and a "stop transfer" sequence. The protease recognition site is located between the C-terminal of the transmembrane region and the N-terminal of the
gtgctgggactgtacaacactctgaaccctgaagcatctgcctcgccttgctgcatgccc
                                                                                                                                                                                                                                                                                                                          /*tag= d
/note= "wild-type codon = ATG. May be replaced by
any other codon to give mutant sequence"
1216..1239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Transforming growth factor beta 3 proteins, precursors and mutants - obtd. from polypeptide and antibodies, with optimal therapeutic use due to genetic manipulation of coding sequence
                                                                                                                                                                                                                                                                                              /*tag= c
/note= "nucleotides 1163-1471 of TGF-beta3"
1213..1215
                                                                                                                                                                                                                                                                                                                                                            /*tag= e
/note= "nucleotides 1475-1498 of TGF-beta3"
                                                                                                                                                                                                                                    /*tag= a
/note= "nucleotides 263-1150 of TGF-beta3"
889..903
                                                                                                                                                                                                                                                            /*tag= b
/note= "encodes Factor Xa cleavage site
followed by a methionine residue"
                                                                                                                                                                Mutant transforming growth Factor beta 3 coding sequence.
                                                Haley JD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tendijke P,
                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 12; Page 66; 107pp; English
                                                                                                               BP.
                                                                                                             AAQ22229 standard; cDNA; 1239
                                                                                                                                                                                                                                                                                                                                                                                                                         91WO-US04541.
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                                                                                                                                                (first entry)
                                                                                                                                                                                 TGF-beta 3; homodimer; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                          (ONCO-) ONCOGENE SCI INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Foulkes JG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1992-041510/05.
P-PSDB; AAR22038.
                                                                                                                                                                                                                                                                                                                  misc_difference
                                                                                                                                                                                                                           misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                       25-JUN-1991;
                                                                                                                                                05-MAY-1992
                                                                                                                                                                                                                                                      misc_feature
                                                                                                                                                                                                                                                                                         misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                         25-JUN-1990;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Iwata KK,
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                                                                                                                               AAQ22229;
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tacattgacttccgacaggatctgggctggaagtgggtccatgaacctaagggctactat 120
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                                                                                                                                                                                                                                                                                                                                                                         gctttggacaccaattactgcttccgcaacttggaggagaactgctgtgtgcgcccctc
                                                                                                                                                                                                                                                                                                          gocaacttctgctcaggcccttgcccatacctccgcagtgcagacacaacccacaggcacg
TGF-beta 3 precursor. Mature TGF-beta 3 can then be efficiently cleaved from the membrane. See also AAQ20576 and AAR20622.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tumour growth inhibitor; carcinoma; melanoma; leukaemia; arteriosclerosis; inflammation; psoriasis; therapy; vulnerary;
                                                                                                     Length 1239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product= tumour_growth_inhibitor_precursor
/note= "see AAR86771"
159..160
                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tissue-derived tumour growth inhibitor-1 coding sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product= mature_tumour_growth_inhibitor
/note= "see AAR86770"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /*tag= b
/note= "the codons at positions -40 to
                                               Sequence 1239 BP; 308 A; 348 C; 328 G; 248 T; 7 other;
                                                                                                     Score 333; DB 13;
Pred. No. 2.3e-85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAT06496 standard; cDNA; 498
                                                                                                 Ouery Match 98.2%;
Best Local Similarity 99.1%;
Matches 333; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             87EP-0109866
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/*tag=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12-JUN-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20-OCT-1987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20-OCT-1986;
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psoriasis; ss.

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                                                                                                                                                   The sequence encodes a 112 amino acid tumor growth inhibitor (TGI)

(AAR86770) or a 205 precursor TGI (AAR86771) comprising TGI with an additional 93 amino acid residues at the N-terninus. However, the nuclectides representing codons -40 to -10 f the precursor TGI are not specified in Figure 29, i.e. the cDNA is 498 nucleotides in length, but should be 615 nucleotides long. The DNA is used to produce the inhibitors by recombinant methods i.e. vector expression in bacterium or eukaryotic host cells, e.g. carcinoma, melanoma or leukaemia cells, in the treatment of proliferative disorders e.g. arteriosclerosis, inflammation and composition of the treatment of burns to facilitate wound healing. They can also be used as immunomodulators. Although the proteins proteins are not rensiforming growth factor-beta-1 or -beta-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             gccaacttctgctcaggcccttgcccatacctccgcagtgcagacacaacccacagcacg 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        340 gigcigggacigiacaacactcigaacccigaagcatcigcciggccitgcigcgigccc 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                caggacctggagccctgaccatcctgtactatgttggaggaccccaaagtggagagcag 300
                                                                                                                                                                                                                                                                                                                                                                                                                             caggacctggagccctgaccatcctgtactatgttgggaggaccccaaaagtggagcag 459
                                                                                    Tissue-derived growth inhibitor and corresponding genes - useful for detection of tumours, inhibition of tumour growth, treatment of proliferative disorders and healing of burns and wounds.
                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                  getttggacaccaattactgetteegeaacttggaggagaactgetgtgtgegeeeete 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TGI; carcinoma; melanoma; leukaemia; arteriosclerosis; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             280 gecaacticigeicageceetigeceataceicegeagigeagaeacaaeceaeageaeg
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                                                                                                                                                                                                                                                                                                                                                                        DB 17; Length 498;
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                                                                                                                                                                                                                                                                                                                                      Sequence 498 BP; 122 A; 136 C; 129 G; 111 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                       Score 332.6; DB 17;
Pred. No. 2.4e-85;
0; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence encoding tumour growth inhibitor.
                                 Stephenson JR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ВР
                                                                                                                               Claim 6; Fig 29; 83pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAQ06845 standard; cDNA; 2530
                                                                                                                                                                                                                                                                                                                                                                       Query Match 98.1%;
Best Local Similarity 98.8%;
Matches 335; Conservative
                                                                P-PSDB; AAR86770, AAR86771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
           (ONCO-) ONCOGENE SCI INC
                               Iwata KK,
                                                    WPI; 1996-000991/01
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                               Gold LI,
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Gold LI, Foulkes JG;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tacattgacttccgacaggatctgggctggaagtgggtccatgaacctaagggctactat 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          caggacctggagccctgaccatcctgtactatgttgggaggaccccaaagtggagcag 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The plasmid was isolated from a human cDNA library prepd. from the DNA of a chronic myelocytic leukaemia cell line (K562). The sequence can be used to produce the tumour growth inhibitor (TGI) by recombinant techniques. The protein may also be isolated from human umbilical cord and placental tissues. It can be used to inhibit tumour cell growth, to treat burns, to facilitate the healing of wounds or to treat proliferative disorders. The protein and Abs raised to it can be used for detection and typing of tumours. The Abs can also be used to inhibit the activity of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9tgctgggactgtacaacactctgaaccctgaagcatctgcctcgccttgctgctgctgctgccc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gctttggacaccaattactgcttccgcaacttggaggagaactgctgtgtgcgcccctc
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tissue-derived tumour growth inhibitors - comprise specified protein sequences used to detect, and treat tumours, burns a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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llarity 97.6%; Pred. No. 2.4e-83;
Conservative 0; Mismatches 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Franco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tendijke P,
                                      Socation/Qualifiers
263..1501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 10; Fig 41; 190pp; English.
                                                                                                                                                                                                                                                                                                                                              86US-0847931.
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                                                                                                                                                                                                                                                                                                          89US-0353410.
85US-0725003.
                                                                                                                                                                                                                                                                                                                                                                                      87US-0111022
                                                                        /*tag= a
2506..2511
/*tag= b
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Stephenson JR,
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2529
/*tag=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P-PSDB; AAR08264
Homo sapiens
                                                                                            polyA_signal
                                                                                                                                                                                                                                                                                                        17-MAY-1989;
19-APR-1985;
07-APR-1986;
                                                                                                                                                                                        WO9014360-A.
                                                                                                                                                                                                                                                                      17-MAY-1990;
                                                                                                                                                                                                                                29-NOV-1990
                                                                                                                                                                                                                                                                                                                                                                    20-0CT-1986
                                                                                                                                                                                                                                                                                                                                                                                                            20-APR-1988
                                                                                                                                                                                                                                                                                                                                                                                      20-0CT-1987
                                                                                                                                  polyA_site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 331;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local S
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                                      Key
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AAV52934
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                                                                                                                                                                                                                                                                     Nucleotide sequence encoding transforming growth factor beta-3 -used as a probe, or to produce TGF beta 3, for inhibition of growth of normal and neoplastic cells, eg A549.
                                                                                                                                                                                                                                                                                                                This sequence encodes porcine transforming growth factor-beta 3 (TGF-beta 3) polypeptide. The nucleic acid sequence encoding this subtype is useful as a probe or to produce TGF-beta 3 for both normal and neoplastic cell growth inhibition.
240
                                                                                                                                                                                                                                                                                                                                                                                                                                        tacattgacttccgacaggatctgggctggaagtgggtccatgaacctaagggctactat 120
                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                 Transforming growth factor beta-3 (TGF beta 3); tumour cells; growth inhibition.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181 gtgctgggactgtacaacactctgaaccctgaagcatctgcctcgccttgctgcgtgccc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          caggacctggagccctgaccatcctgtactatgtgggaggacccccaaagtggagcag
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                                                                                                                                                                                                                                                                                                                                                     Sequence 2676 BP; 704 A; 705 C; 699 G; 568 T; 0 other;
                   cDNA sequence encoding porcine TGF-beta 3.
                                                                                                                                                                                                                                                                                                   Disclosure; Fig. 4; 61pp; English.
                                                                       AAQ02819 standard; DNA; 2676 BP
                                                                                                                                                                                      88WO-US01945
                                                                                                                                                                                                    88WO-U001945
                                                                                                     (first entry)
                                                                                                                                                                                                                                 Goeddel DV;
                                                                                                                                                                                                                  (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                               WPI; 1990-007474/01.
P-PSDB; AAR04080.
                                                                                                                                                                                     08-JUN-1988;
                                                                                                                                                                                                    08-JUN-1988;
                                                                                                     31-MAY-1989
                                                                                                                                                       WO8912101-A.
                                                                                                                                                                                                                                 Dernyck RM,
                                                                                                                                                                      14-DEC-1989
                                                                                      AAQ02819;
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transforming growth factor beta 3 precursor (prefer-beta 3, see AAW78786). A porcine ovarian cDNA library was screened using human of Gre-beta 1 cDNA (see AAV52933) as probe. A hybridising clone, cosignated lambda 11.3, was used to rescreen the library to designated lambda 10. The was combined with clone lambda 11.3 combined with clone lambda 11.3 combined to provide the 10+11.3 sequence. The invention relates to the recombinant production of TGF-beta. Biologically active TGF-beta is defined as being capable of inducing EGF-potentiated anchorage independent growth of target cell lines and/or growth inhibition of coplastic cell lines. Nucleic acids encoding TGF-beta have been isolated and cloned into vectors which are replicated in bacteria cand expressed in cukaryotic cells. TGF-beta recovered from transformed cells is used in known therapeutic applications.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA encoding transforming growth factor-beta precursor sequence - useful for analysis to perform manipulations to increase yield of recombinant production of the protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This nucleotide sequence, termed 10+11.3, codes for the porcine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 2639;
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                                                                                                                                                                                                                                                                                                                                                                                                                                  growth factor-beta 3; TGF-beta 3; pig; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /transl_except= (pos:481..483, aa:Met)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 302.2; DB 19;
Pred. No. 1.6e-76;
Pig transforming growth factor-beta 3 cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
127..1497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 6; Fig 4a-c; 26pp; English.
                                                                                                                                                                                                   AAV52934 standard; cDNA; 2639 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 87US-0025423.
85US-0715142.
89US-0389929.
92US-0845893.
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93.2%;
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95US-0454468
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                    21-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                     Transforming
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22-MAR-1985;
04-AUG-1989;
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05-NOV-1993
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0 other;

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Sequence 2669 BP; 706 A; 702

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   Gaps
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                                                                                                                                                                      gtgctgggactgtacaacactctgaaccctgaagcatctgcctcgccttgctgcgtgccc
                                                                                                                                                                                                  caggacctggagccctgaccatcctgtactatgttgggaggaccccaaagtggagcag
                                                                                                            gccaacttctgctcaggcccttgcccatacctccgcagtgcagacacaacccacagcacg
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                                                                                                                                                                                                                                                                                                                                                                                                             TGF-beta-1; TGF-beta-2; transforming growth factor beta-1; transforming growth factor beta-3; recombinant; wound healing; vulnerary; ss.
   Indels
  23;
                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Fig 4a-c; 25pp; English.
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89US-0389929
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 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleic acid sequences diagnostic probes, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1994-056343/07.
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                                                                                                                                                                                                                                                                                                                                                                                          Pig TGF-beta-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13-MAR-1987;
04-AUG-1989;
04-MAR-1992;
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316;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sus scrofa
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 Matches
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                                                                                                               1219 tacattgacttccgacaggatctgggctggaagtgggtccatgaacctaagggctactat 1278
                                                                                                                                                                                                240
                                                                                         tacattgacttccgacaggatctgggctggaagtgggtccatgaacctaagggctactat 120
                                              9
                                                                                                                                                                                                                                                                                                                                                                                                                                Entire porcine transforming growth factor (TGF) beta-3 cDNA sequence.
                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Porcine transforming growth factor (TGF) beta-3; human ovarian cDNA; human transforming growth factor (TGF) beta-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CDNA library to
                                              gctttggacaccaattactgcttccgcaacttggaggagaactgctgtgtgcgcccctc
                                                                                                                                                                                    gtgctgggactgtacaacactctgaaccctgaagcatctgcctcgccttgctgcgtgccc
                                                                                                                                                                                                                                  caggacctggagccctgaccatcctgtactatgttgggaggacccccaaagtggagcag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       host
 Length 2669;
                      ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic acid encoding transforming growth factor-beta cloned into expression vectors for expression in eukaryotic
                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  T; 0 other;
Score 302.2; DB 15;
Pred. No. 1.6e-76;
0; Mismatches 23;
 DB 15;
                                                                                                                                                                                                                                                                                           301 ctctccaacatggtggtgaagtcttgtaaatgtagctga 339
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2671 BP; 706 A; 705 C; 699 G; 561
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                                                                                                                                                                                                                                                                                                                                                             ВР
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                                                                                                                                                                                                                                                                                                                                                            AAQ03303.standard; DNA; 2671
Query Match 89.1%;
Best Local Similarity 93.2%;
Matches 316; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cells for therapeutic use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1990-051338/07.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Derynck RMA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13-MAR-1987;
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of the human isoforms TGF-betal, TGF-beta2 and TGF-beta3 (see AAQ41599, AAQ41601 and AAQ41601, respectively). The hinge points between parts derived from different parent isoforms are pref. between amino acids 44 and 45, 56 and 57, 79 and 80, 90 and 91, or 22 and 23. Of the 30 possible hybrids using these hinge points and one part each from two of the isoforms, 6 are preferred including the hybrid TGF-betal(44/45)beta3. The hybrid molecules promote cell migration, inhibit the growth of A375 melanoma cells, accelerate the healing of partial-thickness burn wounds and full-thickness incisional wounds and increase formation of fibrous granular tissue. See AAQ41602-Q41607 for the most pref. hybrids.

    241 caggacctggagcccctgaccatcctgtactatgttgggaggacccccaaagtggagcag 300
    241 caggacctggagcccctgaccatcctgtactatgttgggaggacccccaaagtggagcag 300

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                                                                                                                                                                                                                                                              1 gctttggacaccaattactgcttccgcaacttggaggagaactgctgtgtgcgcccctc
                                                                                                                                                                                                                    181 gigetgggaetgtacaacaetetgaaceetgaageatetgeetegeettgetgegtgeee
                                                                                                                                                                Length 336;
                                                                                                                                                        ; DB 14;
1.9e-75;
24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TGF-beta
                                                                                                                               Sequence 336 BP; 75 A; 109 C; 86 G; 66 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Transforming growth factor type beta; TGF-beta protein renaturation; protein folding; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                              Score 297.6;
Pred. No. 1.9
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                                                                                                                                                              Query Match 87.8%;
Best Local Similarity 92.9%;
Matches 312; Conservative
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P-PSDB; AAR92775.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cerletti N;
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                                                                                  1159 gecetggacaccaactactgetteegeaatttggaggagaactgetgtgtgegeeetete 1218
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention covers hybrid TGF-beta molecules consisting of parts
                                                                                                                                                                                            getttggacaccaattactgcttccgcaacttggaggagaactgctgtgtgcgcccctc
                                                                                                                                                                                                                                       caggacctggagcccttgaccatctgtactatgttgggaggaccccaaagtggagcag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New hybrid transforming growth factor-beta molecules - comprise portions of mature TGF-beta isoforms; useful as wound healants, cardioprotective, antiinflammatory and immunosuppressive agents
                      Length 2671;
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"TGF-betal=1-132, TGF-beta3=133-336"
                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                          hTGF-betal; hTGF-beta3; hybrid protein; wound healing; cancer treatment; bone repair; growth regulation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                        Growth Factor-betal(44/45)beta3 hybrid
             Score 302.2; DB 11;
Pred. No. 1.6e-76;
                                                                                                                                                                                                                                                                              Kuhla J;
                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8; Page 26-27; 48pp; English
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                                                                                                                                                                                                                                                                                                                                                          BP
                                                                                                                                                                                                                                                                                                                                                       AAQ41603 standard; cDNA; 336
                      89.1%;
93.2%;
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                Query Match
Best Local Similarity 93.2°
Matches 316; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             03-NOV-1992;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
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                                                              A DNA sequence (AAT17237) codes for a recombinant hybrid of human transforming growth factor-beta, TGF-beta 1-3 (AAR92775), in which the N-terminal 44 amino acids are from TGF-beta 1 (see also AAR92773) and the C-terminal 68 amino acids from TGF-beta 3 (see also AAR92773). The DNA was subcloned in pPLMu, yielding plasmid pPLMu, hTGF-beta 1(44/45)beta3. Non-soluble, monomeric hybrid TGF-beta 1-3 was recovered from E. coll transformants. A blologically active, dimeric form of the hybrid was obtd. by refolding the monomer in detergent-free buffer contq. DNSO and/or DNF. Hybrid dimers TGF-beta 2-3 (AAR92776) and TGF-beta 3-2 (AAR927777) were similarly
                                                                                                                                                                                                                                                                                               240
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                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                             gtgctgggactgtacaacactctgaaccctgaagcatctgcctcgccttgctgctgcgtgccc
                                                                                                                                                                                                                                                                                                                                                                                                                   caggacctggagcccctgaccatcctgtactatgttgggaggacccccaaagtggagcag
                                                                                                                                                                                                                                                                                                                                                                                                                            Prodn. of dimeric biologically active transforming growth factor by refolding denatured monomer in detergent-free folding buffer contg. specific organic solvent to improve yield
                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                 Score 297.6; DB 17; Length 336;
Pred. No. 1.9e-75;
0; Mismatches 24; Indels 0;
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/note= "encodes N-terminal 44 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cDNA encoding human TGF-beta-like protein, TGF-beta-1-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           growth factor beta; TGF; regulator; method;
n; differentiation; wound healing; solvent;
                                                                                                                                                                                    Sequence 336 BP; 75 A; 109 C; 86 G; 66 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ctctccaacatggtggtgaagtcttgtaaatgtagc 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product= hybrid_TGF-beta-1-3
                                                                                                                                                                                                                                      0; Mismatches
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                                             Example 10; Page 36-37; 54pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAT15465 standard; cDNA to mRNA; 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                 Query Match 87.8%;
Best Local Similarity 92.9%;
Matches 312; Conservative
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AATIS465 encodes transforming growth factor (TGF) beta-like protein, TGF-beta-1-3. TGF beta-1-3 is a hybrid of TGF-1 and TGF-3. TGF beta hybrids were made using a new process of producing dimeric, biologically active TGF beta-like proteins. The new process involves treating denatured TGF beta monomers with folding buffer contg. a mild detergent (CHAPS, CHAPSO or digitonin) and at least one of the solvents DMSO (dimethyl sulphoxida), DMSO2 (dimethylsulphoxe) and DMF (dimethyl formamide). The detergent allows folding of the monomer such that, after dimerisation, the TGF beta-like protein retains biological activity and remains in soluble form. The method allows relatively high yields of biologically active TGF beta-like proteins in thair native dimeric form. TGF-beta like proteins are multifunctional regulators of cellular activity and a typical use is to stimulate wound
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                                                      of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Prodn. of dimeric, biologically active transforming growth f
beta – by refolding denatured monomer in buffer contg. mild
detergent and specific organic solvents to improve yields
                                                      amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 17;
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                       /*tag= c
/note= "encodes C-terminal 68
TGF-beta-3"
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                                                                                                                                                                                                                                                  95WO-EP02718
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133..336
                                                                                                                                                                                                                                                                                                                                                                (CIBA ) CIBA GEIGY AG.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P-PSDB; AAR91959
                                                                                                                                                                                                                                                  12-JUL-1995;
                                                                                                                                                                                                                                                                                                       25-JUL-1994;
mat_peptide
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The specification describes a method for growing stem cells. The method involves providing stem cells with supporters which are genetically modified in order to provide externally regulatable interactions between the supporters and the stem cells, and applying an external signal for starting or stopping the interactions. The cells are useful for curing diseases by gene therapy and/or cell therapy in combination with tissue engineering, when the functional expression of stem cells is helped with engineered architecture of the tissue, which diseases are related to insufficient and/or lack and/or disorders of stem cells. The present sequence represents a vector, which is used in the method of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tacattgacttccgacaggatctgggctggaagtgggtccatgaacctaagggctactat 120
                                                                                                                                                                                                                                                                                                                                                                                                              Growing stem cells useful as therapeutic, involves providing stem celwith supporters which are genetically modified to provide externally regulatable interactions, and applying an external signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gctttggacaccaattactgcttccgcaacttggaggagaactgctgtgtgcgcccctc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                              gene therapy; cell therapy; stem cell disorder; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 4382 BP; 1153 A; 1120 C; 1091 G; 1018 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 291; DB 22; Length 4 Pred. No. 2.7e-73; O: Mismatches 30; Indels
                                                                                                                Nucleotide sequence of the vector puhd10-3-tgf.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Fig 26; 92pp; English.
                           AAF55131 standard; DNA; 4382 BP.
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                                                                                                                                                                                                                                                                                               99EP-0116533
                                                                                      (first entry)
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hes 309; Conservative
                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-218440/22.
                                                                                                                                                                                                       WO200114530-A2
                                                                                                                                                                                                                                                                                              24-AUG-1999;
                                                                                                                                                                                                                                                                                                                         (CHEN/) CHEN
                                                                                      29-MAY-2001
                                                                                                                                                                                                                                      01-MAR-2001
                                                                                                                                               Stem cell;
                                                                                                                                                                            Synthetic
                                                        AAF55131;
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               AAF55131
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The invention covers hybrid TGF-beta molecules consisting of parts of the human isoforms TGF-beta1, TGF-beta2 and TGF-beta3 (see AAQ41599, AAQ41600 and AAQ41601, respectively). The hinge points between parts derived from different parent isoforms are pref. between amino acids 44 and 45, 56 and 57, 79 and 80, 90 and 91, or 22 and 23. Of the 30 possible hybrids using these hinge points and one part each from two of the isoforms, 6 are preferred including the hybrid TGF-beta2(44/45)beta3. The hybrid molecules promote cell migration, inhibit the growth of A375 melanoma cells, accelerate the healing of partial-thickness burn wounds and full-thickness incisional wounds and increase formation of fibrous granular tissue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tacattgacttccgacaggatctgggctggaagtgggtccatgaacctaagggctactat 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New hybrid transforming growth factor-beta molecules - comprise portions of mature TGF-beta isoforms; useful as wound healants, cardioprotective, antiinflammatory and immunosuppressive agents etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gotttggatgcggcctattgctttagaaatgtgcaggataattgctgcctacgtccactt 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14; Length 336;
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"TGF-beta2=1-132, TGF-beta3=133-336"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              37; Indels
                                                                                                                                                                                                                    hTGF-beta2; hTGF-beta3; hybrid protein; wound healing; cancer treatment; bone repair; growth regulation; ss.
                                                                                                                                                                                            Transforming Growth Factor-beta2(44/45)beta3 hybrid.
Sequence 336 BP; 81 A; 94 C; 84 G; 77 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             See AAQ41602-Q41607 for the most pref. hybrids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   81.7%; Score 276.8; DB 1
89.0%; Pred. No. 1.5e-69;
11ve 0; Mismatches 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kuhla J;
                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 8; Page 29-30; 48pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cerletti N,
                                                                                                        ВР
                                                                                                     AAQ41605 standard; cDNA; 336
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    McMaster GK,
                                                                                                                                                               26-AUG-1993
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                                                                                                                                  AAQ41605;
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                                                                                                                                                                                                                                                181 gigologgacigiacaacacicigaacceigaagcateigecigeciigeigegigece
                  1 gettiggacaccaattactgetteegcaactiggaggagaactgeigigigegeeeete
                                       Prodn. of dimeric, biologically active transforming growth factor beta - by refolding denatured monomer in buffer contg. mild detergent and specific organic solvents to improve yields
                                                                                                                                                                                                                                                                                  caggacctggagcccctgaccatcctgtactatgttgggaggaccccaaagtggagcag
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/note= "encodes C-terminal 68 amino acids of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cowth factor beta; TGF; regulator; method;
differentiation; wound healing; solvent; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cDNA encoding human TGF-beta-like protein, TGF-beta-2-3,
                                                                                                                                                                                                                                                                                                                                                /*tag= a
/product= hybrid_TGF-beta-2-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
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                                                                                               A DNA sequence (AAT17238) codes for a recombinant hybrid of human transforming growth factor-beta, TGF-beta 2-3 (AAR92776), in which the N'terminal 44 amino acids are from TGF-beta 2 (see also AAR92774). The DNA was subcloned in pPLMu, yielding plasmid pPLMu.hTGF-beta 2 (44/45)beta3. Non-soluble, monomeric hybrid TGF-beta 1-3 was recovered from E. coli LC137 transformants. A biologically active, dimeric form of the hybrid was obtd. by refolding the monomer in detergent-free buffer contg. DMSO and/or DMF. Hybrid dimers TGF-beta 1-3 (AAR92775) were similarly
61 tacattgatttcaagagggatctagggtggaaatggatacacgaacccaaagggtacaat 120
                                  gccaacttctgctcaggcccttgcccatacctccgcagtgcagacacaacccacagcacg 180
                                                               121 gccaacttctgctcaggcccttgcccatacctccgcagtgcagacacaacccacagcacg 180
                                                                                                                                                                               241 caggacctggagccctgaccatcctgtactatgttgggaggaccccaaagtggagcag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Prodn. of dimeric biologically active transforming growth factor by refolding denatured monomer in detergent-free folding buffer contg. specific organic solvent to improve yield
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 276.8; DB 17; Length 336; Pred. No. 1.5e-69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Transforming growth factor type beta; TGF-beta 2; TGF-beta 3; protein renaturation; protein folding; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 336 BP; 81 A; 94 C; 84 G; 77 T; 0 other;
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Matches 299; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hybrid TGF-beta 2-3 DNA.
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                   AAT15466 encodes transforming growth factor (TGF) beta-like protein, TGF-beta-2-3. TGF beta-2-3 is a hybrid of TGF-2 and TGF-3. TGF beta hybrids were made using a new process of producing dimeric, biologically active TGF beta-like proteins. The new process involves treating denatured TGF beta monomers with folding buffer contg. a mild detergent (CHAPS, CHAPSO or digitonin) and at least one of the solvents DMSO (dimethyl sulphoxide), DMSO2 (dimethylsulphone) and DMF (dimethyl formamide). The detergent allows folding of the monomer such that, after dimerisation, the TGF beta-like protein retains biological activity and remains in soluble form. The method allows relatively high yields of biologically active TGF beta-like proteins in their native dimeris form. TGF-beta like proteins are multifunctional requiators of cellular activity and a typical use is to stimulate wound
                                                                                                                                                                                                                                                                                         tacattgacttccgacaggatctgggctggaagtgggtccatgaacctaagggctactat 120
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/note= "TGF-beta3=1-132, TGF-beta1=133-336"
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89.0%; Pred. No. 1...
0; Mismatches
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Claim 17; Page 42; 59pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hTGF-betal; hTGF-beta3; hybrid cancer treatment; bone repair;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAQ41606 standard; cDNA; 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
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Matches 299; Conservative
                                                                                                                                                                           Sequence 336 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
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The invention covers hybrid TGF-beta molecules consisting of parts of the human isoforms TGF-beta1 (see AAQ41599, AAQ41600 and AAQ41601, respectively). The hinge points between parts derived from different parent isoforms are pref. between amino acids to possible hybrids using these hinge points and one part each possible hybrids using these hinge points and one part each from two of the isoforms, 6 are preferred including the hybrid TGF-beta3(44/45)beta1. The hybrid molecules promote cell migration, inhibit the growth of A375 melanoma cells, accelerate the healing of partial-thickness burn wounds and full-thickness incisional wounds and increase formation of fibrous granular tissue.
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                                                                                                                                                                                                                                                                                         New hybrid transforming growth factor-beta molecules - comprise portions of mature TGF-beta isoforms; useful as wound healants, cardioprotective, antiinflammatory and immunosuppressive agents etc.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 336 BP; 63 A; 109 C; 98 G; 66 T; 0 other;
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Pred. No. 4.2e-59;
0; Mismatches 60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             increase formation of fibrous granular tissue.
See AAQ41602-Q41607 for the most pref. hybrids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            301 ctctccaacatggtggtgaagtcttgtaaatgtagc 336
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                                                                                                                                                                                                                                                                                                                                                                                                     Claim 8; Page 30-31; 48pp; English.
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                                                                                                                                                           Cerletti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CDNA; 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 70.8%;
Best Local Similarity 82.1%;
Matches 276; Conservative
92EP-0810845.
                                                  91EP-0810870
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                                                                                                                                                           Cox D,
                                                                                                                                                                                                                WPI; 1993-161126/20.
                                                                                                       GEIGY
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                                                                                                                                                                                                                                            P-PSDB; AAR39645
                                                                                                       (CIBA ) CIBA
                                                                                                                                                           McMaster GK,
                                               11-NOV-1991;
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                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention covers hybrid TGF-beta molecules consisting of parts AAQ41600 and AAQ41601, respectively. The hinge points between parts derived from different parent isoforms are pref. between amino acids 44 and 45, 56 and 57, 79 and 80, 90 and 91, or 22 and 23. Of the 30 possible hybrids using these hinge points and one part each from two of the isoforms, 6 are preferred, esp. the hybrid TGF-beta3(44/45)beta2. The hybrid molecules promote cell migration, inhibit the growth of A375 melanown cells, accelerate the healing of partial-thickness burn wounds and full-thickness incisional wounds and increase formation of fibrous granular tissue.

See AAQ41602-Q41606 for the other pref. hybrids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tacattgacttccgacaggatctgggctggaagtgggtccatgaacctaagggctactat 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gecaacttetgeteaggecettgeceatacetecgeagtgeagacaeaacecaeageaeg 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gccaacttctgtgctggagcatgcccgtatttatggagttcagacactcagcacagcagg 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      caggacctggagccctgaccatcctgtactatgttgggaggacccccaaagtggagcag 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 getttggacaccaattactgcttccgcaacttggaggagaactgctgtgtgcgcccctc 60
                                                                                                                                                                                                                                                                                                                                                             New hybrid transforming growth factor-beta molecules - comprise portions of mature TGF-beta isoforms; useful as wound healants, cardioprotective, antiinflammatory and immunosuppressive agents etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gtgctgggactgtacaacactctgaaccctgaagcatctgcctcgccttgctgcggtgccc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match 70.8%; Score 240; DB 14; Length 336; Best Local Similarity 82.1%; Pred. No. 4.2e-59; Matches 276; Conservative 0; Mismatches 60; Indels
                                                                                        a
"TGF-beta3=1-132, TGF-beta2=133-336"
cancer treatment; bone repair; growth regulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 336 BP; 88 A; 87 C; 71 G; 90 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ctctccaacatggtggtgaagtcttgtaaatgtagc 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kuhla J;
                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                      Cerletti N,
                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 9; Page 32; 48pp; English.
                                                                                                                                                                                            92EP-0810845.
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/*tag=
/note= '
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                                                                                                                                                                                                                                                                                    McMaster GK, Cox D,
                                                                                                                                                                                                                                                                                                                WPI; 1993-161126/20.
P-PSDB; AAR39646.
                             Homo sapiens
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A DNA sequence (AAT17239) codes for a recombinant hybrid of human transforming growth factor-beta, TGF-beta 3-2 (AAR92777), in which the N-terminal 44 amino acids are from TGF-beta 3 (see also AAR92772) and the C-terminal 68 amino acids from TGF-beta 2 (see also AAR92774). The DNA was subcloned in pPLMu, yielding plasmid pPLMu.hTGF-beta 3 (44/45)beta2. Non-soluble, monomeric hybrid TGF-beta 3-2 was recovered from E. coll LC137 transformants. A biologically active, dimeric form of the hybrid was obtd. by refolding the monomer in detergent-free buffer contg. DNSO and/or DNF. Hybrid dimers TGF-beta 1-3 (AAR92775) and TGF-beta 2-3 (AAR92776) were similarly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Prodn. of dimeric biologically active transforming growth factor by refolding denatured monomer in detergent-free folding buffer contg. specific organic solvent to improve yield
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                                                                                                                                                                                                           Transforming growth factor type beta; TGF-beta 2; TGF-beta 3; protein renaturation; protein folding; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 336 BP; 88 A; 87 C; 71 G; 90 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 240; DB 17;
Pred. No. 4.2e-59;
0; Mismatches 60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 10; Page 41-42; 54pp; English.
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82.1%;
AAT17239 standard; DNA; 336
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                                                                                                     (first entry)
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                                                                                                                                                           DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (CIBA ) CIBA GEIGY AG
                                                                                                                                                           Hybrid TGF-beta 3-2
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Best Local Similarity
Matches 276; Conserv
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                                                                                                                                                                                                                                                                                                                                           WO9603433-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                12-JUL-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25-JUL-1994;
                                                                                                        17-JUL-1996
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                                                                                                                                                                                                                                                                                        Synthetic.
                                                     AAT17239;
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; 0 90 T; 0 other;

Sequence 336 BP; 88 A; 87 C; 71 G;

SO

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AATIS467 encodes transforming growth factor (TGF) beta-like protein, TGF-beta-3-2. TGF beta-3-2 is a hybrid of TGF-3 and TGF-2. TGF beta hybrids were made using a new process of producing dimeric, biologically active TGF beta-like proteins. The new process involves treating denatured TGF beta-like proteins. The new process involves treating denatured TGF beta-nonears with folding buffer conty. a mild detergent (CHAPS, CHAPSO or digitonin) and at least one of the solvents DMSO (dimethyl sulphoxidal, DMSO) (dimethylsulphone) and DMF (dimethyl formamide). The detergent allows folding of the monomer such that, after dimerisation, the TGF beta-like protein retains biological activity and remains in soluble form. The method allows relatively high yields of biologically active TGF beta-like proteins in their native dimeric form. TGF-beta like proteins are multifunctional regulators of cellular activity and a typical use is to stimulate wound
factor
                                                                                                                                                                                                                                                                                                                                                                                                                   of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Prodn. of dimeric, biologically active transforming growth f
beta - by refolding denatured monomer in buffer contg. mild
detergent and specific organic solvents to improve yields
                                                                                                                                                                                                                                                                             ф
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       amino acids
                                                                                                                                                                                                                                                          Transforming growth factor beta; TGF; regulator; method; proliferation; differentiation; wound healing; solvent;
                                                                                                                                                                                                                                   cDNA encoding human TGF-beta-like protein, TGF-beta-3-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       68
                                                     /*tag= a
/product= hybrid_TGF-beta-3-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                         /*tag= c
/note= "encodes C-terminal
                                                                                                                                                     вР
                                                                                                                                                 AAT15467 standard; cDNA to mRNA; 336
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                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                              TGF-beta-3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGF-beta-2"
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                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Prepn. of transforming growth factor-beta fusion protein – useful to reduce surgery recovery time and to prepare artificial skin \,
                                                      9
                                                                                                                                                                                                                                                                                                                                           TGF-betal active fragment of a TGF-beta fusion protein encoding cDNA.
                                                                                                            1 gotttggacaccaattactgcttccgcaacttggaggagaactgctgtgtgcgcccctc
                                                                                                                                                                                                    241 caagatttagaacctctaaccattctctactacattggcaaaacacccaagattgaacag
                                                     1 gettiggacaccaattactgetteegeaacttggaggagaactgetgtgtgegeeeette
                                               ;
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                                                                                                                                                                                                                                                                                                                                                            Transforming growth factor-beta fusion protein; wound healing; artificial skin; surgery recovery time; ss.
Length 336;
                  Indels
                  90;
Score 240; DB 17;
Pred. No. 4.2e-59;
0; Mismatches 60;
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Query Match 70.8%;
Best Local Similarity 82.1%;
Matches 276; Conservative
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P-PSDB; AAW08173.
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(HALL/) HALL F L.
(NIMN/) NIMNI M E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TUAN T.
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(NIMN/)
(TUAN/)
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Human TGF-beta 1 cDNA.
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                                                                                                                                                                                                          comprises a purification tray and a TGF active fragment. The present sequence encodes a specifically claimed TGF active fragment, TGF-betal. Additionally, the fusion protein may comprise proteinse-sensitive additionally, the fusion protein may comprise proteinse-sensitive inher sites and binding domain so the protein sequence may contain some or all of the following elements: purification tag:proteinase site:TGF-beta. TGF-beta promotes site:ECM binding site:proteinase site:TGF-beta. TGF-beta promotes wound healing, and the fusion protein can be used to reduce surgery recovery time and in the preparation of artificial skin. The inclusion of a purification tag facilitates purification of the fusion protein. The proteinase site is included to permit cleavage and release of the purification tag after purification if desired. The extracellular matrix binding site facilitates delivery of the TGF-beta to the site to be treated reduces the amount of TGF-beta required to be administered to be effective and reduces the concentration of circulating TGF-beta
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Best Local Similarity 75.5%; Pred. No. 1.7e-49;
Matches 256; Conservative 0; Mismatches 83
                                                         Page 44-45; 59pp; English.
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fragment. The protein can be used in place of a bone morphogenetic active fragment to create the fusion proteins of the invention. When a bone morphogenetic active fragment is used, the fusion proteins are designated bone morphogenetic fusion proteins. The bone morphogenetic fusion proteins. The bone morphogenetic fusion proteins. The bone morphogenetic fusion protein as morphogenetic fusion protein as site, an EcM/bone binding site, a second proteinase site, and a bone morphogenetic fusion proteins can be used for enhancing wound the bone morphogenetic fusion proteins can be used for enhancing wound
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    present sequence encodes a transforming growth factor beta active
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                                                                                                                                                                                                                                                                                                                                                                                                     New bone morphogenetic fusion proteins - comprising a purification tag and a bone morphogenetic active fragment, used for enhancing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 339 BP; 66 A; 113 C; 100 G; 60 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             wound healing or bone growth
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Matches 256; Conservative
98WO-US11189
                                                  97US-0868452
                                                                                                                                                                                                                                                                  Nimni ME,
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P-PSDB; AAW84207.
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SHORS E C.
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02-JUN-1998;
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                                              AAX15245 standard; cDNA; 339
                                      AAX15245
ID AAX1
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ctctccaacatggtggtgaagtcttgtaaatgtagctga 339

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cDNA encoding the mature form of transforming growth factor-beta-1. Transforming growth factor-beta-1; TGF-beta-like protein; 8-sulphonated TGF-beta-like protein; wound treatment; cancer; bone repair; tissue repair; bone marrow protective agent; cardioprotection; anti-inflammatory; immunosuppressive; Producing biologically active dimeric Transforming Growth Factor-beta - by refolding new monomeric Transforming Grow Factor-beta, useful for treatment of wounds and cancer McMaster GK, Meyhack B, Example 1; Page 28; 32pp; English. 90EP-0810922 89GB-0027546 (first entry) Cox D, (NOVS ) NOVARTIS AG ulcer; bed sore; ds 1999-083520/08 P-PSDB; AAW97091. Homo sapiens 28-APR-1999 27-NOV-1990; 06-DEC-1989; EP891985-A1 20-JAN-1999 Cerletti N, AAX15245; Query Match 61 61 ò 셤 δ g ö The coding sequence (AAT17235) of human transforming growth factor TGF-beta 1 (AAR92773) was cloned into plasmid pGEM-5ZF(+) (Promega) and the construct used to transform E. coli 171090. Subcloning in pPLMu yielded plasmid pPLMu.hTGF-beta 1. Non-soluble, monomeric TGF-beta 1 was recovered from E. coli LC 137/ppLMu.hTGF-beta 1 (DSM 5656) transformants. A biologically active, dimeric form of TGF-beta 1 was obtd. by refolding this monomer in detergent-free buffer contg. DMSO and/or DMF. Dimers of TGF-beta 3 (AAR92772) and TGF-beta 2 (AAR92774), and hybrid dimers (see also AAR92775-77), were 240 300 tacattgacttccgacaggatctgggctggaagtgggtccatgaacctaagggctactat 120 gecaacticigeicaggecetigeceataecticegeagigeagaeacaaeceacageaeg 180 tacattgacttccgcaaggacctcggctggaagtggatccacgagcccaagggctaccat 120 gccaacttctgcctcgggccctgccctacatttggagcctggacacgcagtacagcaag 180 caggogottggagoogotgcccatcgtgtactacgtgggccgcaagcccaaggtggagcag 300 gctttggacaccaattactgcttccgcaacttggaggagaactgctgtgtgcgcccctc 60 Gaps 1 gecetggacaccaactattgettcagetecacggagaagaactgetgegtgeggeagetg 60 gtgctgggactgtacaacactctgaaccctgaagcatctgcctcgccttgctgcggtgccc caggacctggagccctgaccatcctgtactatgttgggaggaccccaaagtggagcag Prodn. of dimeric biologically active transforming growth factor by refolding denatured monomer in detergent-free folding buffer contg. specific organic solvent to improve yield ö Length 339; Score 204.6; DB 17; Length Pred. No. 4.8e-49; 0; Mismatches 84; Indels Sequence 339 BP; 66 A; 114 C; 100 G; 59 T; 0 other; Transforming growth factor type beta; TGF-beta 1; protein renaturation; protein folding; ds. Example 1B; Page 20-30; 54pp; English. 60.4%; 95WO-EP02719 94EP-0810439 Best Local Similarity 75.2 Matches 255; Conservative AG WPI; 1996-117000/12. GEIGY P-PSDB; AAR92773 also produced (CIBA ) CIBA Prodn. of dim by refolding Homo sapiens 25-JUL-1994; 12-JUL-1995; 38-FEB-1996 Cerletti N;

Query Match

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The present sequence encodes the mature form of transforming growth factor-beta-1. Dimeric, biologically active TGF-beta-like protein can be produced by subjecting the denatured monomeric form to refolding conditions. The new monomeric S-sulphonated TGF-beta-like protein is useful for the production of the dimeric, biologically active TGF-beta-like protein is useful for the treatment of wounds furface or internal) and cancer in a mammal, in bone and tissue repair, as a bone marrow protective agent, a mediator of cardioportection, for the production of an anti-inflammatory or immunosuppressive preparation. Treatment is useful for animals, especially humans, and wound treatment (e.g. ulcers, bed sores etc.) is tacattgacttccgacaggatctgggctggaagtgggtccatgaacctaagggctactat 120 240 241 caggacctggagcccctgaccatcctgtactatgttgggaggacccccaaagtggagcag 300 9 1 gotttggacaccaattactgcttccgcaacttggaggagaactgctgtgtgcgcccctc tacattgacttccgcaaggacctcggctggaagtggatccacgagcccaagggctaccat gecaacticigectegggeectgeectacattiggagectggaeacgeagtacageaag 181 gtcctggccctgtacaaccagcataacccgggcgcctcggcggcggcgtgctgcgtgccg gtgctgggactgtacaacactctgaaccctgaagcatctgcctcgccttgctgcgtgccc DB 20; Length 339; Indels Sequence 339 BP; 66 A; 114 C; 100 G; 59 T; 0 other; 60.4%; Score 204.6; DB 20; 75.2%; Pred. No. 4.8e-49; Live 0; Mismatches 84; particularly useful for the elderly Best Local Similarity 75.2 Matches 255; Conservative 121 121 181 g οy a δ δ

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/product=monkey transforming growth factor-beta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 1303;
                                                                                                                                                                                                                                                                                                                                                             Inhibition of proliferation of epidermal cells - used to treat psoriasis by contacting cells with compositions containing transforming growth factor-beta.
                                                                                                                                                                                                                                                                                                                                                                                                             TGF-beta may be used in the treatment of hyperplasia associated with acanthosis-categorised skin diseases, and in alleviating psoriatic symptoms associated with cytokine-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            84; Indels
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                                                                                                                                                                                                                                                                                                                         Stevens V;
                                                                                                                                            Transforming growth factor-beta; simian; psoriasis;
                                                                                                                                                                                                                                                                                                                                                                                                                                      induced phenomena. See also AA003268 and AAR03750.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 11;
                       Score 204.6; DB 1
Pred. No. 6.7e-49;
                                                                                                                             Monkey transforming growth factor-beta cDNA.
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                                                                                                                                                                                                                                                                                                                       Ranchalis JE,
                                                                                                                                                                                    Location/Qualifiers
                                                                               BP
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                                                                             AAQ09317 standard; cDNA; 1303
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/*tag= a
836..1170
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les 255; Conserv
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Best Local Si
Matches 255;
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                     Hypertension therapy; hypotensive agent; blood pressure modulator;
gtgctgggactgtacaacactctgaaccctgaagcatctgcctcgccttgctgcgtgccc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence encoding simian transforming growth factor (TGF) beta-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A new method for treating hypertension comprises administering
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Use of transforming growth factor (TGF)-beta and their antagonists - for modulating blood pressure, for treating hypertension and hypotension
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 267 T; 0 other;
                                                                                                                                                                           Sequence 1559 BP; 300 A; 546 C; 446 G;
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262..282
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Length 1559;

DB 13;

Score 204.6;

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                                                                                                                                                                                                                                           gtgctgggactgtacaacactctgaacctgaagcatctgctcgccttgctgctgctgct
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Pred. No. 7e-49;
); Mismatches 84; Indels
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transfected eucaryotic cells,
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 75.28;
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88US-0147842
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                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cercopithecus aethiops.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1988-347488/49
 Best Local Similarity
Matches 255; Conserv
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25-JAN-1988;
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expressed in eukaryotic cells in plasmid pSV2. There is 100% between mature simian and human TGF-beta 1. The plasmid also the SV40 promoter and a selection marker, esp. DHFR.
                                                                                                        Score 204.6; DB 9; Length 1560; Pred. No. 7e-49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                contg. transforming growth factor beta - inhibitions of HIV infection and replication in vivo.
                                                                                                                                      Indels
                                                           Sequence 1560 BP; 301 A; 547 C; 445 G; 267 T; 0 other,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIV; vaccine; AZT; CD4; cytokines; growth
                                                                                                                                   84;
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                                                                                                        60.48;
75.28;
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                                                                                                                     Best_Local Similarity 75.2
Matches 255; Conservative
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P-PSDB; AAR05663.
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                                                                                                        Query Match
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                                                                                                                                                                                                                                                                                                                                  TGF-beta may be used in vivo to prevent formation of synctia and inhibit HIV infection. {\tt TGF} may also be used with other HIV treatments (AZT, soluble CD4 etc.).
                                                                                                                                                                                                                                                                                                                                                                                   121 gocaacttctgctcaggcccttgcccatacctccgcagtgcagacacaccacagcacg 180
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/product=human transforming growth factor-beta
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                                                                                                            Sequence 1560 BP; 301 A; 547 C; 445 G; 267 T; 0 other;
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                                                                                                                                                                 DB 11;
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                                                                                                                                                                 60.4%; Score 204.6; DB 75.2%; Pred. No. 7e-49;
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                                                                         Disclosure; Fig 1; 20pp; English
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1096..1431
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Matches 255; Conservative
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P-PSDB; AAR03743.
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                                                                                                                                                                 Query Match
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vaccine; A2T; CD4; cytokines; transforming growth factor;
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Inhibition of proliferation of epidermal cells - used to treat psoriasis by contacting cells with compositions containing transforming growth factor-beta.
                                                                                                                                                                                                                                                     TGF-beta may be used in the treatment of hyperplasia associated with acanthosis-categorised skin diseases, and in alleviating psoriatic symptoms associated with cytokine-induced phenomena. See also AAQ03269 and AAR03750.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1561 BP; 301 A; 547 C; 446 G; 267 T; 0 other;
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Pred. No. 7e-49;
0; Mismatches 84;
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ilarity 75.2%;
Conservative
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255; Conserv
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ds.
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TGF-betal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mat_peptide
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Best Local $
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Stevens V;

26

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caggacctggagccctgaccatcctgtactatgttgggaggacccccaaagtggagcag 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gtgctgggactgtacaacactctgaaccctgaagcatctgcctcgccttgctgcgtgccc
                                                                                                                                   Inhibition of proliferation of epidermal cells - used to treat psoriasis by contacting cells with compositions containing transforming growth factor-beta.
                                                                                                                                                                                                               TGF-beta may be used in the treatment of hyperplasia associated with acanthosis-categorised skin diseases, and in alleviating psoriatic symptoms associated with cytokine-induced phenomena. See also AAQ03268 and AAR03743.
                                                                                                                                                                                                                                                                                   Sequence 1571 BP; 299 A; 563 C; 443 G; 266 T; 0 other
                                                                                                                                                                                                                                                                                                                          Score 204.6; DB 11;
Pred. No. 7e-49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ctctccaacatggtggtgaagtcttgtaaatgtagctga 339
                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                    Purchio AF, Ranchalis JE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
512..1684
                                                                                                                                                                                        Disclosure, fig 1; 20pp; English.
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                                                                                                                                                                                                                                                                                                                        Query Match 60.4%;
Best Local Similarity 75.2%;
Matches 255; Conservative
                 88US-0229133
                                           (ONCO-) ONCOGEN LTD PARTNER
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512..598
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599..1684
                                                                                            WPI; 1990-038499/06.
P-PSDB; AAR03750.
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                                                                  Fwardzik DR,
                 05-AUG-1988;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20-NOV-1991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TGF-beta may be used in vivo to prevent formation of synctia and inhibit HIV infection. TGF may also be used with other HIV treatments (AZT, soluble CD4 etc.).
                                                                                                                                                                                                                                                                                                                                                                                       180
                                                                                                                                                                                                                                                                             1 gctttggacaccaattactgcttccgcaacttggaggagaactgctgtgtgcgcccctc 60
                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                             Length 1569;
                                                                Compsns. contg. transforming growth factor beta - used for inhibitions of HIV infection and replication in vivo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product-human transforming growth factor-beta
                                                                                                                                                                                                                          Score 204.6; DB 11; Length
Pred. No. 7e-49;
0; Mismatches 84; Indels
                                                                                                                                                                                  Sequence 1569 BP; 295 A; 565 C; 444 G; 265 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              301 ctctccaacatggtggtgaagtcttgtaaatgtagctga 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Transforming growth factor-beta; psoriasis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human transforming growth factor-beta cDNA
  À;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
 Purchio
                                                                                                                                                        Disclosure; Fig 1; 20pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAQ03269 standard; DNA; 1571 BP
                                                                                                                                                                                                                         Query Match 60.4%;
Best Local Similarity 75.2%;
Matches 255; Conservative (
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Lioubin M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22..63
/*tag=
                        WPI; 1990-068723/10.
P-PSDB; AAR05664.
Brankovan V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             04-AUG-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12-AUG-1990
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Gaps

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84; Indels

Length 1571;

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61 tacattgacttccgacaggatctgggctggaagtgggtccatgaacctaagggctactat 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                           The gene product is known to stimulate cell proliferation and inhibit anchorage-dependent growth of a variety of human cancer cell lines, it is esp. useful in treatment of burns and the promotion of surface and internal wound healing. TGF-beta may be expressed from a transformed CHO cell line.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 getttggacaccaattactgetteegcaacttggaggagaactgetgtgtgegeeeete 60
                                                                                                                                                                                                                                                                                                                                                                     TGF-beta prodn. from transformed hosts - useful esp. for treating wounds (J6 2/9/86).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 gecaacttetgeteaggeeettgeeeataeeteeggagagacacaaageacg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1796 gccaacttctgcctcgggccctgcccctacatttggagcctggacacgcagtacagcaag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181 gtgctgggactgtacaacactctgaaccctgaagcatctgcctcgccttgctgcgtgccc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          241 caggacctggagccctgaccatcctgtactatgttgggaggaccccaaagtggagcag
                            /*tag= a
/note= "Sequence can form stable hairpin loops"
842..2014
/*tag= b
/*tag= c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          84;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            60.4%; Score 204.6; DB 775.2%; Pred. No. 7.9e-49; iive 0; Mismatches 84
Location/Qualifiers 37..113
                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Fig 1b; 26pp; English
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                                                                                                                                                                                                                     85US-0715142
87US-0025423
                                                                                                                                                                                          86EP-0302112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 255; Conservative
                                                                                                                                                                                                                                                                 (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                           WPI; 1986-326875/50.
                                                                                                                                                                                                                                                                                                                                        P-PSDB; AAP61468
                misc_structure
                                                                                                                                                                                          21-MAR-1986;
                                                                                                                                                                                                                     22-MAR-1985;
13-MAR-1987;
                                                                                                                                                                                                                                                                                              Derynck RMA;
                                                                                                                                                               10-DEC-1986
                                                                                       mat_peptide
                                                                                                                                EP200341-A.
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Best Local S
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                                                           CDS
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                                                                                                                                                                                                                                                                                                                                                                    The DNA sequence encodes human prepro-TGF-beta 1 which can produced by recombinant methods, it has osteogenetic and tumoricidal activity.
                                                                                                                                                                                                                                                                            Human pro-TGF-beta 1 prodn., for osteo-genetic activity - h
preparing DNA chain contg. base sequence coding for human
pre:pro-TGF-beta 1, forming expression vector etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Transforming growth factor beta; cancer; wound healing.
                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1821 BP; 326 A; 679 C; 508 G; 308 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -
/*tag= c
/note= "pro-TGF-beta
1346..1684
                                          /*tag= e
/note= "TGF-beta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BP
                                                                                                                                                                                                                                                                                                                                        Claim 1; Fig 1; 16pp; Japanese.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence encoding preTGF-beta.
                                                                                                                                              89JP-0318243.
                                                                                                                                                                           89JP-0318243
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 75.2
Matches 255; Conservative
                                                                                                                                                                                                        (KIRI ) KIRIN BREWERY KK
                                                                                                                                                                                                                                   WPI; 1991-271579/37.
                                                                                                                                                                                                                                                  P-PSDB; AAR13813.
                                                                                    JP03180192-A
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                            mat_peptide
                                                                                                                 06-AUG-1991
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                                   encoding human pre-transforming growth factor-beta-1 (pre-TGF-beta-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 It was obtained by an analysis of several overlapping cDNAs and gene fragments, leading to the detn. of a continuous sequence corresp. to tl TGF-beta-1 precursor mRNA. It is useful in constructing vectors that encode biologically active transforming growth factor (TGF-beta), operably linked to DNA that encodes a secretory leader (SL). It, or a nucleic acid capable of hybridising with it, can also be labelled and used in diagnostic assays for DNA or mRNA encoding TGF-beta or related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic acid encoding transforming growth factor-beta -
cloned into expression vectors for expression in eukaryotic host
cells for therapeutic use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2537 BP; 473 A; 893 C; 739 G; 432 T; 0 other;
                                                                                                                                                                                                                                                  /*tag= d
/note="G-C rich sequence
and a downstream TATA-like sequence"
                                                                    Transforming growth factor-beta-1 (TGF-beta-1); neoplastic cell line inhibition; EGF-potentiated anchorage-independent growth;
                                                                                                                                                                                                                  /*tag= c
/note="stable hairpin loops
                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fig 1b; 28pp; English.
                                                                                                                                                                 1676.2011
/*tag= b
37.113
                                                                                                                                                                                                                                                                                                                                                                      87US-0025423
                                                                                                                                                                                                                                                                                                                                               87US-0U25423
                                                                                                                                                                                                                                        2015..2100
            (first entry)
                                                                                                                                                        842..2014
                                                                                                                                                                                                                                                                                                                                                                                                                      Derynck RMA, Goeddel DV;
                                                                                                                                                                                                                                                                                                                                                                                              (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1990-051338/07.
P-PSDB; AAR05258.
                                                                                                                                                                                                      misc_difference
                                                                                                                                                                                                                                       misc_feature
                                                                                                                                                                                                                                                                                                                                               13-MAR-1987;
                                                                                                                                                                                                                                                                                                                                                                      13-MAR-1987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure;
            05-AUG-1990
                                                                                                                      sapiens
                                                                                                                                                                                                                                                                                                US4886747-A
                                                                                                                                                                                                                                                                                                                       12-DEC-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       proteins
                                                                                                                     Homo
                                    CDNA
                                                                                                                                            Key
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Sequence encodes the 390 amino acid (AA) precursor transforming growth factor-beta 1 (pre-TGF-beta 1) polypeptide. The 5' untranslated region of the TGF-beta 1 mRNA is 841 bases long, is purine rich and has a region of potential secondary structure. The TATA-like sequence in the 3' untranslated region of the gene is presumably a polyadenylation signal. Mature TGF-beta 1 comprises the C-terminal 112 AA's of pre-TGF-beta 1 and is cleaved at the Arg-Arg dipeptide preceding its NH2 terminus. The nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleotide sequence encoding transforming growth factor beta-3 -used as a probe, or to produce TGF beta 3, for growth inhibition of certain normal and neoplastic cells, eg A549.
                                                                                               Transforming growth factor beta-3 (TGF beta 3); tumour cells; growth
                                                                                                                                                                                                                               /*tag c
2093..2099
/*tag d
/label=TATA-like sequence
37..113
                                                                                                                                                                                                                                                                                                                    /*tag= f
/label=hydrophobic domain
                                                                                                                                                                                                         TGF-beta 1
                                                                                                                                                                    /label=pre-TGF beta
1677..2011
                                                                                                                                  .ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Fig. 1b; 61pp; English.
 ВP
                                                                      Sequence of pre-TGF-betal cDNA
                                                                                                                                                                                              /*tag= b
/label=mature
AAQ02814 standard; cDNA; 2537
                                                                                                                                                                                                                                                                                                                                                                                                     88WO-US01945
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                                                                                                                                                                                                                   2015. . 2092
                                               (first entry)
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                                                                                                                                            842..2011
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                                                                                                                                                                                                                                                                                            /*tag=
863..91
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1990-007474/01.
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                                                                                                                                                                                                                                            misc_feature
                                                                                                                                                                                                                                                                                                       misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                     08-JUN-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                             08-JUN-1988;
                                               31-MAY-1989
                                                                                                                                                                                                                                                                                                                                                      WO8912101-A
                                                                                                                                                                                                                                                                                                                                                                               14-DEC-1989
                                                                                                          inhibition
                                                                                                                                                                                                                                                                              stem_loop
                       AAQ02814;
                                                                                                                                                                                                                     GC_signal
                                                                                                                                  Key
                                                                                                                                                                                 CDS
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.; 0

Gaps

; 0

Indels

84;

0; Mismatches

60.4%; Score 204.6; DB 1 llarity 75.2%; Pred. No. 7.9e-49; Conservative 0; Mismatches 84

Similarity

Best Local Sim Matches 255; Query Match

DB 11; Length 2537;

1676

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1736

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61

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1796

121

ð

1 getttggacaccaattactgcttccgcaacttggaggagagaactgctgtgtgcgcccctc 60

tacattgacttccgacaggatctgggctggaagtgggtccatgaacctaagggctactat 120

gccaacttctgctcaggcccttgcccatacctccgcagtgcagacacaacccacagcacg 180

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Derynk RMA,
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25-JAN-1980
                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAT15720;
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5'UTR
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acid encoding the second subtype of TGF-beta (TGF-beta 3) is useful as probe or to produce TGF-beta 3 for inhibition of growth of normal and
                                                                                                                                                                                                               1736 tacattgacttccgcaaggacctcggctggaagtggatccacgagcccaagggctaccat 1795
                                                                                                                                                                                               1856 gtcctggccctgtacaaccagcataacccgggcgcctcggcggcgcgtgctgcgtgccg 1915
                                                                                                                   tacattgacttccgacaggatctgggctggaagtgggtccatgaacctaagggctactat 120
                                                                                                                                                  gccaacttctgctcaggcccttgcccatacctccgcagtgcagacacaacccacagcacg 180
                                                                                                                                                                                 Gaps
                                                                                    gctttggacaccaattactgcttccgcaacttggaggagaactgctgtgtgcgcccctc 60
                                                     Score 204.6; DB 11; Length 2537; Pred. No. 7.9e-49; 0; Mismatches 84; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                TGF-beta-1; TGF-beta-2; transforming growth factor beta-1; transforming growth factor beta-3; recombinant; wound healing;
                               Sequence 2537 BP; 473 A; 893 C; 739 G; 432 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                               /*tag= a
/note= "possible hairpin loop region"
                                                                                                                                                                                                                                                      301 ctctccaacatggtggtgaagtcttgtaaatgtagctga 339
                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                    BP
                                                                                                                                                                                                                                                                                                   AAQ56923 standard; cDNA; 2537
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87US-0025423.
89US-0389929.
92US-0845893.
                                                     60.4%;
ilarity 75.2%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    85US-0715142
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1676..2011
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2515..2521
/*tag= d
                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                             842..2014
                                                                                                                                                                                                                                                                                                                                                  Human pre-TGF-beta-1.
                                                    Query Match
Best Local Similarity
Matches 255; Conserv
               neoplastic cells.
                                                                                                                                                                                                                                                                                                                                                                                                                        misc_structure
                                                                                                                                                                                                                                                                                                                                                                                 vulnerary; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22-MAR-1985;
13-MAR-1987;
04-AUG-1989;
04-MAR-1992;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22-MAR-1985;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1856 gicciggiccigiacaaccagcataacccgggcgccicggcggcggcgicgigcigcggicg 1915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tacattgacttccgacaggatctgggctggaagtgggtccatgaacctaagggctactat 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 gccaacttctgctcaggcccttgcccatacctccgcagtgcagacacaacccacagcacg 180
                                                                                                                                                                                                                                                                                                               cDNA sequences were determined for human pre-TGF-beta-1 (AAQ56923), pig TGF-beta-3 (AAQ56925) and human TGF-beta-3 (AAQ56926), and the corresponding amino acid sequences were determined (AAA46227-29, respectively). A genomic fragment corresponding to a human TGF-beta-1 exon (AAQ56924) was also isolated and its amino acid sequence determined (AAR46230). The sequences have been used in the construction of vectors for the expression of recombinant TGF-beta.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 gctttggacaccaattactgcttccgcaacttggaggagaactgctgtgtgcgcccctc 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          241 caggacctggagccctgaccatcctgtactatgttgggaggaccccaaagtggagcag
                                                                                                                                                                                        Nucleic acid sequences encoding transforming growth factor-beta diagnostic probes, and for use in therapeutics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 15; Length 2537;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2537 BP; 473 A; 890 C; 742 G; 432 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1976 ctgtccaacatgatcgtgcgctcctgcaagtgcagctga 2014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              transforming growth factor beta 1; wound healing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      301 ctctccaacatggtggtgaagtcttgtaaatgtagctga 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 204.6; DB 1 Pred. No. 7.9e-49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pre-transforming growth factor beta 1 cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                      Disclosure; Fig 1b; 25pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 60.4%;
Best Local Similarity 75.2%;
Matches 255; Conservative C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          recombinant production; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                    Goeddel DV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /*tag=
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(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (revised)
                                                                                                       WPI; 1994-056343/07
P-PSDB; AAR46227.
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ВP

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tacattgacttccgcaaggacctcggctggaagtggatccacgagcccaagggctaccat 1795
                                          caggacctggagccctgaccatcctgtactatgttgggaggacccccaaagtggagcag
                                 gccaacttctgctcaggcccttgcccatacctccgcagtgcagacacaacccacagcacg
                                                                          gtgctgggactgtacaacactctgaaccctgaagcatctgcctcgccttgctgcggtgccc
                                                                                                                                                                                                                                                                                                                      Transforming growth factor-beta 1; TGF-beta 1; human; ss.
                                                                                                                                                                      ctctccaacatggtggtgaagtcttgtaaatgtagctga 339
                                                                                                                                                                                                                                                                                               Human pre-transforming growth factor-beta 1 cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                   /*tag= c
/note= "GC-rich sequence"
2514..2520
/*tag= d
                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
842..2014
                                                                                                                                                                                                                                                                                                                                                                                                                         /*tag= b
/note= "putative
2015..2100
                                                                                                                                                                                                                                  AAV52933 standard; cDNA; 2537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      87US-0025423.
85US-0715142.
89US-0389929.
92US-0845893.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    85US-0715142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               93US-0147364
95US-0454468
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1676..2011
/*tag= b
37..113
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P-PSDB; AAW78785.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13-MAR-1987;
22-MAR-1985;
04-AUG-1989;
04-MAR-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Derynck RMA,
                                                                                                                                                                                                                                                                           21-DEC-1998
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                                                                                                                                                                                                                                                                                                                                                                                             mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US5801231-A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-NOV-1993
                                                                                                                                                                                                                                                                                                                                                                                                                 stem_loop
                                                                                                                                                                                                                                                      AAV52933;
           1736
                                                                                                                                                                                                              RESULT 50
                                                    1796
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                                                                                                                   241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The cDNA encodes the pre-transforming growth factor (TGF) beta 1 protein. The nucleotide sequence was obtd. by an analysis of several overlapping cDNAs and gene fragments. The DNA is useful for the recombinant production of TGF beta 1, which can be used in, e.g. wound healing. (Revised entry submitted to correct sequence analysis breakdown.)
                    "GC-rich region forms stable hairpin loops;
similar to structural organisation of c-myc RNA,
could play role in mRNA stability or in
regulation of transcription
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New recombinant human transforming growth factor-beta prods. - produced using Chinese hamster ovary cells, for use in diagnostic applications
                                                                                                                                             "GC-rich region; possibly responsible for the fact 3'UTR of mRNA could not be cloned as cDNA; may be important for transcription efficiency"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 gotttggacaccaattactgcttccgcaacttggaggagaactgctgtgtgcgcccctc
                                                                                                                                                                                                             /*tag= g
/note= "TATA-like sequence; no evidence that this
                                                                                                                                                                                                                                                                                   "consensus sequence immediately precedes polyA-tail (Benoist et al)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 60.4%; Score 204.6; DB 17; Length Best Local Similarity 75.2%; Pred. No. 7.9e-49; Matches 255; Conservative 0; Mismatches 84; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2537 BP; 473 A; 893 C; 739 G; 432 T; 0 other;
                                                                                                                                                                                                                                functions a promoter"
                                                                                                               mature_TGF_beta_1
                                                                                   pre-TGF_beta_1
                    /note= "GC-rich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 3; Fig 1; 26pp; English.
                                                                                                                                                                                                                                                                                                                                                                                        85US-0715142.
89US-0389929.
92US-0845893.
93US-0147364.
                                                                                                              /product= ma
2015..2100
/*tag= e
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2529..2536
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2094..2100
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           Д
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37..113
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/note=
           /*tag=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1996-076891/08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P-PSDB; AAR90827.
                                                                                                                            repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        or in therapy
misc_feature
                                                                                                                                                                                                                                                                                                                                                                                          22-MAR-1985;
04-AUG-1989;
04-MAR-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Derynck RMA,
                                                                                                                                                                                                                                           polyA_signal
                                                                                                                                                                                                                                                                                                                  US5482851-A.
                                                                                                                                                                                                                                                                                                                                                           22-MAR-1985;
                                                                                                                                                                              repeat_unit
                                                                                                                                                                                                                                                                                                                                       09-JAN-1996
                                                                                           mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                13-MAR-1987
                                                                                                                                                                                                                                                                                                                                                                                                                       05-NOV-1993
                                                                                                                                                                                                 TATA_signal
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stable hairpin loop"

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precursor sequence -
                                                                                                                           DNA encoding transforming growth factor-beta useful for analysis to perform manipulations recombinant production of the protein
                                                                                                                                                                                                                                       Example 3; Fig 1B 1-3; 26pp; English
Goeddel DV;
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1676 gecetigacaceaactattgetteagetecacggagaagaactgetgegtgeggeagetg 1735 tacattgacttccgacaggatctgggctggaagtgggtccatgaacctaagggctactat 120

61

g

12-OCT-1995.

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macrophage inducible nitric oxide synthase; iNOS; constitutive NOS; interleukin-1-beta; transforming growth factor-beta; TGF-beta; IL1-beta; nitric oxide production; hypotension; inflammation; septic shock;
         This nucleotide sequence codes for the human transforming growth factor-beta 1 precursor (preTGF-beta 1, see AAW78785). It is a composite of overlapping CDNA clones isolated from different cDNA libraries (placenta, A172 glioblastoma, HT1080 flbroblastoma) using TGF-beta exon (see AAV52936) restriction fragments as probes. The 3' region of the sequence was determined using cloned genomic TOR. The invention relates to the recombinant production of TGF-beta. Biologically active TGF-beta is defined as being capable of inducing EGF-potentiated anchorage independent growth of target cell lines and/or growth inhibition of neoplastic cell lines. Nucleic acids encoding TGF-beta have been isolated and cloned into evectors which are replicated in bacteria and expressed in cukaryotic cells. TGF-beta recovered from transformed cells is used in known therapeutic applications. TGF-beta nucleic acids are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gtectggccctgtacaaccagcataacccgggcgcctcggcggcgccgtgctgcgtgccg 1915
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                                                                                                                                                                                                                                                                                   also useful in diagnosis and identification of TGF-beta clones.
                                                                                                                                                                                                                                                                                                                                                                                  DB 19; Length 2537;
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/*tag= a
/product= transforming growth factor-beta 1
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                                                                                                                                                                                                                                                                                                                                                                                60.4%; Score 204.6; DB 1
75.2%; Pred. No. 7.9e-49;
                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
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The cDNA encodes transforming growth factor-beta 1 (TGF-beta 1) which has been found to inhibit inducible nitric oxide synthase (1NOS) gene transcription, esp. in interleukin-1-beta (ILI-beta) stimulated rat smooth muscle cells, and at a dose which does not inhibit constitutive NOS. TGF-beta 1 or 2 (AAR83055) or their active fragments, can be used in the treatment of Appotension, such as that associated with severe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1679 gccctggacaccaactattgcttcagctccacggagaagaactgctgcggcggcagctg 1738
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                                                                                                                                                                                                                                                                                                                                                                                                                   Treatment of hypotension, esp. in septic shock - by administering transforming growth factor-beta e.g. to inhibit inducible nitric oxide synthase gene transcription
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Pred. No. 8e-49;
0; Mismatches 84;
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75.2%;
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                                                                                                                         94WO-US03705
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                                                                                                                                                                                         (HARD ) HARVARD COLLEGE.
                                                                                                                                                                                                                                                        Perrella MA;
                                                                                                                                                                                                                                                                                                                     WPI; 1995-358443/46.
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255; Conserv
                                                                                                                                                                                                                                                                                                                                                          P-PSDB; AAR83054.
                                                            05-APR-1994;
                                                                                                                         05-APR-1994;
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Best Local 9
                                                                                                                                                                                                                                                        Lee M,
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A chimeric gene (AAT16516) codes for a fusion protein (AAR89470) between the helical region of human collagen I(a) and human transforming growth factor beta-1 (TGF-beta-1). The collagen moiety was cloned from human fibroblast AG02261A cells by PCR amplification. The construct was inserted into a pMal vector for expression in E. coli. The fusion protein provides sustained release and delivery of TGF-beta-1 to a target tissue. The TGF increases efficacy of the body's normal soft tissue repair response and also induces
                                                                                                                                                                                                                                                                                                                                                                                                            Chimaeric DNA encoding protein contg. extracellular matrix protein domain - and cellular regulatory factor domain, partic. useful as osteogenic agents, also related vectors, transformed cells and
                                           /*tag= a
/product= collagen IA/TGF-beta-1 fusion protein
                                                                                                                                                           the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 3541 BP; 504 A; 1143 C; 1188 G; 704 T; 2 other;
                                                                                               /note= "base 2679 is not identified in specification"
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/note= "base 2688 is not identified in
specification"
               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Fig 2; 59pp; English.
                                                                                                                                                                                                                                                        95CA-2151547
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                                                                                    *tag= b
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                                                                                                                                                                                                                                                                                  10-JUN-1994;
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               Key
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protein. The method may be used to make host cells assimilate and incorporate trans-4-hydroxyproline into proteins. This is especially useful in the recombinant production of proteins such as collagen, fibrinogen and fibronectin whose ability to self aggregate and produce functional proteins depends on the post translational hydroxylation of proline. The method is also useful in studying the structure and function of polypeptides which do not normally contain trans-4-hydroxyproline. The present sequence encodes a chimeric collagen I (alphal)/transforming growth factor-betal (TGF-betal) protein, which may be produced using the method of the invention.
                                                                                                                                                                                                                                                                                  Extracellular matrix protein; self aggregation; hydroxylated proline; trans-4-hydroxyproline; a hydroxproline; recombinant protein production; collagen; fibrinogen; fibronectin; post translational hydroxylation; ss. transforming growth factor-betal; TGF-betal; chimera; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              matrix protein or its fragment. The extracellular matrix protein is capable of self aggregating in a cell which does not ordinarily hydroxylated prolines. The method comprises optimising a nucleic acid sequence for expression in the cell by substitution of codons preferred by that cell for naturally occurring codons not preferred by the cell; incorporating the nucleic acid sequence into the cell; and contacting the cell with a hypertonic growth medium containing at least one amino acid, selected from the group consisting of trans-4-hydroxyproline and 3-hydroxyproline to allow at least one of the amino acids to be assimilated into the cell and incorporated into the extracellular matrix
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Production of extracellular matrix proteins containing 4-trans-hydroxyproline results in native self aggregating proteins,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The specification describes a method for producing an extracellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product= "chimeric collagen 1 (alpha1)/TGF-beta1
    protein"
/transl_except= (pos: 2591..2593, aa: Gly)
                                                                                                                                                                                                                                               cDNA encoding a chimeric collagen 1 (alpha1)/TGF-beta1 protein.
Connolly K;
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20..3535
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                                                                                                                               AAA12498 standard; cDNA; 3541
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                                                                                                                                                                                                          25-JUL-2000
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                                                                                                                                                                                                                                                                                                                                                                               Chimeric
Chimeric
                                                                                                                                                                      AAA12498;
                                                                                              RESULT 53
                                                                                                              AAA12498
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TGF-betal; biologically active protein production;
                                                                                       (PERE/) PEREZ
                                                 22-JUN-1992;
                                                                   22-JUN-1992;
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            FR2692594-A.
                              24-DEC-1993.
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                                                                                                          Perez J;
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                                                                            3377 gtcctggccctgtacaaccagcataacccgggcgcctcggcggcgccgtgctgcgtgccg 3436
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                                                                                                                                               gccaacttctgctcaggcccttgccatacctccgcagtgcagacacaacccacagcacg 180
                                                                                                                                                                                      240
                                                                                                          tacattgacttccgacaggatctgggctggaagtgggtccatgaacctaagggctactat 120
                                                 Gaps
                                                                  3317 gccaacttctgcctcgggccctgccctacatttggagcctggacacgcagtacagcaag
                                                                                                                                                                                    caggacctgagaccctgaccatctgtactatgttgggaggaccccaaagtggagcag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              has used T instead of U in full-length mRNA"
                             DB 21; Length 3541;
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                                                                                                                                                                                                                                                                                                                                                                                                               Transforming Growth Factor beta 1; TGF; non-coding region; coding region; resonance; interaction; optimisation; ss.
                                                Indels
Sequence 3541 BP; 504 A; 1145 C; 1188 G; 704 T; 0 other;
                           Score 204.6; DB 21;
Pred. No. 8.6e-49;
0; Mismatches 84;
                                                                                                                                                                                                                                                                 /*tag= a
/note= "the inventor
the TGFbetal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /*tag= g
/product= TGFbetal
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/note= "N2 region"
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                            Query Match 60.4%;
Best Local Similarity 75.2%;
Matches 255; Conservative (
                                                                                                                                                                                                                                                                                                                                   AAQ55624 standard; DNA; 4105
                                                                                                                                                                                                                                                                                                                                                                                             TGFbetal 5'-UTR-CDS-3'-UTR.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The TGFbetal mRNA was divided into 3 regions (i.e. 5'-UTR, CDS and 3'-UTR) for various "perturbation" experiments. The relative order of the 3 regions was altered, e.g. the 3'-UTR was positioned upstream of the CDS and the 5'-UTR was positioned downstream of the CDS. The experiments showed that interactions between coding and noncoding regions are destroyed by such perturbations.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Application of optimised gene expression - for scientific, industrial and therapeutic purposes
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llarity 75.2%; Pred. No. 8.9e-49;
Conservative 0; Mismatches 84
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92FR-0007571
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Best Local Similarity
Matches 255; Conserv
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Human transforming growth factor beta 1 encoding cDNA.
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                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                      WO9603432-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                           12-JUL-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25-JUL-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGF-betal is one example of a novel TGF-beta produced as a dimeric, biologically active protein using the method of the invention. This coding sequence was isolated from the CI-215 human glioma cell line. It was incorporated into an appropriate vector to transform Saccharomyces cerevisiae or E.coli. Monomeric TGF-betal was purified, denatured and dissolved in 140ml 50mM Tris/HCl pH8. IM NaCl. 5mM EDTA, After 72 hrs at 4 deg C, pH was adjusted to 2.5 and the mixture was conc. 10 times. The conc. soln was diluted to the original vol. with 10mM HCl and conc to a final vol of 10 ml. The supernatant from centrifigation at 5000g for 30 min contained disulphide-linked dimeric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           240
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                                                                                                                                                                                                                                                                                       Schmitz A, Meyhack B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               85; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ctctccaacatggtggtgaagtcttgtaaatgtagctga 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 203; DB 12;
Pred. No. 1.4e-48;
0; Mismatches 85;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 27; 35pp; English.
                                                                                                                                                                                                                                                                                    Cox D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  59.98;
74.98;
                                                                                                                90EP-0810922
                                                                                                                                                                    89GB-0027546
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                                                                                                                                                                                                                                                                                    McMaster GK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 59.9
Best Local Similarity 74.9
Matches 254; Conservative
                                                                                                                                                                                                                       (CIBA ) CIBA GEIGY AG
                                                                                                                                                                                                                                                                                                                                     WPI; 1991-180005/25.
                                                                                                                                                                                                                                                                                                                                                                  P-PSDB; AAR12402
                                                                                                             27-NOV-1990;
                                                                                                                                                                    06-DEC-1989;
                                                                                                                                                                                                                                                                                 Cerletti N,
                                                      19-JUN-1991
EP433225-A
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AATI5462-T15464 encode transforming growth factor (TGF) beta-1,
TGF beta-2 and TGF beta-3 which are produced using recombinant
CTGF beta-2 and TGF beta-1ike proteins in
DNA technology and used to produce TGF beta-like proteins in
CTGT dimeric form. The TGF beta-1ike proteins produced are hybrids of
CTGT different types of TGF beta-1ike proteins of
CTGT beta morphogenic proteins e.g. BMP-2. The TGF beta hybrids were
made using a new process of producing dimeric, biologically active
TGF beta monomers with folding buffer contg. a mild detergent (CHAPS,
CTGF beta monomers with folding buffer contg. a mild detergent (CHAPS,
CTGF beta monomers with folding buffer contg. a mild detergent (CHAPS,
CTGF beta monomers with folding buffer contg. a mild detergent (CHAPS,
CTGF beta monomers with folding buffer contg. a mild detergent (CHAPS,
CTGF beta monomers with folding buffer contg. a mild detergent (CHAPS,
CTGF beta monomers with folding buffer contg. a mild detergent (CHAPS,
CTGF beta monomers with folding buffer contg. a mild detergent clamethylsulphone) and bmr (dimethyl formamide).
The detergent allows folding of the monomer such that, after
and remains in soluble form. The method allows relatively high yleids
of biologically active TGF beta-like proteins in their native dimeric
form. TGF-beta like proteins are multifunctional regulators of
cellular activity and a typical use is to stimulate wound healing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tacattgacttccgacaggatctgggctggaagtgggtccatgaacctaagggctactat 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Prodn. of dimeric, biologically active transforming growth f
beta - by refolding denatured monomer in buffer contg. mild
detergent and specific organic solvents to improve yields
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 339;
Transforming growth factor beta; TGF; regulator; method;
proliferation; differentiation; wound healing; solvent; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      85; Indels
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Pred. No. 1.4e-48;
                                                                                                                                                                                                                                                   /*tag= a
/product= human_TGF-beta-1
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                                                                                                                                                                           Location/Qualifiers
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(first entry)

10-JUN-1996

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ID AAT1
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1344 caggegetggageegetgeeeategtgtaetaegtgggeegeaageeeaaggtggageag 1403

BP

AAQ41602 standard; cDNA; 336

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(first entry)

26-AUG-1993

AAQ41602;

caggacctggagccctgaccatcctgtactatgttgggaggaccccaaagtggagcag

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AAQ41602
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                            caggacctggagcccttgaccatcctgtactatgttgggaggacccccaaagtggagcag
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Transforming growth factor-beta 1; tumour treatment; ss cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Coding sequence of human transforming growth factor-beta 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1569 BP; 295 A; 563 C; 445 G; 266 T; 0 other;
                                                                                                                                      ctctccaacatggtggtgaagtcttgtaaatgtagctga 339
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                                                                                                                                                                                                                                                                                                      AAN81085 standard; DNA; 1569 BP
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88US-0147842
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288.329
/*tag= b
1104.1442
/*tag= c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1988-347488/49.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     simian TGF-beta 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              treating tumours.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27-MAY-1988;
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25-JAN-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                   09-OCT-1990
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241
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a "TGF-beta1=1-132, TGF-beta2=133-336"

/\*tag= /note=

Location/Qualifiers 1..336

mat\_peptide

Key

Homo sapiens

Kuhla J;

Cerletti N,

Cox D,

McMaster GK,

WPI; 1993-161126/20. P-PSDB; AAR39641.

(CIBA ) CIBA GEIGY AG

92EP-0810845. 91EP-0810870

03-NOV-1992; 11-NOV-1991;

19-MAY-1993

EP542679-A.

hTGF-betal; hTGF-beta2; hybrid protein; wound healing; cancer treatment; bone repair; growth regulation; ss. Transforming Growth Factor-betal(44/45)beta2 hybrid.

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The invention covers hybrid TGF-beta molecules consisting of parts AQ41600 and AAQ41601, respectively). The hinge points between parts derived from different parent isoforms are pref. between amino acids 44 and 45, 56 and 57, 79 and 80, 90 and 91, or 22 and 23. Of the 30 possible hybrids using these hinge points and one part each from two of the isoforms, 6 are preferred including the hybrid TGF-betal(44/45)beta2. The hybrid molecules promote cell migration, inhibit the growth of A375 melanoma cells, accelerate the healing of partial-thickness burn wounds and full-thickness incisional wounds and full-thickness incisional wounds and increase formation of fibrous granular tissue.
New hybrid transforming growth factor-beta molecules - comprise portions of mature TGF-beta isoforms; useful as wound healants, cardioprotective, antiinflammatory and immunosuppressive agents etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 336 BP; 90 A; 92 C; 72 G; 82 T; 0 other;
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Gaps

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85; Indels

0; Mismatches

Matches 254; Conservative

Query Match Best Local Similarity

59.9%; Score 203; DB 9; Length 1569; 74.9%; Pred. No. 2e-48;

1164 tacattgacttccgcaaggacctcggctggaagtggatccacgaggcccaagggctaccat 1223

gccaacttctgctcaggcccttgcccatacctccgcagtgcagacacaacccacagcacg 180

tacattgacttccgacaggatctgggctggaagtgggtccatgaacctaagggctactat 120

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                                                                                                                   etc.
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                                                     ô
       Length 336;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hTGF-betal; hybrid protein; wound healing; cancer treatment; bone repair; growth regulation; ss.
                                                     84; Indels
  DB 14;
  Score 201.6; DB 1 Pred. No. 3.4e-48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 301 ctctccaacatggtggtgaagtcttgtaaatgtagc 336
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                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
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59.5%;
75.0%;
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                                                  Conservative
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P-PSDB; AAR39638.
                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mature human
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                                                  252;
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Query Match
Best Local :
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                                                Matches
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AAQ41599
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44 and 45, 56 and 57, 79 and 80, 90 and 91, or 22 and 23. The hybrid molecules promote cell migration, inhibit the growth of A375 melanoma cells, accelerate the healing of partial-thickness burn wounds and full-thickness incisional wounds and increase formation of fibrous granular tissue. See e.g. AAQ41602-Q41607 for pref. hybrids.
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                                                                                                                                                 gctttggacaccaattactgcttccgcaacttggagagaactgctgtgtgcgcccctc
                                                                                                                                                                               tacattgacttccgacaggatctgggctggaagtgggtccatgaacctaagggctactt
                                                                                                                                                                                                                                                                 gtgctgggactgtacaacactctgaaccctgaagcatctgcctcgccttgctgcggtgccc
                                                                                                                                                                                                                                                                           gecaacttetgeteaggecettgeceatacetecgeagtgeagacaeaacecaeageaeg
                                                                                                                                                                                                                                                                                                         caggacctggagccctgaccatcctgtactatgttgggaggacccccaaagtggagcag
                                                                                                                   ó
                                                                                              Length 345;
                                                                                                                    86; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     derived from TGF-beta2."
                                                               A; 115 C; 102 G; 60 T; 0 other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Transforming growth factor; TGF-beta; cancer; CHO;
                                                                                             DB 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   encoding chimeric simian TGF-betal/beta2
                                                                                             Score 200.4; DB 1. Pred. No. 7.5e-48;
                                                                                                                                                                                                                                                                                                                                                 ctctccaacatggtggtgaagtcttgtaaatgtagctg 338
                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
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/note="Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                         BP
                                                                                                                                                                                                                                                                                                                                                                                                                        AAQ04908 standard; DNA; 1561
                                                                                            tch 59.1%;
al Similarity 74.6%;
252; Conservative
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/*tag= b
1120..1155
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Circopithecus aethiops.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Purchio AF, Madisen L;
                                                               Sequence 345 BP; 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1990-187401/25.
P-PSDB; AAR05492.
                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  insertion_seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                18-OCT-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13-DEC-1989;
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                                                                                                                    Matches
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AAQ04908
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beta pro-protein"

37

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/*tag= o
/note= "Feature not labelled in the specification"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Compsn. comprising new chimeric TGF-B (TGF-beta 1-beta 2) -
inhibits proliferation of vascular endothelial cells, useful for
treating cancer and to promote wound healing
                                                                                                                                                                                                                                                                                    /*tag= n
/note= "Mutagenic linker"
                                                                                                                                                                                                                                                                                                                                                                                                                                         Purchio AF;
                                                                                                                                                                                                                                                                                                                                                                                                                     (BRIM ) BRISTOL-MYERS SQUIBB CO.
  "TGE-5
                                                                            /*tag= g
/label= T11V
1129..1131
                                                                                                                                                                 /*tag= j
/label= V17L
1150..1152
/*tag= k
/label= Q19P
1168..1170
                                                                                                                                                                                                                                                      /*tag= m
/label= K26R
1120..1155
                                                 /*tag= f
/label= S10N
1126..1128
                                                                                                       /*tag= h
/label= E120
1132.1134
                                                                                                                                     /*tag= i
/label= K13D
1144..1146
                     /*tag= e
/label= S9R
1123..1125
                                                                                                                                                                                                                                   /label= R25K
1171..1173
                                                                                                                                                                                                                                                                                                                                                                                92WO-US01993
                                                                                                                                                                                                                                                                                                                                                                                                  91US-0669171
  /note= "TGF
1120..1122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1992-348938/42.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                         old_sequence
                                                                                                                                                                                                                                                                                                      misc_feature
                                                                                                                                                                                                                                                                                                                                                                                13-MAR-1992;
                                                                                                                                                                                                                                                                                                                                                                                                  14-MAR-1991;
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                                                                                                                                                                                                                                                                                                                                                              01-OCT-1992.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Madisen L,
            mutation
                                                                                                                                                        mutation
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                                        mutation
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|||||||||||||||
tacattgacttcaagagggacctcggctggaagtggatccacgagcccaagggctaccat 1215
                                                                                                                                                                                                                                                                                           1276 gtcctggccctgtacaaccagcataacccgggcgcctcggcggcgccgtgctgcggtgccg 1335
                                                                                                                                                                                                                                                                                                                                                                               1336 caggcgctggagccactgcccatcgtgtactacgtgggccgcaagcccaaggtggagcag 1395
                                                                                                                                                                                                                                                                                                                        240
                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Transforming growth factor; TGF; TGF-beta; TGF-5 beta; simian;
Simian virus 40; SV40; expression vector; Chinese Hamster ovary; CHO;
vascular endothelial cell; ss.
                                                                                                                                                                                                      1 getttggacaccaattactgcttccgcaacttggaggagaactgctgtgtgcgcccctc 60
                                                                Chimeric gene has TGF activity and may be more desirable than its parents TGF-betal. GHO cells expressing the product from a plasmid vector (p5beta/dhfr) are 2.5 times more bioactive than normal. The product is useful in treatment of cancer and wound
                                                                                                                                                                                                                                                                                                                       gtgctgggactgtacaacactctgaaccctgaagcatctgcctcgccttgctgcggtgccc
                                                                                                                                                                                                                                                                                                                                                           caggacctggagccctgaccatcctgtactatgttgggaggaccccaaagtggagcag
                                                                                                                                                                                    ő
                                                                                                                                                                Length 1561;
         New chimeric transforming growth factor -
with TGF-beta biological activity and increased secretion
                                                                                                                                                                                    Indels
                                                                                                                                    Sequence 1561 BP; 304 A; 543 C; 443 G; 271 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /*tag= c
/note= "TGF-5 beta pre-pro-protein"
349..1095
/*tag= d
                                                                                                                                                                                                                                                                                                                                                                                               Score 195; DB 11;
Pred. No. 3.7e-46;
0; Mismatches 90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /*tag= a
1096..1431
/*tag= b
/note=_Mature TGF-5 beta"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TGF-beta 1/beta 2 chimeric gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BP
                                               Claim 2; Fig 1; 18pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAQ29177 standard; DNA; 1561
                                                                                                                                                               Query Match 57.5%;
Best Local Similarity 73.5%;
Matches 249; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
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                                                                                                                See also EP-373994
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                             efficiency
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                                                                                                         healing
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The sequence given encodes a hybrid transforming growth factor (TGF) beta termed TGF-beta 1/Deta 2 (or TGF-5 Deta). The mutations indicated in the features table represent replacements of TGF-beta 1 bases with those from the corresponding positions of TGF-beta 2. Simian codon usage was maintained. This DNA sequence could be placed under the control of Simian virus 40 (SV40) expression regulatory region within an expression vector and used to transfect Chinese Hamster ovary (CHO) cells. CHO transfectants can be seen to synthesise and secrete high levels of mature TGF-5 beta. TGF-5 beta induces effects on the proliferation of vascular endothelial cells equivalent to those produced by TGF-beta 1. Length 1561; Sequence 1561 BP; 306 A; 541 C; 443 G; 271 T; 0 other; Score 195; DB 13; Pred. No. 3.7e-46; Disclosure; Fig 1; 45pp; English. 57.5%; 73.5%;

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line. It was incorporated into an appropriate vector to transform Saccharomyces cerevisiae or E.coli. Monomeric TGF-betal was purified, denatured and dissolved in 140ml 50m Yris/HCl pH8. IM NaCl. 5mM EDTA, 2mM reduced glutathione, 1mm oxidised glutathione and 33mM Chaps. After 72 hrs at 4 deg C, pH was adjusted to 2.5 and the mixture was conc. 10 times. The conc. soln was diluted to the original vol. with 10mM HCl and conc to a final vol of 10 ml. The supernatant from centrifugation at 5000g for 30 min contained disulphide-linked dimeric
                                                                                                                                                                                           1335
                                                                                180
                                                                                                                                                                    240
                                                                       tacattgacttccgacaggatctgggctggaagtgggtccatgaacctaagggctactat 120
   Gaps
                         9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 coding sequence was isolated from the CI-215 human glioma cell
                                                                                                                                                                 gctttggacaccaattactgcttccgcaacttggaggagaactgctgtgtgcgcccctc
                                                                                                                    gccaacttctgctcaggcccttgcccatacctccgcagtgcagacacaacccacagcacg
                                                                                                                                                                                                                 caggacctggagccctgaccatcctgtactatgttgggaggaccccaaagtggagcag
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'n,
  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Meyhack
                                                                                                                                                                                                                                                                                                                                                                                                                                            TGF-beta2; biologically active protein production; ss.
 90;
                                                                                                                                                                                                                                                                                      ctgtccaacatgatcgtgcgctccgtcaaatgcagctga 1434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 339 BP; 98 A; 77 C; 70 G; 94 T; 0 other;
                                                                                                                                                                                                                                                               ctctccaacatggtggtgaagtcttgtaaatgtagctga 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Schmitz A,
 Mismatches
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                                                                                                                                                                                                                                                                                                                                               AAQ11994 standard; DNA; 339
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                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
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 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1991-180005/25.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               06-DEC-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cerletti N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19-JUN-1991
249;
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Matches
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The invention covers hybrid TGF-beta molecules consisting of parts of the human isoforms TGF-betal, TGF-beta2 and TGF-beta3 (see AAQ41599,
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                                                                               tacattgacttccgacaggatctgggctggaagtgggtccatgaacctaagggctactat 120
                     Gaps
                                         9
                                                           9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             portions of mature TGF beta isoforms; useful as wound healants, cardioprotective, antiinflammatory and immunosuppressive agents etc
                                                                                          gctttggacaccaattactgcttccgcaacttggaggagaactgctgtgtgcgcccctc
                                                    gecaacttetgeteaggecettgeceataceteegeagtgeagacacaaccacagcacg
                                                                                                                                                                        caggacctggagccctgaccatcctgtactatgttgggaggaccccaaagtggagcag
                                                                                                                                          gecaacttetgtgetggageatgeeegtatttatggagtteagacacteageaeag
                                                                                                                                                              gtgctgggactgtacaacactctgaaccctgaagcatctgcctcgccttgctgcgtgccc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       comprise
                     ;
0
  339;
                                                                                                                                                                                                                                                                                                                                                                                            protein; wound healing; cancer treatment;
   Length
                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New hybrid transforming growth factor-beta molecules
  DB 12;
                     98;
                                                                                                                                                                                                                                            ctctccaacatggtggtgaagtcttgtaaatgtagctga 339
                                                                                                                                                                                                                                                       Score 182.2; DB 1
Pred. No. 1.1e-42;
                                                                                                                                                                                                                                                                                                                                                                         Mature human Transforming Growth Factor-beta2
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                    0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                      bone repair; growth regulation; ss
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                                                                                                                                                                                                                                                                                                                 BP
53.78;
71.18;
                                                                                                                                                                                                                                                                                                                AAQ41600 standard; cDNA; 339
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                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                                             hTGF-beta2; hybrid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (CIBA ) CIBA GEIGY
            Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           03-NOV-1992;
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                                                                                                                                                                                                                                                                                                                                                                                                                           sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19-MAY-1993
                     241;
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  Query Match
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            Best Local
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                     Matches
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ö
AAQ41600 and AAQ41601, respectively). The hinge points between parts derived from different parent isoforms are pref. between amino acids 44 and 45, 56 and 57, 79 and 80, 90 and 91, or 22 and 23. The hybrid molecules promote cell migration, inhibit the growth of A375 melanoma cells, accelerate the healing of partial-thickness burn wounds and full-thickness incisional wounds and increase formation of fibrous granular tissue. See e.g. AAQ41602-Q41607 for pref. hybrids.
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Pred. No. 1.1e-42;
0; Mismatches 98;
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Best Local Similarity 71.1%;
Matches 241; Conservative
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P-PSDB; AAR92774.
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TGF-beta 2 (AAR92774) was cloned into plasmid pGEM-5ZF(+) (Promega) and the construct used to transform E. coli Y1090. Subcloning in ppLMu yielded plasmid ppLMu.hTGF-beta 2. Non-soluble, monomeric TGF-beta 2 was recovered from E. coli LC 137/ppLMu.hTGF-beta 2 (DSM 5657) transformants. A biologically active, dimeric form of TGF-beta 2 was obtd. by refolding this monomer in detergent-free buffer contg. DMSO and/or DMF. Dianers of TGF-beta 1 (AAR92773) and TGF-beta 3 (AAR92772), and hybrid dimers (see also AAR92775-77), were
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healing; solvent;
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                                     (AAT17236) of human transforming
                                                                                                                                                                                                                 Score 182.2; DB 17;
Pred. No. 1.1e-42;
                                                                                                                                                                                     Sequence 339 BP; 98 A; 77 C; 70 G; 94 T; 0 other;
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           Example 1B; Page 31-32; 54pp; English.
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ilarity 71.1%;
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TGF-beta 2
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                                                              Prodn. of dimeric, biologically active transforming growth f
beta - by refolding denatured monomer in buffer conty. mild
detergent and specific organic solvents to improve yields
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llarity 71.1%; Pred. No. 1.1e-42;
Conservative 0; Mismatches 98;
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P-PSDB; AAR91957.
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Best Local Similarity
Matches 241; Conserv
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A novel transforming growth factor-beta (TGF-beta) fusion protein comprises a purification tag and a TGF active fragment. The present sequence encodes a specifically claimed TGF active fragment. The present sequence encodes a specifically claimed TGF active fragment. Additionally, the fusion protein may comprise proteinase-sensitive linker sites and binding anothe protein sequence may contain some or all of the following elements: purification tag:proteinase site:ECM binding site-proteinase site:TGF-beta. TGF-beta promotes wound healing, and the fusion protein can be used to reduce surgery recovery time and in the preparation of artificial skin. The inclusion of a purification tag facilitates purification of the fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The proteinase site is included to permit cleavage and release of the purification tag after purification if desired. The extracellular matrix binding site facilitates delivery of the fusion protein to the desired site of action. Delivery of the TGF-beta to the site to be treated reduces the amount of TGF-beta required to be administered to be effective and reduces the concentration of circulating TGF-beta
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                  growth factor-beta fusion protein; wound healing;
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Pred. No. 1.1e-42;
0; Mismatches 98; Indels
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                                                                                                  ocation/Qualifiers
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Matches 241; Conservative
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                                                                                                                                                                                                                                                                                                                  CHEUNG D T.
HALL F L.
NIMNI M E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1997-043065/04 P-PSDB; AAW08174.
                                                                                                                                                                                                                                                                                                                                                                    TUAN T.
                                                                  Homo sapiens
                                                                                                                                                                                   WO9639430-A1
                                                                                                                                                                                                                                                05-JUN-1996;
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                                                                                                                                                                                                                   12-DEC-1996.
                                                                                                                                                                                                                                                                                                                                                                                                                    Cheung DT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  of
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(NIMN/)
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TGF active fragment of a TGF-beta fusion protein encoding cDNA.

tgfb3n.rng

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1 gctttggatgcggcctattgctttagaaatgtgcaggataattgctgcctacgtccactt
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence encodes the mature form of transforming growth factor-beta-2. Dimeric, biologically active TGF-beta-like protein can be produced by subjecting the denatured monomeric form to refolding conditions. The new monomeric S-sulphonated TGF-beta-like protein is useful for the production of the dimeric, biologically active TGF-beta-like protein, which is useful for the treatment of wounds (surface or internal) and cancer in a mammal, in bone and tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       repair, as a bone marrow protective agent, a mediator of
cardioprotection, for the production of an anti-inflammatory or
immunosuppressive preparation. Treatment is useful for animals,
especially humans, and wound treatment (e.g. ulcers, bed sores etc.) is
241 caagatttagaacctctaaccattctctactacattggcaaaacacccaagattgaacag 300
                                                                                                                                                                                                                                                                                                           cDNA encoding the mature form of transforming growth factor-beta-2.
                                              caggacctggagccctgaccatcctgtactatgttgggaggaccccaaagtggagcag
                                                                                                                                                                                                                                                                                                                                                      S-sulphonated TGF-beta-like protein; wound treatment; cancer; bone repair; tissue repair; bone marrow protective agent; cardioprotection; anti-inflammatory; immunosuppressive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Producing biologically active dimeric Transforming Growth Factor-beta - by refolding new monomeric Transforming Growth Factor-beta, useful for treatment of wounds and cancer
                                                                                                                                                                                                                                                                                                                                      Transforming growth factor-beta-2; TGF-beta-like protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ä
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                                                                                                         ctctccaacatggtggtgaagtcttgtaaatgtagctga 339
                                                                                                                       Meyhack B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     particularly useful for the elderly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cox D, McMaster GK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 1; Page 29; 32pp; English.
                                                                                                                                                                                                                  BP
                                                                                                                                                                                                               AAX15246 standard; cDNA; 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             90EP-0810922.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          89GB-0027546
                                                                                                                                                                                                                                                                           (first entry)
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P-PSDB; AAW97092.
                                                                                                                                                                                                                                                                                                                                                                                                      ulcer; bed sore; ds
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The present sequence encodes a transforming growth factor beta active fragment. The protein can be used in place of a bone morphogenetic active fragment to create the fusion proteins of the invention. When a bone morphogenetic active fragment is used, the fusion proteins are designated bone morphogenetic fusion proteins. The bone morphogenetic fusion proteins. The bone morphogenetic fusion proteins. The bone morphogenetic purification may contain some or all of the following elements: a purification tag, a proteinase site, an ECM/bone binding site, a second proteinase site, and a bone morphogenetic protein active fragment. The bone morphogenetic fusion proteins can be used for enhancing wound
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Proteinase site; bone morphogenetic fusion protein; bone binding site; bone morphogenetic protein; transforming growth factor beta; active fragment; wound healing; bone growth; purification tag; ds.
                                 61 tacattgatttcaagagggatctagggtggaaatggatacacgaacccaaagggtacaat 120
                                                                  180
                                                                                                                                   240
                                                                                                                                                                                                    300
                                                                                                                                                                                                                           New bone morphogenetic fusion proteins - comprising a purification tag and a bone morphogenetic active fragment, used for enhancing wound healing or bone growth
61 tacattgacttccgacaggatctgggctggaagtgggtccatgaacctaagggctactat
                                                                                                    121 gecaacttetgtgetggageatgeeegtatttatggagtteagacaeteageaegg
                                                                                                                                                     241 caggacctggagcccctgaccatcctgtactatgttgggaggacccccaaagtggagcag
                                                                      gccaacttctgctcaggcccttgcccatacctccgcagtgcagacacaacccacagcacg
                                                                                                                                     181 gtgctgggactgtacaacactctgaaccctgaagcatctgcctcgccttgctgcgtgccc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cDNA encoding a transforming growth factor beta active fragment.
                                                                                                                                                                                                                                                                                           301 ctctccaacatggtggtgaagtcttgtaaatgtagctga 339
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                                                                                                                                                                                                                                                                                                                                                                                               BP.
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SHORS E C.
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(WULL/)
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gctttggacaccaattactgcttccgcaacttggaggagaactgctgtgtgcgcccctc 60

tch 53.7%; Score 182.2; DB 20; Length 339; al Similarity 71.1%; Pred. No. 1.1e-42; 241; Conservative 0; Mismatches 98; Indels 0:

Best Local Similarity Matches 241; Conserv

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Query Match

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macrophage inducible nitric oxide synthase; iNOS; constitutive NOS; interleukin-1-beta; transforming growth factor-beta; TGF-beta; IL1-beta; nitric oxide production; hypotension; inflammation; septic shock;
                                                                                                                                          gccaacttctgctcaggcccttgcccatacctccgcagtgcagacacaacccacagcacg 180
                                                                                                                                                                                                                                                      caggacctggagccctgaccatcctgtactatgttgggaggaccccaaagtggagcag 300
                                                                                                                              tacattgacttccgacaggatctgggctggaagtgggtccatgaacctaagggctactat 120
                                                                                                                                                                                                                                                              1 gctttggacaccaattactgcttccgcaacttggaggagaactgctgtgtgcgcccctc 60
                                                                                                   gtgctgggactgtacaacactctgaaccctgaagcatctgcctcgccttgctgcgtgccc
                                                                                                                                                                                                                        Treatment of hypotension, esp. in septic shock - by administering transforming growth factor-beta e.g. to inhibit inducible nitric
                                                 Length 339;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /*tag= a
/product= transforming growth factor-beta
                                                                      Indels
                                                  DB 20;
                                                                      98;
                    94 T; 0 other;
                                                                                                                                                                                                                                                                                           ctctccaacatggtggtgaagtcttgtaaatgtagctga 339
                                                                                                                                                                                                                                                                                                       cDNA encoding transforming growth factor-beta 2.
                                                 53.7%; Score 182.2; DB 271.1%; Pred. No. 1.1e-42;
                                                                    0; Mismatches
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182..1426
                   C; 70 G;
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                   BP; 98 A; 77
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                                                                      Conservative
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or bone growth.
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P-PSDB; AAR83055.
                                                           Similarity
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                   Sequence 339
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                                                          Best Local Simi
Matches 241;
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                                                  Query Match
healing
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The cDNA encodes transforming growth factor-beta 2 (TGF-beta 2) which has been found to inhibit inducible nitric oxide synthase (INOS) gene transcription, esp. in interleukin-1-beta (ILI-beta) stimulated rat smooth muscle cells, and at a dose which does not inhibit constitutive NOS. TGF-beta I or 2 (AAR83055) or their active fragments, can be used in the treatment of hypotension, such as that associated with severe inflammation or septic shock.
                                                                                                                                                                                                                                                                                                                                                      1267
                                                                                                                                                                                                                                               tacattgatttcaagagggatctagggtggaaatggatacacgaacccaaagggtacaat 1207
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                                                                                                                                                                                                                                                                                                                                         Hypertension therapy; hypotensive agent; blood pressure modulator;
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                                                                                                                                                                                 Length 1695;
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                                                                                                                                                                                                         Indels
                                                                                                                                              Sequence 1695 BP; 523 A; 386 C; 354 G; 432 T; 0 other;
                                                                                                                                                                              Score 182.2; DB 16;
Pred. No. 1.6e-42;
); Mismatches 98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        301 ctctccaacatggtggtgaagtcttgtaaatgtagctga 339
                                                                                                                                                                                                       0; Mismatches
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262..282
                       Disclosure; Fig 16; 52pp; English.
 oxide synthase gene transcription
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BP.
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                                                                                                                                                                              53.7%;
ilarity 71.1%;
Conservative
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325..1095
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283..324
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beta-1/beta-2
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/_c_s This entire SQ is replaced with AAT in simian TGF-beta-2-414 cDNA"
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/note="Possible sequencing error"
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1698
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466..1794
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                                                                                                                                                                                                                                                                                                                                                                       misc_difference 1143
                                                                                                                                                                                                                                                                            misc_difference 1053
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 Homo sapiens
                                  misc_feature
                                                                                                                                    misc_feature
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                                                                                                                 mat_peptide
                                                                                           sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DE3833897-A
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                        Key
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1216 gccaacttctgtgctggagcatgcccgtatttatggagttcagacactcagcagagg 1275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tacattgacttccgacaggatctgggctggaagtgggtccatgaacctaagggctactat 120
                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                            A new method for treating hypertension comprises administering a transforming growth factor (TGF)-beta to an individual at a dose effective for lowering blood pressure; the TGF-beta may be e.g. mature TGF-beta, TGF-beta, a mature TGF-betal/beta2 hybrid, TGF-betal precursor, a latent TGF-betal precursor, hybrid TGF-betal/TGF-betal precursor, a latent TGF-betal complex or a latent TGF-betal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          human transforming growth factor (TGF) beta-2 precursor
                                                                                                                                                                                                                                                                                                                                                                                                        1 gottttggacaccaattactgcttccgcaacttggaggagaactgctgtgtgcgcccctc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 gecaacttetgeteaggeeettgeecataceteegeagtgeagacacaaeceacageaeg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181 gigotgggacigiacaacacicigaacccigaagcaicigccicgccitgcigcgigccc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             caggacctggagcccctgaccatcctgtactatgttgggaggacccccaaagtggagcag
                                                                                                                                                                                                                                                                                                                                                          Length 2208;
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                                                                                                                                                         Use of transforming growth factor (TGF)-beta and their antagonists - for modulating blood pressure, for treating hypertension and hypotension
                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                        Sequence 2208 BP; 599 A; 576 C; 534 G; 499 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                        Score 182.2; DB 13;
Pred. No. 1.7e-42;
0; Mismatches 98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cell differentiation; cell proliferation; ss
                                                                                                                                                                                                       Disclosure; Fig 3; 42pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAN90767 standard; cDNA; 2568
                                                                                                                                                                                                                                                                                                                                                          Query Match 53.7%;
Best Local Similarity 71.1%;
Matches 241; Conservative
                                91WO-US04449
                                                     90US-0541221
                                                                            (BRIM ) BRISTOL-MYERS SQUIB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                   Oleson FB, Comereski CR;
                                                                                                                         WPI; 1992-024199/03
                                                                                                                                     P-PSDB; AAR20126
                                20-JUN-1991;
                                                     20-JUN-1990;
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05-DEC-1989;
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                                                                                                                                                               Query Match
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                                                              PolyA-RNA was isolated from the tamoxifen-treated, human prostatic adenocarcinoma cell line PC-3 and converted to cDNA. TGF DNA is used for control of the SV40 promoter and expressed in CHO cells. The simian
                                                                                                                                                                                  getttggatgcggcctattgctttagaaatgtgcaggataattgctgcctacgtccactt 1515
                                                                                                                                                     0; Gaps
                                                                                                                                                                                                                                            gtgctgggactgtacaacactctgaaccctgaagcatctgcctcgccttgctgcggtgccc
                                                                                                                                                                                                                                                                       caggacctggagccctgaccatcctgtactatgttgggaggacccccaaagtggagcag
                                                                                                                                                                                                               gccaacttctgctcaggcccttgcccatacctccgcagtgcagacacaacccacagcacg
                                                                                                                         DB 10; Length 2568;
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                            DNA sequence encoding transforming growth factor beta
for large scale expression in eucaryotic cells
                                                                                                                       Query Match 53.7%; Score 182.2; DB 10; Length Best Local Similarity 71.1%; Pred. No. 1.8e-42; Matches 241; Conservative 0; Mismatches 98; Indels
                                                                                                   Sequence 2568 BP; 772 A; 597 C; 513 G; 686 T; 0 other;
                                                                                                                                                                                                                                                                                                             ctctccaacatggtggtgaagtcttgtaaatgtagctga 339
                                                                                                                                                                                                                                                                                                                                                                                                                 Human TGF-Beta2 precursor; cancer; tumorcide;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
467..1792
                                                                                                                                                                                                                                                                                                                                                                                                  Human TGF-Beta2-442 precursor cDNA
                                                  Disclosure; Fig la; 27pp; German.
                                                                                                                                                                                                                                                                                                                                                        BP.
                                                                                                                                                                                                                                                                                                                                                      AAQ05126 standard; DNA; 2569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 88US-0285140.
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1457..1792
/*tag= b
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     WPI; 1989-138796/19.
                                                                                     SQ is also claimed
             P-PSDB; AAP91889
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                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic
                            DNA
                                   nseq
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1457 getttggatgeggectattgettttagaaatgtgeaggataattgetgectaegteeaett 1516
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGF-Beta2 may be used in treatment of tumors at effective doses, and may also be useful in augmenting wound healing by stimulating cell proliferation. The growth factor can be produced at high levels from a CHO expression system.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypertension therapy; hypotensive agent; blood pressure modulator;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gccaacttctgctcaggcccttgcccatacctccgcagtgcagacacaaccacagcacg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gtgctgggactgtacaacactctgaaccctgaagcatctgcctcgccttgctgcgtgccc
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                                                                                                                                                                                                                                                                                                                                                                                                            Length 2569;
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0
                                                                                                                                                                                                                                                                                                                                                                                          Score 182.2; DB 11; Leuy...
Pred. No. 1.8e-42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                encoding human transforming growth factor (TGF)-
                                                                                                                                                                                                                                                                                                                                                  other;
                                                                                                                                         Cloning and expression of transforming growth factor used for treatment of tumors or for augmenting wound
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2569 BP; 772 A; 598 C; 512 G; 687 T; 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
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467..475
                                         ż
                                                                                                                                                                                                   Claim 1; Fig 1a; 58pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                        53.7%;
nilarity 71.1%;
Conservative
(ONCO-) ONCOGEN LTD PARTNER
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478..525
/*tag= b
526..1456
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                                         Purchio AF, Madisen
                                                                          WPI; 1990-203127/27.
P-PSDB; AAR05748.
                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 241;
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1484 gctttggatgcggcctattgctttagaaatgtgcaggataattgctgcctacgtccactt 1543
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COS or CHO cell, containing a recombinant vector encoding this sequence under the control of a 2nd nucleotide sequence that regulates gene expression, preferably the SV40 promoter, so the least produces active TGF-beta2. The produced TGF-beta2 protein be used to regulate cellular differentiation and proliferation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hybrid transforming growth factor beta-1/TGF-beta-2 precursor -
to produce biologically active, mature TGF-beta-2
                                                                                                          TGF-betal; TGF-betal; transforming growth factor; protein; cell differentiation; cell proliferation; CHO; Chinese hamster; ovary; COS; monkey kidney; animal; mammal; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                        /*tag= c
/note= "putative signal sequence cleavage site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This DNA sequence is expressed in a host cell, preferably a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 53.7%; Score 182.2; DB 16; Length Best Local Similarity 71.1%; Pred. No. 1.8e-42; Matches 241; Conservative 0; Mismatches 98; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2592 BP; 772 A; 613 C; 516 G; 691 T; 0 other;
                                                       Human transforming growth factor-2 cDNA.
                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Fig.1a; 52pp; English.
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88US-0285140.
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1484..1819
     (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P-PSDB; AAR79922
                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                            misc_feature
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     28-MAY-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                05-DEC-1989;
                                                                                                                                                                                                                                                                                                  sig_peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   transforming growth factor (TGF)-beta to an individual at a dose effective for lowering blood pressure; the TGF-beta may be e.g. mature TGF-beta, a mature TGF-beta, pbeta2 precursor, a latent TGF-beta2 hybrid TGF-beta1/TGF-beta1/TGF-beta2 precursor, a latent TGF-beta1 complex or a latent TGF-beta1 complex
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Use of transforming growth factor (TGF)-beta and their antagonists - for modulating blood pressure, for treating hypertension and hypotension
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2569 BP; 772 A; 598 C; 513 G; 686 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 182.2; DB 13;
Pred. No. 1.8e-42;
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71.1%;
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/*tag= d
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Best Local Similarity 71.1
Matches 241; Conservative
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P-PSDB; AAR20125.
                                                                                                                                                                                                                                                                   20-JUN-1991;
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                      mat_peptide
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241

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Gaps 9

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Length 2592

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241

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AAT04116 standard; cDNA; 2592

1757

AAT04116;

AX SX

tacattgatttcaagagggatctagggtggaaatggatacacgaacccaaagggtacaat 120

121 181 181

Qγ a ò Dp ò g δ qq

61 121

240 240 300

ctctccaacatggtggtgaagtcttgtaaatgtagc 336

301

241

AAQ03510 standard; DNA; 2206

AAQ03510

caggacctggagccctgaccatcctgtactatgttgggaggacccccaaagtggagcag

gtgctgggactgtacaacactctgaaccctgaagcatctgcctcgccttgctgcgtgccc

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The invention covers hybrid TGF-beta molecules consisting of parts nof the human isoforms TGF-beta1, TGF-beta2 and TGF-beta3 (see AAQ41599, AAQ41601, respectively). The hinge points between parts derived from different parent isoforms are pref. between amino acids possible hybrids using these hinge points and one part each from two of the isoforms, 6 are preferred including the hybrid TGF-beta2(44/45)beta1. The hybrid molecules promote cell migration, inhibit the growth of A375 melanoma cells, accelerate the healing of partial-thickness burn wounds and full-thickness incisional wounds and increase formation of fibrous granular tissue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New hybrid transforming growth factor-beta molecules - comprise portions of mature TGF-beta isoforms; useful as wound healants, cardioprotective, antiinflammatory and immunosuppressive agents etc.
                                                                                                                                                                                                                                                                                                         /*tag= a
/note= "TGF-beta2=1-132, TGF-beta1=133-336"
                                                                                                                                                                                                        hTGF-betal; hTGF-beta2; hybrid protein; wound healing; cancer treatment; bone repair; growth regulation; ss.
                                                                                                                                                                                 Transforming Growth Factor-beta2(44/45)beta1 hybrid.
Kuhla J;
                                                                                                                                                                                                                                                                              Location/Qualifiers
1..336
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                                                                                              AAQ41604 standard; cDNA; 336 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 8; Page 28; 48pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                      92EP-0810845.
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                                                                                                                                                      (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1993-161126/20.
P-PSDB; AAR39643.
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                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                      03-NOV-1992;
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                                                                                                                                                      26-AUG-1993
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Human Transforming growth factor from TGF-Beta2-442 cDNA.

14-AUG-1990 (first entry)

AAQ03510;

SIV; vaccine; AZT; CD4; cytokines; growth

ds.

factors;

Key

AIDS;

Location/Qualifiers

/\*tag= a 1091..1429

mat\_peptide

260..1429

mature TGF-Beta2

/\*tag= label=

1094 gctttggatccggcctattgctttagaaatgtgcagcataattgctgcctacgtccactt 1153 TGF-beta may be used in vivo to prevent formation of synctia and inhibit HIV infection. TGF may also be used with other HIV treatments (AZT, soluble CD4 etc.). gctttggacaccaattactgcttccgcaacttggaggagaactgctgtgtgcgcccctc 60 Length 2206; ö Compsns. contg. transforming growth factor beta - used for inhibitions of HIV infection and replication in vivo. Score 180.6; DB 11; Lengtn Pred. No. 5e-42; Sequence 2206 BP; 600 A; 577 C; 530 G; 499 T; 0 other; 0; Mismatches Disclosure; Fig 2; 20pp; English. 53.3%; 70.8%; Conservative WPI; 1990-068723/10. P-PSDB; AAR05665. Query Match Best Local Similarity Matches 240; Conserv Dp δy

Brankovan V, Lioubin M, Purchio A;

(ONCO-) ONCOGEN LTD PARTNER

89EP-0115719. 88US-0236698.

25-AUG-1989; 25-AUG-1988;

07-MAR-1990

EP356935-A

Gaps

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Gaps

tacattgacttccgacaggatctgggctggaagtgggtccatgaacctaagggctactat 120

61

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53.3%; Score 180.8; DB 14; Length 336; llarity 71.1%; Pred. No. 2.7e-42; Conservative 0; Mismatches 97; Indels 0;

Query Match Best Local Similarity Matches 239; Conserv

Sequence 336 BP; 71 A; 99 C; 97 G; 69 T; 0 other;

1274

240

1154

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241

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tacattgacttccgacaggatctgggctggaagtgggtccatgaacctaagggctactat
                                                                                      gocaacttctgctcaggcccttgcccatacctccgcagtgcagacacaacccacagcacg
                                                                                                           1215 gecaacttetgtgetggaggatgeegtatttatggagtteagacaeteageaggg
                                                                                                                                                                                     241 caggacctggagccctgaccatcctgtactatgttgggaggaccccaaagtggagcag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGF-Beta2 may be used in treatment of tumors at effective doses, and may also be useful in augmenting wound healing by stimulating cell proliferation. The growth factor can be produced at high levels from a CHO expression system.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cloning and expression of transforming growth factor beta 2 - used for treatment of tumors or for augmenting wound healing.
                                                                                                                                                                                                                                                                                                                                                                                                         Human TGF-Betal/TGF-Beta2 hybrid precursor cDNA expressing
                                                                                                                                                                                                                                      Human TGF-Beta2 precursor; cancer; tumorcide;
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261..1430
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                                                                                                                                                                                                                                                                                                                               AAQ05127 standard; DNA; 2207
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89US-0446020.
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/*tag= b
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P-PSDB; AAR05749.
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05-DEC-1989;
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          TGF-beta may be used in vivo to prevent formation of synctia and inhibit HIV infection. TGF may also be used with other HIV treatments (AZT, soluble CD4 etc.).
                                                                                                                                                            caggacctggagccctgaccatcctgtactatgttgggaggaccccaaagtggagcag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   53.3%; Score 180.6; DB 11; Length 2207; 70.8%; Pred. No. 5e-42; tive 0; Mismatches 99; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Compsns. contg. transforming growth factor beta -
used for inhibitions of HIV infection and replication in vivo.
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                                                                                                                                                                                                                                                                                                                                                                                                      HIV; AIDS; SIV; vaccine; AZT; CD4; cytokines; growth
                                                                                                                                                                                                                                                                                                                                                                               Hybrid transforming growth factor TGF-betal/beta2.
                                                                                                                                                                                                                          301 ctctccaacatggtggtgaagtcttgtaaatgtagctga 339
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267..1437
/*tag= a
1103..1437
/*tag= b
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                                                                                                                                                                                                                                                                                                    BP
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P-PSDB; AAR05666.
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Matches 240; Conserv
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Key

Sequence 2207 BP; 600 A; 577 C; 532 G; 498 T; 0 other;

1 getttggacaccaattactgcttccgcaacttggaggagaactgctgtgtgcgcccctc 60

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Query Match

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05-OCT-1988;
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                           1 gctttggacaccaattactgcttccgcaacttggaggagaactgctgtgtgcgcccctc
                                                     tacattgacttccgacaggatctgggctggaagtgggtccatgaacctaagggctactat
                                                                                                     gtgctgggactgtacaacactctgaaccctgaagcatctgcctcgccttgctgcgtgccc
                                                                                                                              caggacetggagecetgaceatectgtactatgttgggaggaceceaaagtggageag
                                                                             gccaacttctgctcaggcccttgcccatacctccgcagtgcagacacaacccacagcacg
                ;
0
    Length 2207;
                Indels
     . 5e-42;
    DB 11;
                                                                                                                                                      'note="Possible sequencing error"
   Score 180.6; Di
Pred. No. 5e-42
0; Mismatches
                                                                                                                                                                                                                                                       Cell differentiation; cell proliferation;
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1114..1116
/*tag= h
/codon=(seq:ccg,aa:Ala)
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2217
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'note="Claimed"
   53.3%;
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/*tag= b
289..330
/*tag= c
1102..1440
/*tag= d
1161
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                240; Conservative
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       Best Local Similarity
Matches 240; Conserv
                                                                                                                                                                                                                                                                                                                                                                     misc_difference
                                                                                                                                                                                                                                                                                                                                             misc_difference
                                                                                                                                                                                                                                            precursor DNA
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                                                                                                                                                                                                                                                                                      misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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/note= "hybrid TGF-betal/TGF-beta2 precursor"
257...1084
                                                                                                                                                                                   New DNA sequence encoding transforming growth factor beta 2 used for large scale expression in eucaryotic cells
                                                                                                                                                                                                                                                                                                                                                                                        Query Match 53.3%; Score 180.6; DB 10; Length Best Local Similarity 70.8%; Pred. No. 5e-42; Matches 240; Conservative 0; Mismatches 99; Indels
                                                                                                                                                                                                                                                                                                                                        Sequence 2217 BP; 600 A; 577 C; 531 G; 499 T; 10 other;
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                                                                                                    Webb
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88DE-3833897
                               88US-0234065
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                                                                                                  ù
                                                                                                Purchio AF, Madisen
                                                                                                                                  WPI; 1989-138796/19
                                                                                                                                                     P-PSDB; AAP91900
                                                                 (ONCO-) ONCOGEN
                             18-AUG-1988;
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(first entry)

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                                                                                                                                                                                                                                                                                                                                                                                   This hybrid DNA sequence is expressed in a host cell, preferably a COS or CHO cell, containing a recombinant vector encoding this sequence under the control of a 2nd nucleotide sequence that regulates gene expression, preferably the SV4O promoter, so the host cell produces active TGF-beta2. The produced TGF-beta2 protein can be used to regulate cellular differentiation and proliferation.
                                                                                                                                                                                                                                                                                                                      orid transforming growth factor beta-1/TGF-beta-2 precursor - used produce biologically active, mature TGF-beta-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       52.3%; Score 177.4; DB 16; Length 2200; 70.2%; Pred. No. 4e-41; ive 0; Mismatches 101; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2200 BP; 597 A; 588 C; 517 G; 498 T; 0 other;
/*tag= b
/note= "simian TGF-betal precursor"
                                                     precursor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 301 ctctccaacatggtggtgaagtcttgtaaatgtagctga 339
                                                    TGF-beta2
                                                                                                                                                                                                                                                                                                                                                            Claim 1, 2 and 3; Fig.1b; 52pp; English
                                      /*tag= c
/note= "human T
278..319
/*tag= d
                                                                                                                                                                                                                                                      Webb
                                                                                                                                                          89EP-0104223
                                                                                                                                                                                  89US-0446020
88US-0285140
                       1085..1423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 52.3
Best Local Similarity 70.2
Matches 238; Conservative
                                                                                                                                                                                                                                                    Madisen L, Purchio AF,
                                                                                                                                                                                                                                                                             WPI; 1995-346094/45.
P-PSDB; AAR79921.
                                                                                                                                                                                                                            (ONCO ) ONCOGEN LP.
                                                                                                                                                          14-DEC-1989;
                                                                                                                                                                                  05-DEC-1989;
16-DEC-1988;
                          mat_peptide
                                                               sig_peptide
                                                                                                       EP676474-A1
                                                                                                                              11-0CT-1995
                                                                                                                                                                                                                                                                                                                     Hybrid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121
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AAQ29178 standard; DNA; 1565

81

AAQ29178

AA029178

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The sequence given encodes the human transforming growth factor (TGF)-beta 1. This was used within the scope of the invention to compare to a similar TGF hybrid termed TGF-beta 1/Deta 2 (or TGF-5 beta) (see also AAQ29177). The chimeric DNA sequence could be placed under the control of Simian virus 40 (SV40) expression regulatory region within an expression vector and used to transfect Chinese Hamster ovary (CHO) cells. CHO transfectants can be seen to synthesise and secrete high levels of mature TGF-5 beta induces effects on the proliferation of vascular endothelial cells equivalent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1220 gccaacttctgcctcgggccctgccctacatttggagcctggacacgcagtacagcaag 1279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1106 gccctggacaccaactattgcttcagaaatgtgcaggataattgctgcctacgtccgctt 1165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Transforming growth factor; TGF; TGF-beta; TGF-5 beta; simian; Simian virus 40; SV40; expression vector; Chinese Hamster ovary; CHO; vascular endothelial cell; TGF-beta 1; TGF-beta 2; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 gctttggacaccaattactgcttccgcaacttggaggagaactgctgtgtgcgcccctc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tacattgacttccgacaggatctgggctggaagtgggtccatgaacctaagggctactat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gocaacttctgctcaggcctttgccatacctccgcagtgcagacacaaccacagcacg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   inhibits proliferation of vascular endothelial cells, useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 1565;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Compsn. comprising new chimeric TGF-B (TGF-beta 1-beta 2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                 /*tag= a
//note= "Signal peptide, pre-pro-protein"
356.1105
/*tag= b
//note= "Pro-protein"
/*tag= c
/*tag= c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1565 BP; 300 A; 553 C; 439 G; 273 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 176.2; DB 13;
Pred. No. 8.1e-41;
0; Mismatches 88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cancer and to promote wound healing
                                                                                                                                                        Location/Qualifiers
269..355
                                                                                                                                                                                                                                                                                                                                                                                                                                                Purchio AF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Fig 1; 45pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        to those produced by TGF-beta 1.
                                                                                                                                                                                                                                                                                                                                                                                                                    (BRIM ) BRISTOL-MYERS SQUIBB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 52.0%;
Best Local Similarity 72.3%;
Matches 245; Conservative
                                                                                                                                                                                                                                                                                                                                                           92WO-US01993
                                                                                                                                                                                                                                                                                                                                                                                      91US-0669171
                                                                                                                                                                                                                                                                                                                                                                                                                                                Merwin J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1992-348938/42.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P-PSDB; AAR29657.
                                                                                                                                                                                                                precursor_RNA
                                                                    Transforming
Simian virus
                                                                                                                                                        Key
sig_peptide
                                                                                                                                                                                                                                                                                                                                                          13-MAR-1992;
                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                      14-MAR-1991;
                                                                                                                                                                                                                                                                                                   WO9216228-A.
                                                                                                                                                                                                                                                        mat_peptide
                                         TGF-beta 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                treating
                                                                                                                                                                                                                                                                                                                                                                                                                                              Madisen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ductal
for the
pancreatic ductal trophic factor (PDTF)"
                                                                                                                                                                                                                                                        Pancreatic ductal trophic factor; PDTF; mesenchyme cell; transforming growth factor-beta; TGF-beta; pancreatic tissue growth; pancreatic duct tissue outgrowth; diabetes; ss.
                                 241 caggacctggagccctgaccatcctgtactatgttgggaggaccccaaagtggagcag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Inducing outgrowths of pancreatic duct tissue, using pancreatic trophic factors expressed by e14.5 pancreatic mesenchyme cells,
                                                                                                                                                                                                                                  cDNA encoding a pancreatic ductal trophic factor (PDTF).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2754 BP; 905 A; 525 C; 599 G; 725 T; 0 other;
                                                                                           301 ctctccaacatggtggtgaagtcttgtaaatgtagctga 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 73-75; 76pp; English.
                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
504..1652
                                                                                                                                                                 BP.
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                                                                                                                                                              AAA63944 standard; cDNA; 2754
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B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2000WO-US03424
                                                                                                                                                                                                                                                                                                                                                    /*tag= a
/product=
504..566
/*tag= b
567..1649
/*tag= c
                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Guicherit O, Pang K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (ONTO-) ONTOGENY INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2000-524488/47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P-PSDB; AAB08338
                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200047243-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10-FEB-2000;
                                                                                                                                                                                                                                                                                                     Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10-FEB-1999;
                                                                                                                                                                                                            04-DEC-2000
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                                                                                                                                                                                                                                                                                                                                                                         sig_peptide
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                                                                                                                                                                                     AAA63944;
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                                                                                                                                         RESULT 8
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Staphylococcal Protein A to a second Fb fragment"
                                                                                                                                                                                                                                                                                                                                                                           B of Staphylococcal Protein A
                                                                                                                                                                                                                                                                                                                                                                                                                /*tag= e
/product= truncated TGF-beta containing 6 x Cys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Recombinant truncated transforming growth factor-beta analogues
                                                                                                                                                                                                                                                                                                              /*tag= a
/note= "modified trp-LE leader sequence"
                                                                                                                                                                                                                                                 Encodes Fb-Fb-truncated (6 Cys)-TGF-beta
                                                                                                                                                                                                                                                                                                                                            /product= fragment B of /note= "directly linked
                                                                                                                                                                                                                                                                                                                                                                                     /*tag= d
/product= hinge region
565..843
                                                                                                                                                                                                                                                                Transforming Growth Factor beta; AIDS;
                                                                                                                                                      ||||| | |||||| || || || ||||||||| tggtaaggtcttgcaactgcagctga 1652
                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                    /*tag= c
/product= Fragment
553..564
                                                                                                                                              tggtgaagtcttgtaaatgtagctga
                                                                                                                                                                                                   BP
                                                                                                                                                                                                   852
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (CREA-) CREATIVE BIOMOLECUL
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                                                                                                                                                                                                                                                                                                                                                           376..552
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                                                                                                                                                                                                  AAQ11774 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P-PSDB; AAR11956
                                                                                                                                                                                                                                                                                                                                                                                   misc_structure
                                                                                                                                                                                                                                 23-JUL-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18-OCT-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18-OCT-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                       WO9105565-A.
                                                                                                                                                                                                                                                                                                      sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                       02-MAY-1991
                                                                                                                                                                                                                                                                                                                                                                                                         mat_peptide
                                                                                                                                                                                                                                                                               Synthetic.
                                                                                                                                                                                                                  AAQ11774;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cohen CM;
                                                                                                                                                                                                                                                                                                                              misc_RNA
                                                                                                                                                                                                                                                                                                                                                            misc_RNA
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Gaps

Score 161.2; DB 21; Length 2754; Pred. No. 1.7e-36; 0; Mismatches 103; Indels 0;

Similarity 68.4%; Similarity 68.4%; Conservative

Query Match Best Local Simi Matches 223;

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Disclosure; Fig. 2; 61pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P-PSDB; AAR04075
                                                                                                                                                                                                                                                                                                                                                                                                                            Transforming
Derynck RMA;
                                                                                                                                                                                                                                                                                                                                                                                         31-MAY-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                08-JUN-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  08-JUN-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO8912101-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14-DEC-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                       inhibition
                                                                                                                                                                                                                                                                                                                                                                       AAQ02815;
                                                                                                                                                                                                                                                                                                                                     RESULT 85
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                                                                                                                                                                                                       118 tatgccaacttctgctcaggcccttgcccatacctccgcagtgcagacacaacccacagc 177
                                                                                                                                                                                                                                                    684
                                                                                                                                                                                                                                                                      237
                                                                                                                                                                                                                                                                                                         coccaggacotggagocotgacoatcotgtactatgttggggaggacocccaaagtggag 297
                                                                                                                                                                                                                                                                                                                   codons inferred from known amino acid sequences and observations of partial homology with known genes of the TGF-beta family. It was assembled from chemically synthesised oligonucleotides and can be expressed in prokaryotic host cells. The truncated 6 Cys TGF-beta protein is cleaved from the Fb-Fb domain at the hinge region to give
                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                    catgecaacttetgeetgggeeettgteegtacatetggtetetggatacecagtactee
                                                                                                                                                                                                                                                                       acggtgctggggactgtacaacactctgaaccctgaagcatctgcctcgccttgctgcgtg
                                                                                                                                                                                                                                                                                       aaggtgctggctctgtacaatcagcataacccggggggctagcgcagctccgtgctgttt
                                            synthetic gene was designed based on reported sequence data,
                                                                                                                                                                           ö
                                                                                                                                                          Length 852;
capable of inducing an anti-proliferative effect in mammalian epithelial cells in vitro
                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Transforming growth factor beta; cancer; wound healing
                                                                                                                             Sequence 852 BP; 216 A; 222 C; 225 G; 189 T; 0 other;
                                                                                                                                                          DB 12;
                                                                                                                                                                           88;
                                                                                                                                                         Score 134.2; DB 1
Pred. No. 5.8e-29;
                                                                                                                                                                                                                                                                                                                                              cagctctccaacatggtggtgaagtcttgtaaatg 332
                                                                                                  the truncated product.
See also AAQ11775, AAR11942-7 and AAR11954.
                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                       Genomic sequence encoding TGF-beta exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                          Claim 23; Fig 2; 42pp; English.
                                                                                                                                                         39.6%;
68.0%;
                                                                                                                                                                                                                                                                                                                                                                                                           AAN60973 standard; DNA; 975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 86EP-0302112
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87US-0025423
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/*tag= a
348..500
/*tag= b
501..975
/*tag= c
                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                 Best Local Similarity 68.0
Matches 187; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-MAR-1986;
                                                                                                                                                                                                                                                                                                                                                                                                                                               28-OCT-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22-MAR-1985;
13-MAR-1987;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EP200341-A.
                                                                                                                                                                                                                                                                                                                                                                                                                             AAN60973;
                                                                                                                                                          Query Match
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                                            This
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                              The gene product is known to stimulate cell proliferation and inhibit anchorage-dependent growth of a variety of human cancer cell lines, it is esp. useful in treatment of burns and the promotion of surface and internal wound healing. TGF-beta may be expressed from a transformed CHO cell line.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     growth factor beta-3 (TGF beta 3); tumour cells; growth
                                              - useful esp. for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                ;
0
                                                                                                                                                                                                                                                                                                                                                                                    Length 975;
                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence of genomic fragment encoding a TGF-beta 1 exon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      141 ttgcccatacctccgcagtgcagacacaacccacagcacggtgc 184
                                                                                                                                                                                                                                                                                                             Sequence 975 BP; 274 A; 184 C; 338 G; 179 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 461 ctgcccctacatttggagcctggacacgcagtacagcaaggtac
                                                                                                                                                                                                                                                                                                                                                                                                                              42;
                                                                                                                                                                                                                                                                                                                                                                             Score 96.8; DB 7;
Pred. No. 2.5e-18;
0; Mismatches 42;
                                              from transformed hosts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers 348..500
                                                                                                            Disclosure; Fig 2; 26pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BP.
                                                                                                                                                                                                                                                                                                                                                                                Query Match 28.6%;
Best Local Similarity 74.4%;
Matches 122; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA; 975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         88WO-US01945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     88WO-U001945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dernyck RM, Goeddel DV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (GETH ) GENENTECH INC.
WPI; 1986-326875/50.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1990-007474/01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAQ02815 standard;
                                         TGF-beta prodn. fr
wounds (J6 2/9/86)
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         This sequence encodes an exon of transforming growth factor-beta 1 (TGF-beta 1) polypeptide corresponding to AA's 288-338 of mature TGF-beta 1. The nucleic acid sequence encoding the second subtype of TGF-beta (TGF-beta 3) is useful as a probe or to produce TGF-beta 3 for both normal and neoplastic cell growth inhibition.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New recombinant human transforming growth factor-beta prods. - produced using Chinese hamster ovary cells, for use in diagnostic applications
                                                                                                                                                                                                       tctgggctggaagtgggtccatgaacctaagggctactatgccaacttctgctcaggccc 140
                                                                                                                                                                                                                   Gaps
                                                                                                                                                            cttccgcaacttggaggagactgctgtgtgcgcccctctacattgacttccgacagga 80
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0
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/note= "encodes TGF beta 1 residues 252 to 302"
                                                                                                                 Length 975;
                                                                                                                                      42; Indels
                                                                                                                                                                                                                                                   ttgcccatacctccgcagtgcagacacaacccacagcacggtgc 184
                                                                                                                                                                                                                                                                 BP; 274 A; 183 C; 339 G; 179 T; 0 other;
                                                                                                               28.6%; Score 96.8; DB 11;
74.4%; Pred. No. 2.5e-18;
ive 0; Mismatches 42;
                                                                                                                                                                                                                                                                                                                                                                                                                Partial pre-transforming growth factor beta 1 DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                       growth factor beta 1; wound healing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers 347..500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  using Chinese hamster ovary cells, or in therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 2; Fig 2; 26pp; English
                                                                                                                                                                                                                                                                                                                                   BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       87US-0025423.
85US-0715142.
89US-0389929.
                                                                                                                                                                                                                                                                                                                                AAT15721 standard; DNA; 975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   85US-0715142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         92US-0845893
93US-0147364
                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                  recombinant production; ss
                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                                                                 (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Goeddel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1996-076891/08.
P-PSDB; AAR90828.
                                                                                                                         Best Local Similarity
Matches 122; Conserv
                                                                             Sequence 975
                                                                                                                                                                                                                                                                                                                                                                                                                                      transforming
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Derynck RMA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22-MAR-1985;
04-AUG-1989;
04-MAR-1992;
05-NOV-1993;
                                                                                                                                                                                                                                                                                                                                                                              24-JUL-1997
25-JAN-1980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22-MAR-1985;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09-JAN-1996
                                                                                                                                                                                                                                                                                                                                                       AAT15721;
                                                                                                               Query Match
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The transforming growth factor (TGF) beta 1 exon was identified using the "long probe" strategy used previously for TGF-alpha. Long oligonucleotides (T1572-23) designed on the basis of the partial protein sequence were used as hybridisation probes for the exon in a human genomic DNA library. The TGF beta 1 exon was then used as a probe for the isolation of TGF beta 1 cDNA (see AAT15270). DNA encoding TGF beta 1 is useful for the recombinant production of the protein, which is useful in, e.g. wound healing.
                                                                                                                                                                                                                   81 tctgggctggaagtgggtccatgaacctaagggctactatgccaacttctgctcaggccc 140
                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                        80
                                                                                                                                                                                                    21 cttccgcaacttggaggagaactgctgtgtgcgccccctctacattgacttccgacagga
                                                                                              (Revised entry submitted to correct sequence analysis breakdown.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA encoding transforming growth factor-beta precursor sequence
                                                                                                                                                                                 ö
                                                                                                                                                          Length 975;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          transforming growth factor-beta gene exon fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Transforming growth factor-beta 1; TGF-beta 1; human; ss.
                                                                                                                                                                                Indels
                                                                                                                    Sequence 975 BP; 274 A; 184 C; 338 G; 179 T; 0 other;
                                                                                                                                                                                                                                                                                                 141 ttgcccatacctccgcagtgcagacacacacacaggacggtgc 184
                                                                                                                                                                                                                                                                                                               Score 96.8; DB 17;
Pred. No. 2.5e-18;
                                                                                                                                                                                 42;
                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                     BP
                                                                                                                                                       28.68;
74.48;
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890S-0389929.
920S-0845893.
930S-0147364.
950S-0454468.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              347.500
/*tag= b
501.976
/*tag= c
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                                                                                                                                                                 Best Local Similarity 74.4
Matches 122; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1998-494840/42.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P-PSDB; AAW78788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                04-MAR-1992;
05-NOV-1993;
30-MAY-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Derynck RMA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
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04-AUG-1989;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-SEP-1998
                                                                                                                                                                                                                                                                                                                                                                                                          AAV52936;
                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human
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                                                                                                                                                                                                                                                                                                                         461
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Derynk RMA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic
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                                                                                                                                                                                                                                                                                                       81 tctgggctggaagtgggtccatgaacctaagggctactatgccaacttctgctcaggccc 140
                                                                                                                                                                                                                                                                                                                                                 transforming growth factor-beta 1 (TGF-beta 1) gene incorporating an exon and flanking intron sequences. It was isolated from a human genomic library using probes based on a partial protein sequence of TGH-beta 1. The exon encodes amino acids 288-338 (see AAW78788) of TGF-beta 1. Restriction fragments of the isolated exon were used as probes for the isolation of TGF-beta 1 cDNAs (see AAV52933). The invention relates to the recombinant production of TGF-beta. Nucleic acids encoding TGF-beta have been isolated and cloned into vectors which are replicated in bacteria and expressed in eukaryotic cells. TGF-beta recovered from transformed cells is used in known therapeutic applications. TGF-beta nucleic acids are also useful in diagnosis and identification of TGF-beta
                                                                                                                                                                                                                                                                                           21 cttccgcaacttggaggagaactgctgtgtgcgcccctctacattgacttccgacagga 80
useful for analysis to perform manipulations to increase yield of recombinant production of the protein
                                                                                                                                                                                                                                                                       .;
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                                                                                                                                                                                                                                                Length 975;
                                                     This nucleotide sequence comprises a fragment of the human
                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                  461 ctgcccctacatttggagcctggacacgcagtacagcaaggtac 504
                                                                                                                                                                                                                Sequence 975 BP; 274 A; 184 C; 338 G; 179 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                141 ttgcccatacctccgcagtgcagacacaccacaggacacggtgc 184
                                                                                                                                                                                                                                                28.6%; Score 96.8; DB 19; 74.4%; Pred. No. 2.5e-18;
                                                                                                                                                                                                                                                                       42;
                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /codon_start= 348..350
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                                Example 2; Fig 2; 26pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               85US-0715142.
87US-0025423.
89US-0389929.
92US-0845893.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAQ56924 standard; DNA; 975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           85US-0715142
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                                                                                                                                                                                                                                                                      Matches 122; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1..975
/*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human pre-TGF-beta-1.
                                                                                                                                                                                                                                                             Best Local Similarity
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04-AUG-1989;
04-MAR-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22-MAR-1985;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22-MAR-1985;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      08-FEB-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   vulnerary.
                                                                                                                                                                                                                                                  Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  81 tctgggctggaagtgggtccatgaacctaagggctactatgccaacttctgctcaggccc 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      401 ceteggetggaagtggatecaegageecaagggetaecatgecaaettetgeetegggee 460
                                                                                                                                                                                                                                                            cDNA sequences were determined for human pre-TGF-beta-1 (AAQ56923), pig TGF-beta-3 (AAQ56925) and the corresponding amino acid sequences were determined (AAR46227-29, respectively). A genomic fragment corresponding to a human TGF-beta-1 exon (AAQ56924) was also isolated and its amino acid sequence determined (AAR46230). The sequences have been used in the construction of vectors for the expression of recombinant TGF-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "only contains 6 Cys residues; sequence disclosed in specification omits 50 bases"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21 cttccgcaacttggaggagaactgctgtgtgcgccccctctacattgacttccgacagga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /*tag= b
/product= fragment B of Staphylococcal Protein A
/note= "directly linked to a second Fb fragment"
                                                                                                                                Nucleic acid sequences encoding transforming growth factor-beta diagnostic probes, and for use in therapeutics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product= truncated TGF-beta containing 8 x Cys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 975;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /*tag= a
/note= "modified trp-LE leader sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 975 BP; 274 A; 181 C; 341 G; 179 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          141 ttgcccatacctccgcagtgcagacacaacccacagcacggtgc 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 95.2; DB 15;
Pred. No. 7.1e-18;
0; Mismatches 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Encodes Fb-Fb-truncated "(8 Cys)"-TGF-beta.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Transforming Growth Factor beta; AIDS; ss
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                                                                                                                                                                                                             Disclosure; Fig 2; 25pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 28.1%;
Best Local Similarity 73.8%;
Matches 121; Conservative
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Goeddel
                                                    WPI; 1994-056343/07
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Best Local Similarity
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         263 tcctgtactatgttgggaggaccccaaagtggagcagctctccaacatggtggtgaagt 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    615 glocglacalcingglototologalacocaglaciocaaggigiligicininini
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     675 ataacccgggggctagcgcagctccgtgctgttccacaggccttggaaccgctgccga 734
                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                This synthetic gene was designed based on reported sequence data, codons inferred from known amino acid sequences and observations of partial homology with known genes of the TGF-beta family. It was assembled from chemically synthesized oligonucleotides and can be expressed in prokaryotic host cells. The sequence is that given in the specification, however, 50 bases should be inserted between nucleotides 600 and 601 of this sequence: the two "missing" Cys codons are presumably contained in the omitted sequence. The truncated TGF-beta protein is cleaved from the Fb-Fb domain at the hinge region to give the truncated product.

See also AAQ11774, AAR11942-7 and AAR11954.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        bovine bone morphogenic protein-6; bone defects; cartilage defects; wound healing; bone repair; cartilage formation; periodontal disease; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                       gcccatacctccgcagtgcagacacaaccacagcacggtgctgggactgtacaacactc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               203 tgaaccctgaagcatctgcctcgccttgctgctgctgcccaggacctggagccctgacca
                                                                                                                                                                     Recombinant truncated transforming growth factor-beta analogues capable of inducing an anti-proliferative effect in mammalian epithelial cells in vitro
                                                                                                                                                                                                                                                                                                                                                                                                                    ;
                                                                                                                                                                                                                                                                                                                                                                                             Score 73.2; DB 12; Length 817;
Pred. No. 1.2e-11;
0; Mismatches 73; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                Sequence 817 BP; 207 A; 213 C; 219 G; 178 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Encodes C-terminal portion of bovine BMP-6.
                                                                                                                                                                                                               Claim 23; Fig 2B; 42pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BP.
                                                                                                                                                                                                                                                                                                                                                                                                21.6%;
61.6%;
                                                    90090SD-0M06
                                                                        89US-0422962
                                                                                            (CREA-) CREATIVE BIOMOLECUL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAQ23678 standard; DNA; 894
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                   117; Conservative
                                                                                                                                     WPI; 1991-148530/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    323 cttgtaaatg 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gttgcaagtg 804
                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                 P-PSDB; AAR11957
                                                   18-OCT-1990;
                                                                        18-OCT-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17-SEP-1992
         W09105565-A
                              02-MAY-1991
                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local S:
Matches 117,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAQ23678;
                                                                                                                 Cohen CM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       90
                                                                                                                                                                                                                                                                                                                                                                                                                                       143
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This sequence was isolated from positive clones in a bovine lambda gt10 library isolated with probes AAQ23673-6, which were then screened with HEL5. One which hybridised positive was sequenced to yield the given sequence. An inframe stop codon indicates it encodes the C-terminal part of bovine BMP-6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     67 gacttccgacaggatctgggctggaagtgggtccatgaacctaagggctactatgccaac 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ttotgotcaggocottgocoatacotcogoagtgoagac-----acaacocacago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7 gacaccaattactgcttccgcaacttggaggagaactgctgtgtgcgcccctctacatt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               acggtgctggggactgtacaacactctgaaccctgaagcatctgcctcgccttgctgcgtg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    565 cccacgaaactgaacgccatctcggtgctctacttcgacgacaactccaatgtcatcctg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    505 atcgtgcagaccctggttcacctcatgaaccccgagtacgtccccaaaccgtgctgcgcg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ccccaggacctggagccctgaccatcctgtactatgttgggaggacc---cccaaagtg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New human bone morphogenic protein-5 derivs. - for treating bone and/or cartilage defects, burns, incisions, ulcers, for wound
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 894;
                                                                         C-terminal part of bovine BMP-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 894 BP; 169 A; 301 C; 277 G; 147 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gagcagctctccaacatggtggtgaagtcttgtaaatgtagctga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               625 aagaagtaccggaacatggtcgtacgagcgtgtggggtgccactga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 54.6; DB 13;
Pred. No. 2.4e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches 154;
                                                                                                                                                                                                                                                                                                                                                                             ט
                                                                                                                                                                                                                                                                                                                                                                             Wozney
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                See also AAO23773-81, and AAR22497-9
                                                                                                                                                                                                                                                                                                                                                                          Е А,
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 4; Page 25; 54pp; English.
                                                                                                                                                                                                                                                                                                                                                                             Wang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16.1%;
51.9%;
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                                                                                                                                                                                                                                                                                                                       (GENE-) GENETICS INST INC
                                                                                                                                                                                                                                                                                                                                                                        Rosen V A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 179; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAQ37567 standard; DNA;
                         . 669
                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1992-132089/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                       26-SEP-1991;
                                                                                                                                                                                                                                                                                                                                                                        Celeste A J,
                                                                                                                                                                                                                                                                          26-SEP-1990;
                                                                                                                       W09205199-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAQ37567;
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565 cccacgaaactgaacgccatctcggtgctctacttcgacgacaactccaatgtcatcctg 624
                        gagcagctctccaacatggtggtgaagtcttgtaaatgtagctga
                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wozney JM;
                                                                                                              BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8703-0031346.
8803-0179100.
8803-0179101.
8903-0329610.
8903-0347559.
9903-043409.
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86US-0880776.
86US-0943332.
87US-0028285.
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93US-0116425.
95US-0469935.
                                                                                                              AAX99261 standard; DNA; 894
                                                                                                                                                                                                                                                                                                                                                                                                                       97US-0788729
                                                                                                                                                                                                                                                                                                                                 /*tag= a
/product=
                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                     699.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rosen VA, Wang EA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1999-468410/39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WANG E A.
WOZNEY J M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ROSEN V A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P-PSDB; AAY28984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tissue repair
                                                                                                                                                                                          DNA encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        08-APR-1988;
08-APR-1988;
28-MAR-1989;
04-MAY-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20-MAR-1987;
26-MAR-1987;
08-APR-1988;
                                                                                                                                                                04-0CT-1999
                                                                                                                                                                                                                                                                                                                                                                       US5939388-A.
                                                                                                                                                                                                                                                                                                                                                                                                                       23-JAN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUL-1986;
17-DEC-1986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-NOV-1989
                                                                                                                                                                                                                                                                                                                                                                                               17-AUG-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                07-SEP-1993
                                                                                                                                        AAX99261;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (ROSE/) I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (MOZN/)
                                                                                                                                                                                                                                                                                 Bos sp.
                                                                                     92
                        295
                                                 625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bone
                                                                                                                                                                                                                                                                                                          Key
                                                                                                   AAX99261
                          ð
                                                 a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          These
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This sequence was isolated using the probes given in AAQ37557-60. The probes were based on the tryptic peptide fragment from bovine bone morphogenic protein (BMP-6) having the sequence XHELVSFS. A further clone representing the carboxy terminal part of the bovine BMP-5 cartilage/bone protein (see also AAQ37566) was isolated under more stringent conditions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ccccaggacctggagccctgaccatcctgtactatgttgggaggacc---cccaaagtg 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gacttocgacaggatctgggctggaagtgggtccatgaacctaagggctactatgccaac 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ttetgetcaggecettgeceatacetcegeagtgeagae-----acaaeceaeage 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             acggtgctggggactgtacaacactctgaaccctgaagcatctgcctcgccttgctgcgtg 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7 gacaccaattactgcttccgcaacttggaggagaactgctgtgtgcgccccctctacatt 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gcctcagactacaacagcagcgagctgaagacggcctgccggaagcatgagctctacgtg 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                agettecaggacetggggtggcaggactggatcattgcccccaagggctacgctgccaac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   atcgtgcagaccctggttcacctcatgaaccccgagtacgtccccaaaccgtgctgcgcg
                        tryptic peptide; bovine; bone morphogenic protein; BMP-6; carboxy terminal; cartilage; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Isolated DNA sequence encoding bone morphogenic protein (BMP-6) useful for treating bone and/or cartilage defects and in wound
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16.1%; Score 54.6; DB 14; Length 894; 51.9%; Pred. No. 2.4e-06; ive 0; Mismatches 154; Indels 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 894 BP; 169 A; 301 C; 275 G; 149 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                   Wozney JM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Table II; 24pp; English.
                                                                                    Location/Qualifiers
1..669
/*tag= a
                                                                                                                                                                                                                                                                                                                                                                                   Wang EA,
                                                                                                                                                                                                              86US-0943332
87US-0943332
87US-0028285
87US-0031346
88US-0179100
88US-0179101
88US-0179101
89US-0329610
89US-0347559.
                                                                                                                                                                                      86US-0880776
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                                                                                                                                                                                                                                                                                                                                                         (GEMY ) GENETICS INST INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       healing and tissue repair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                  Rosen VA,
BMP-6 coding sequence
                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1993-075724/09.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                     P-PSDB; AAR32903
                                                                                                                                                                                                                                                  26-MAR-1987;
08-APR-1988;
08-APR-1988;
08-APR-1988;
28-MAR-1989;
04-MAY-1989;
23-JUN-1989;
                                                                                                                                                                                       01-JUL-1986;
                                                                                                                                                                                                                           17-DEC-1986;
20-MAR-1987;
                                                                                                                                                                                                                                                                                                                                                                                  AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Simi
Matches 179;
                                                                                                                                     US5187076-A
                                                                                                                                                              16-FEB-1993
                                                             Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                  Celeste
                        Probe;
BMP-5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29
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The invention is related to purified bone morphogenic proteins (BMP). Compositions comprising a matrix, a vehicle and a purified dimeric BMP-5 or naturally occurring allelic sequences of BMP-5 are used for inducting bone/and or cartilage or other connective tissue formation in a patient and is useful in wound healing e.g. ulcers, burns and incisions, tissue repair and treating periodortal disease. The composition can be used to treat cell populations e.g. embryonic cells, stem cells to enhance or enrich growth and/or cell differentiation. Tissues that can be treated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bone morphogenic protein; BMP-5; bone formation; cartilage; ulcer; connective tissue; wound healing; burn; incision; tissue repair; BMP-6; periodontal disease; cell differentiation; osteoarthritis; osteoporosis; bone fracture; cosmetic plastic surgery; neuronal survival; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               morphogenic protein composition useful in wound healing and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     carboxy-terminal part of bovine BMP-6 bone protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "BMP-6 carboxy terminal fragment"
Example 4; Columns 19-20; 20pp; English.
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include epidermis, nerve, muscle, liver, lung, cardiac, pancreas and kidney. Osteoarthritis and osteoporosis can also be treated. It is useful for healing bone fractures and cartilage defects in humans and other animals, particularly domestic animals and thoroughbred horses and also has uses in cosmetic plastic surgery. The composition may increase neuronal survival and be useful in transplantation and the treatment of conditions which exhibit a decrease in neuronal survival. The present sequence represents a DNA encoding the carboxy-terminal part of bovine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     - useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gacticcgacaggatetgggetggaagtgggtecatgaacetaagggetaetatgeeaac 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  444
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7 gacaccaattactgcttccgcaacttggaggagaactgctgtgtggggcccctctacatt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               agcttccaggacctggggtggcaggactggatcattgcccccaagggctacgctgccaac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          acggtgctgggactgtacaacactctgaaccctgaagcatctgcctcgccttgctgcgtg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             505 atogtgcagaccetggttcacctcatgaaccecgagtacgtccccaaaccgtgctgcgcg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ccccaggacctggagccctgaccatcctgtactatgttgggaggacc---cccaaagtg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              565 cccacgaaactgaacgccatctcggtgctctacttcgacgacaactccaatgtcatcctg
                                                                                                                                                                                                                                                                                                                                                                                                                                                             12;
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                                                                                                                                                                                                                                                                                                                                                                                                Length 894;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gagcagctctccaacatggtggtgaagtcttgtaaatgtagctga 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     625 aagaagtaccggaacatggtcgtacgagcgtgtgggtgccactga 669
                                                                                                                                                                                                                                                                                                    Sequence 894 BP; 169 A; 301 C; 277 G; 147 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ozkaynak
                                                                                                                                                                                                                                                                                                                                                                                                Score 54.6; DB 20;
Pred. No. 2.4e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches 154;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Consensus gene/probe to osteogenic protein OP1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DC,
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51.98;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    89WO-US01453
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 51.9
Matches 179; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1989-324202/44.
P-PSDB; AAP91200.
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                                                                                                                                                                                                                                                    BMP-6 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Periodontal;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22-MAR-1990
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                                     This is a synthetic consensus gene sequence, used as a probe to isolate natural genes of proteins that induce endochondral bone formation.
                                                                                                                                                                                                  79 gcacgagctgtatgtcagcttccgagacctgggctggcaggactggatcatcgcgcctga 138
                                                                                                                                                                                                                                                                                                                                        281
                                                                                                                                                                                                                                                                                                                                                     gogococototacattgacttocgacaggatotgggctggaagtgggtccatgaacctaa 110
                                                                                                                                                                                                                                                         139 agacttcgacgcctactgctccggagcctgccagttcccctctgcggatcacttcaa 198
                                                                                                                                                                                                                                                                                   221
                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New Growth Differentiation Factor-11 (GDF-11) - with tissue-specific expression in muscle, neural and uterine cells, for detecting cell proliferation disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product= Murine growth differentiation factor-11.
                                                                                                                                                                                                                                                                                                            199 cagcaccaaccacgccgtggtgcagacctggtgaacaacatgaacccggcaaggtacc
                                                                                                                                                                                                                                                                                   agacacacacacagcacggtgctgggactgtacaacactctgaaccctgaagcatctgc
                                                                                                                                                                                                                                                                                                                                        ctcgccttgctgcgtgccccaggacctggagccctgaccatcctgtactatgttgggag
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Growth differentiation factor-11; GDF-11; antibody; detection; disorder; muscle; antisense; suppression; vector; liposome;
                                                                                                                       Length 454;
                                                                                                                                                  Indels
                                                                               86 T; 0 other;
                                                                                                                                                                                                                                gggctactatgccaacttctgctcaggcccttgcccatacctc-
                                                                                                                       Score 53.4; DB 10;
Pred. No. 4.3e-06;
                                                                                                                                                0; Mismatches 116;
                                                                             Sequence 454 BP; 101 A; 146 C; 121 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (UYJO ) UNIV JOHNS HOPKINS SCHOOL MED
                                                                                                                                                                                                                                                                                                                                                                                                                      345
                                                                                                                                                                                                                                                                                                                                                                                            282 gacccccaaagtggagcagctctccaa 308
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198..578
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             Disclosure; fig 1B; 104pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                     319 ttccaccgtggtgctgaagaactacca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BP.
                                                                                                                      15.8%;
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                                                                                                                                                  142; Conservative
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                                                                                                                    Query Match
Best Local Similarity
Matches 142; Conserva
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P-PSDB; AAR88554.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               08-JUL-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO9601845-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        441
                                                                                     Antibodies directed against the growth differentiation factor (GDF) are useful for detecting cell proliferative disorders when contacted with a specimen from a subject suspected of having a GDF-II associated disorder. Antibody binding constitutes a positive result. Detection is performed in muscle cells in vitro or in vivo. The antibodies may also be used in the treatment of such disorders by suppressing GDF-II activity. Antisense GDF-II reagents may also be used. Vectors are utilised in the treatment process e.g. colloidal dispersion systems such as liposomes which are target specific and either anatomically or mechanistically targetted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 actgcttccgcaacttggaggagaactgctgtgtgcgccccctctacattgacttccgac 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Growth differentiation factor-11; GDF-11; mouse; transgenic animal; transforming growth factor-beta; cell proliferation; neuromuscular disorder; muscular dystrophy; muscle atrophy; aging;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  262 actgcgatgaacactcgagtgagtcccgctgctgccgatatcctctcacagtggactttg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gcccttgcccatacctccgcagtgcagacacaacccacagcacggtgctgggactgtaca
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 52.8; DB 17; Length 630;
Pred. No. 7e-06;
0; Mismatches 82; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 630 BP; 155 A; 173 C; 159 G; 143 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mouse growth differentiation factor-11 DNA fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (UYJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
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198..578
                              Claim 3; Page 38-39; 67pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAV07556 standard; DNA; 630 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15.6%;
55.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98WO-US02310.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 15.6
Best Local Similarity 55.4
Matches 102; Conservative
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P-PSDB; AAW65459.
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                                                                                                                                                                                                                                                                                                                                                                        proliferative disorders, especially those involving muscle, nerve and adipose tissue. It was isolated from a murine genomic library using murine GDF-8 as probe. A full-length sequence (see AAV07555) encoding human GDF-11 (see AAV05458) is also provided. Claimed transgenic animals, especially bovine, porcine, ovine or avian animals, have been altered so that production of GDF-11 is reduced or completely disrupted. Such animals have higher than normal levels of muscle tissue, preferably without increased fat and/or chlesterol levels, and are useful as food products. The invention also provides methods for treating a muscle or adipose tissue disorder in an animal, including humans. A GDF-11 antibody, antisense molecule or dominant negative polypeptide (or a polynucleotide encoding a dominant negative polypeptide) can be administered to a patient to treat e.g. a muscle wasting disease, a neuromuscular disorder, muscle atrophy, obesity or other
                                                                                                                                                                                                                           This nucleotide sequence includes a region of an open reading frame that codes for the C-terminal portion (see AAM65459) of murine growth differentiation factor-11 (GDF-11), a new member of the transforming growth factor-beta superfamily that is associated with various cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         321
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Transgenic animal growth differentiation factor-11 is inhibited - by insertion of transgene, also use of GDF-11 inhibitors for treating muscular wasting, neuromuscular disease, obesity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 630 BP; 155 A; 173 C; 159 G; 143 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 52.8; DB 19;
Pred. No. 7e-06;
0; Mismatches 82;
                                                                                                                                                        Example 1; Page 53-54; 89pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 adipocyte cell disorders, and aging.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
198..578
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tch 15.6%; al Similarity 55.4%; 102; Conservative
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Bos taurus

Partial bovine bone morphogenetic protein-11 (BMP-11).

(first entry)

10-AUG-1995

579

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The invention relates to a method for producing animal food products with increased ribs content. The method comprises: (a) introducing a transgene which interferes with expression of growth differentiation factor-11 (GDF-11), into an embryo: (b) allowing the embryo to mature; (c) crossbreeding the transgene-positive progeny; (d) processing these progeny to obtain the foodstuff. Modulators of GDF-11 are useful for treating acute or chronic renal disease, and various other muscle associated disorders or chronic renal disease, and various other muscle associated disorders disorders; adipose tissue disorders and immunologic disorders. The animal food product comprises large amounts of muscle and meagre amounts of fats and cholesterol, hence useful in treating obesity and related disorders. The present sequence represents a genomic DNA encoding a partial mouse
                                                                                                                                                                                                                                                                                                                                 Preparation of transgenic animal food product useful for treating renal and muscular disorders, comprises introducing transgene interfering with expression of growth differentiation factor-11 into embryo -
  'note "the start codon is not indicated"
                                                                                                                                                                                          (UYJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE
                                                                                                                                                                                                                                                                                                                                                                                                              Example 3; Fig 1A; 97pp; English.
                                                                                                                  99WO-US17252
                                                                                                                                                      98US-0123929
                                                                                                                                                                                                                                   McPherron AC;
                                                                                                                                                                                                                                                                       WPI; 2000-195289/17.
P-PSDB; AAY77565.
                                    WO200006716-A1.
                                                                                                                  28-JUL-1999;
                                                                                                                                                      28-JUL-1998;
                                                                          10-FEB-2000
                                                                                                                                                                                                                                   Lee S,
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Sequence 630 BP; 155 A; 173 C; 159 G; 143 T; 0 other;

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                                                                            262 actgcgatgaacactcgagtgagtcccgctgctgccgatatcctctcacagtggactttg 321
                                                 17 actgettecgeaacttggaggagaactgetgtgtgegeeeectetacattgaetteegae 76
                                                                                                      77 aggatotggggctggaagtgggtccatgaacctaagggctactatgccaacttctgctcag
                                                                                                                                322 aggettttggettgggactggatcategeacetaagegetacaaggecaactactgeteeg
                                                                                                                                                                             137 gcccttgcccatacctccgcagtgcagacacaacccacagcacggtgctgggactgtaca
                              ö
15.6%; Score 52.8; DB 21; Length 630; 55.4%; Pred. No. 7e-06; Live 0; Mismatches 82; Indels 0
                                                                                                                                                                                                                                                                                                           AAQ79444 standard; DNA; 789 BP.
                          Conservative
            Best Local Similarity
Matches 102; Conserv
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 Query Match
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A bovine genomic library (strain Bovine Activin WC) in lambda EMBL3
was screened under low stringency conditions with a 1081-1403 base
fragment of human BMP-7 DNA. Positive clones were screened with BMP-
5. -6, and -7 probes under high stringency conditions and one clone
reactive in the first screen but not in the second was selected. The
hybridisation characteristics were localised to a 0.5 kb fragment.
The partial sequence of this clone, lambda 7r-30 (ATCCD 75439) is
(79444. The 5' limit of this exon of the bovein BMP-11 gene is
difficult to define. Clone lambda 7r-30 contains at least one exon/
intron boundary. BMP-11 polypeptide exists as a dimer comprising two
intron boundary. BMP-11 polypeptide exists as a electrodimer with one
mature sequence from BMP-11 and the other being any of BMP 1-10.
The predicted mol. Wt. of the mature active species comprising two
mature protein sequences is approx. 12,000 daltons. Further active
species are contemplated comprising AAs 23-126. Primers C and D
are based on clone lambda 7r-30 (see 079446, Q79447). Nts 375 or

390-704 of Q79444 are claimed. AAs 18-126 of R66147 are claimed.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
                                                                                                                                                                                                                                                                                                                                                                                                                                             New DNA encoding bone morphogenetic protein 11 - and related vectors, transformed cells and polypeptide(s), including heterodimers, useful e.g. in fertility control bone and tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 789;
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                                                                                              /*tag= b
/note= "putative 3' end of intron"
375..701
/*tag= c
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Pred. No. 1.4e-05;
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                                    Location/Qualifiers
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Best Local Similarity 54.9%;
Matches 129; Conservative (
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                                                                    /*tag= a
322..323
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                                                                                                                                                                                                                                                                                                                                                                                                              P-PSDB; AAR66147
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence encodes bovine bone marrow morphogenic protein-11 (BMP-11). The BMP-11 protein may be useful for regulating folliclestimulating hormone (FSH), e.g. for the purpose of contraception or for inducing bone, cartilage and/or other connective tissue formation. The protein is produced by culturing the cells of transformed with the DNA followed by recovering and purifying the BMP-11 sequence from the
                                                                                                                                             BMP-11; regulation; follicle stimulating hormone; FSH; contraception; bone formation; cartilage formation; connective tissue formation; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gtccatgaacctaagggctactatgccaacttctgctcaggcccttgccatacctccgc 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  468 atcatcgctcctaaaacgctacaaggccaactactgctccggccagtgcgagtacatgttt 527
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA encoding bone morphogenetic protein 11\ \mathrm{polypeptide}(s) - useful for regulating follicle-stimulating hormone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Db
1.4e-05;
97;
                                                                                                                   Bovine bone morphogenic protein-11 encoding DNA.
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Pred. No. 1.4
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324..374
                                      BP,
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93US-0061464.
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Best Local Similarity 54.9%;
Matches 129; Conservative
                                    AAT74190 standard; DNA; 789
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P-PSDB; AAW23589.
                                                                                                                                            BMP-11; regulation;
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This sequence represents the coding sequence for the bovine bone morphogenetic protein-11 (BMP-11) of the invention. The human BMP-11 optyeptide (see AMW0817), mature human BMP-11, or its dimers with other inhibin-beta, inhibin-alpha or bone morphogenetic proteins are useful for inducing bone and/or cartilage formation, e.g. for bone, ligament or cartilage repair, wound healing or treatment of periodontal disease. BMP-11 may also be useful for regulating the production of follicle stimulating hormone, for contraception, to stimulate haematopoiesis, and to suppress the development of gondal tumours.
                                                                                                                                                                                                                                                                                                                                                                                      Bone-morphogenetic protein-11; BMP-11; inhibin-beta; inhibin-alpha; bone formation; cartilage repair; wound healing; periodontal disease; follicle stimulating hormone regulator; contraception; haematopoiesis; gondal tumour suppressor; therapy; cow; bovine; ds.
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Pred. No. 1.4e-05;
0; Mismatches 97;
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                                                                                                                                                                                                                                                                                                                                   Bovine BMP-11 coding sequence.
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This is a partial nucleotide sequence of bovine activin WC, or bone morphogenetic protein 11 (BMP-11). The DNA was isolated by screening a bovine genomic library with a fragment of human BMP-7. The DNA probe and with a mixed BMP-5, BMP-6 and BMP-7 probe; the recombinant hybridised positively to the BMP-7 probe under reduced stringency conditions and exhibited weak or no hybridisation to the mixed probe under high stringency conditions. The clone includes an open reading frame encoding at least 126 amino acids (see an open reading frame encoding at least 126 amino acids (see an open reading frame encoding at least 126 amino acids (see in example of a novel family. BMP-11 proteins may be useful to growth factor beta superfamily. BMP-11 proteins may be useful to tissue repair, or for augmenting the activity of other BMP proteins. BMP-11 may also be useful for requiating the production of follicle stimulating hormone (e.g. for contraception), to 468 atcatcgctcctaaacgctacaaggccaactactgctccggccagtgcgagtacatgttt 527 atgcaaaagtatccgcacaccttggtgcaacaggct-----aacccaagaggc 578 Activin WC; bone morphogenetic protein 11; BMP-11; cattle; bovine; bone; cartilage; connective tissue; neuronal tissue; wound healing; tissue repair; vulnerary; contraceptive; transforming growth factor-beta; ds. agtgcagacacaaccacaggacggtgctgggactgtacaacactctgaacctgaagca 579 tctgcggggccctgctgcacacccaagatgtccccaatcaacatgctctact 633 Administration of human or bovine bone morphogenetic protein 11 = 217 totgcctcgccttgctgcgtgccccaggacctggagcccctgaccatcctgtact "putative 3' end of intron" Bovine activin WC (BMP-11) partial DNA sequence. Location/Qualifiers Celeste AJ, Thies SR, Wozney JM; Example 1; Page 55; 62pp; English. BP. AAX58652 standard; DNA; 789 98WO-US23827 97US-0966297 (first entry) ๙ (GEMY ) GENETICS INST INC. /\*tag= b 375..701 24 . . 704 /partial /\*tag= /\*tag= /note= WPI; 1999-327207/27. P-PSDB; AAY06096 W09924058-A2 06-NOV-1998; 07-NOV-1997; 16-AUG-1999 20-MAY-1999 mat\_peptide Bos taurus AAX58652; RESULT 100 AAX58652 intron 157 228 CDS ò g ŏ g

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agtgcagacacaacccacagcacggtgctgggactgtacaacactctgaaccctgaagca 216 Gaps gagaactgctgtgtgcgccccctctacattgacttccgacaggatctggggctggaagtgg 96 528 atgcaaaagtatccgcacacccacttggtgcaacaggct-----aacccaagaggc stimulate haematopoiesis, to suppress the development of gonadal tumours, and especially (claimed) to induce neuronal cell formation, growth differentiation, proliferation and maintenance. Query Match 15.3%; Score 51.8; DB 20; Length 789; Best Local Similarity 54.9%; Pred. No. 1.4e-05; Matches 129; Conservative 0; Mismatches 97; Indels 9 217 tctgcctcgccttgctgcgtgccccaggacctggagccctgaccatcctgtact tctgcggggccctgctgcacaccaccaagatgtccccaatcaacatgctctact Sequence 789 BP; 187 A; 213 C; 223 G; 166 T; 0 other; 37 157 SSSXS셤 g ò à ò 216

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Result

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Post-processing:

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DB DB

Minimum | Maximum |

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Total number

Title: Perfect score:

Sequence:

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Run on:

Scoring table:

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181 gtgctgggactgtacaacactctgaaccctgaagcatctgcctcgccttgctgcgtgcc 240
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                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Nimni, Marcel E.
APPLICANT: Hall, Frederick L.
APPLICANT: Tuan, Tai-Lan
APPLICANT: Wu, Lingtao
APPLICANT: Wu, Lingtao
TITLE OF INVENTION: Transforming Growth Factor B Fusion
TITLE OF INVENTION: and
TITLE OF INVENTION: Their Use in Wound Healing
NUMBER OF SEQUENCES: 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Merchant & Gould
STREET: 11150 Santa Monica Boulevard, Suite 400
CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/470,837
                                                                                                                                                                                                                                                                                                                                            30630-1US01
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 33, Application US/08470837 Patent No. 5800811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 424
ATTORNEX/AGENT INFORMATION:
NAME: STAIP, Janice A.
REGISTRATION NUMBER: 34,051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 30
TELECOMMUNICATION INFORMATION:
TELEPHONE: 310-445-1140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 339 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 310-445-9031 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mat_peptide
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                                                                                                                                                                                                                                                                                   Similarity
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                                                                                                                                                                                                 ; NAME/KEY:
; LOCATION:
US-08-789-588-3
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US-09-123-233-5
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Best Local S
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GENERAL INFORMATION:
APPLICANT: Gerletti, Nico
APPLICANT: Cox, David
APPLICANT: Cox, David
APPLICANT: Cox, David
APPLICANT: Meyhack, Bernd
TITLE OF INVENTION: Process for Refolding Recombinantly
TITLE OF INVENTION: Produced TGF-beta-like Proteins
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Henry P. No. 5922846ak
STREET: 520 White Plains Road, P.O. Box 2005
     Length 339;
                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/789,588
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100.0%; Pred. No. 2.8e-87;
ive 0; Mismatches 0;
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/486,057
FILING DATE: 07-UUN-1995
FILING DATE: 25-FEB-1994
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Tarrytown STATE: New York COUNTRY: 0.S.A. COUNTRY: 0.S.A. ZIP: 10591-9005 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPATIBLE OF COMPUTER: PatentIn Release #1.0, v
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US 07/960,309
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 3, Application US/08789588
Patent No. 5922846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 07
FILING DATE: 13-OCT-1992
PRIOR APPLICATION DATA:
Query Match
Best Local Similarity 100.C
Matches 339; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 339;
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TITLE OF INVENTION: biologically active dimeric protei
NUMBER OF SEQUENCES: 14
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PENTIN Release #1.0, Version #1.30 (EPO)
APPLICATION NUMBER: US/09/123,233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 339; DB 2;
100.0%; Pred. No. 2.8e-87;
tive 0; Mismatches 0;
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FILING DATE: 06-DEC-1989
ATTORNEY/AGENT INFORMATION:
NAME: NO. 5922846ak, Henry P.
REGISTRATION NUMBER: 33200
REFERENCE/DOCKET NUMBER: 4-17861
TELECOMMUNICATION INFORMATION:
TELEPRAM: (908) 277-5110
TELEFAX: (908) 277-5110
TELEFAX: (908) 277-5110
TELEFAX: (908) 277-5110
TELEFAX: (308) 277-5110
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
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INFORMATION FOR SEO ID NO: 5
SEQUENCE CHARACTERISTICS:
LENGTH: 339 base pairs
TYPE: nucleic acid
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; PETER T.; HALEY, JOHN D.
; TITLE OF INVENTION: METHOD FOR OBBTAINING BONE MARROW FREE
; OF TUMOR CELLS USING TRANSFORMING GROWTH FACTOR B3
NUMBER OF SEQUENCES: 9
                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 339; DB 5;
100.0%; Pred. No. 5.2e-87;
tive 0; Mismatches 0;
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                                                                                                                                  ORGANISM: Transforming Growth Factor-Beta IMMEDIATE SOURCE:
CLONE: TGF-B3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/543,341
FILING DATE: 25-UN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 353,410
FILING DATE: 17-MAY-1989
APPLICATION NUMBER: 183,410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 20-APR-1988
APPLICATION NUMBER: 111,022
FILING DATE: 20-OCT-1987
APPLICATION NUMBER: 922,121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 20-OCT-1986
APPLICATION NUMBER: 847,931
 2529 base pairs
                                                                                                               FRAGMENT TYPE: N-terminal ORIGINAL SOURCE: ORGANISM: Transforming
                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                   NAME/KEY: mat_peptide
LOCATION: 263..1498
OTHER INFORMATION:
                                    single
                 NUCLEIC ACID
                                                                                                                                                                                                                                                     OTHER INFORMATION:
                                                linear
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Best Local Similarity
Matches 339; Conserv
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                                                                                                                                                                                                                     NAME/KEY: CDS
                    TYPE: NUCLEIC
STRANDEDNESS:
                                                 TOPOLOGY: 11
MOLECULE TYPE:
                                                                                  HYPOTHETICAL:
ANTI-SENSE: N
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   LENGIH:
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TITLE OF INVENTION: TISSUE DERIVED TUMOR GROWTH INHIBITORS NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                   Indels
                 MOLECULE TYPE: CDNA to MRNA
IMMEDIATE SOURCE:
CLONE: E. coli LC137/ppLMu.hTGF-beta3 (DSM 5658)
                                                                               NAME/KEY: CDS
COCATION: 1..336
COPHER INFORMATION: /product= "human TGF-beta3"
S-09-123-233-5
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                                                                                                                                                                                  100.0%; Score 339; DB 3;
100.0%; Pred. No. 2.8e-87;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 1919/22669-F-PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)977-9550
TELEPHONE: (212)664-0525
TELEFAX: (212)664-0525
TELEX: 42253 GOOP UI
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PCT/US91/04541
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application PC/TUS9104541 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Cooper & Dunham
STREET: 30 Rockefeller Plaza
CITY: New York
STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 10112
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
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                                                                                                                                                                                 Query Match 100.
Best Local Similarity 100.
Matches 339; Conservative
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TOPOLOGY:
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PCT-US91-04541-1
                                                                   FEATURE
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/389,929
FILING DATE: 04-AUG-1989
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APPLICATION NUMBER: US/09/123,233
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 530
INFORMATION FOR SEQ ID NO: 7
SEQUENCE CHARACTERISTICS:
LENGTH: 336 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM:
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Best Local Similarity
Matches 316; Conserv
                                                                                      RESULT 8
5168051-9
; Patent No. 5168051
                                                                                                                                                                                                          LENGTH: 2671
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; Patent No. 5168051
; Patent No. 5168051
; TITLE OF INVENTION: NUCLEIC ACID ENCODING TGF-B ITS
; CURRENT APPLICATION DATA:
; CURRENT APPLICATION NUMBER: US/07/389,929
FILING DATE: 04-AUG-1989
                                                                                                                                                                                                                                                                                                                                                                                          Score 325.4; DB 6;
Pred. No. 3.5e-83;
0; Mismatches 1;
                                                                                               Score 339; DB 6;
Pred. No. 5.2e-87;
0; Mismatches 0;
FILING DATE: 07-APR-1986
APPLICATION NUMBER: 725,003
FILING DATE: 19-APR-1985
                                                                                               Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 339; Conservative 0
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99.4%;
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Best Local Similarity 99.4
Matches 337; Conservative
                                              LENGTH: 2529
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LENGTH: 2233
                                    ; SEQ ID NO:1:
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576 240 61 tacattgacttccgacaggatctgggctggaagtgggtccatgaacctaagggctactat 120 caggacctggagcccctgaccatcctgtactatgttgggaggacccccaaagtggagcag of 0; Length 2671; APPLICANT:
TITLE OF INVENTION: No. 6057430el process for the production
TITLE OF INVENTION: biologically active dimeric protein
NUMBER OF SEQUENCES: 14 USES Patentin Release #1.0, Version #1.30 (EPO) APPLICANT: DERYNCK, RIK M.A.;GOEDDEL, DAVID V. TITLE OF INVENTION: NUCLEIC ACID ENCODING TGF-B ITS NUMBER OF SEQUENCES: 21 DB 6; 615 1.3e-76; 89.1%; Score 302.2; 93.2%; Pred. No. 1.3e ive 0; Mismatches

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RESULT 11
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Patent No. 6057430
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: biologically active dimeric protein
NUMBER OF SEQUENCES: 14
COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                     /product= "hybrid TGF-beta named TGF-betal-3"
                                                                                    FEATURE: NAME/KEY: mat_peptide LOCATION: 1.132 LOCATION: 1.132 OTHER INFORMATION: /product= "N-terminal 44 amino OTHER INFORMATION: acids of human TGF-betal"
                                                          IMMEDIATE SOURCE:
CLONE: E. coli LC137/pPLMu.TGF-betal(44/45)beta3
                                                                                                                                                                                                                                                                                                                                                                    87.8%; Score 297.6; DB 3; 92.9%; Pred. No. 1.4e-75; ive 0; Mismatches 24;
            MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "recombinant hybrid DNA
DESCRIPTION: TGF-betal and TGF-beta3 DNA"
                                                                                                                                                                                                                /product= "C-terminal 68
                                                                                                                                                                                                                                acids of human TGF-beta3
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APPLICATION NUMBER: US/09/123,233
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                  Query Match 87.8
Best Local Similarity 92.9
Matches 312; Conservative
                                                                                                                                                                               NAME/KEY: mat_peptide
                                                                                                                                                                                                LOCATION: 133.336
OTHER INFORMATION:
OTHER INFORMATION:
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CTHER INFORMATION:
CTHER INFORMATION:
US-09-123-233-7
TOPOLOGY: linear
                                                                                                                                                                                                                                                            NAME/KEY: CDS
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es 37; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                      /product= "hybrid TGF-beta2-3"
                                                                   MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "recombinant hybrid DNA
DESCRIPTION: coding for hybrid TGF-beta2-3"
IMMEDIATE SOURCE:
CLONE: E. coli LC137/PPLMu.TGF-beta2(44/45)beta3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 276.8; DB 3;
Pred. No. 1.1e-69;
0; Mismatches 37;
                                                                                                                                                                                                       LOCATION: 1..132
OTHER INFORMATION: /product= "N-terminal 44
OTHER INFORMATION: acids of human TGF-beta2'
                                                                                                                                                                                                                                                                                                           /product= "C-terminal 68 acids of human TGF-beta3'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 11, Application US/09123233
Sequence 11, Application US/09123233
Sequence 11, Patent No. 6057430
Sequence 11
TITLE OF INVENTION: No. 6057430el proc;
TITLE OF INVENTION: biologically activ;
NUMBER OF SEQUENCES: 14
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ver;
CURRENT APPLICATION NUMBER: US/09/123,233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 89.0%;
Matches 299; Conservative
336 base pairs
                                                                                                                                                                                                                                                        FEATURE:
NAME/KEY: mat_peptide
                                                                                                                                                                                 NAME/KEY: mat_peptide
                  TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                          LOCATION: 133.336
OTHER INFORMATION:
OTHER INFORMATION:
FEATURE:
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                                                      linear
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LOCATION:
                                                      TOPOLOGY:
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11150 Santa Monica Boulevard, Suite 400
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                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Sharp, Janice A.
REGIGSTRATION NUMBER: 34,051
REFERENCE/CDCKET NUMBER: 3063
TELECOMMUNICATION INFORMATION:
TELEPHONE: 310-445-1140
TELEFAX: 310-445-9031
                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
SOFTWARE: PatentIn Release #
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Best Local Similarity 75.5%;
Matches 256; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 339 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 310-445-9031
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mat_peptide
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CLASSIFICATION: 424
                         CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: CDNA
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                                                    COUNTRY: USA
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US-08-470-837-29
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US-08-486-057B-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 70.8%; Score 240; DB 3; Length 336; Best Local Similarity 82.1%; Pred. No. 2.7e-59; Matches 276; Conservative 0; Mismatches 60; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    60; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        : Transforming Growth Factor B Fusion : and
                                                                                                                                                                                                                                             OTHER INFORMATION: /product= "N-terminal 44 amino OTHER INFORMATION: acids of human TGF-beta3"
                                                                                     TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "recombinant hybrid DNA
DESCRIPTION: ociding for hybrid TGF-beta3-2"
IMMEDIATE SOURCE:
CLONE: E. coli LC137/PPIMu.TGF-beta3(44/45)beta2
                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: 1..336
OTHER INFORMATION: /product- "hybrid TGF-beta3-2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Their Use in Wound Healing NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: /product= "C-terminal 68
OTHER INFORMATION: acids of human TGF-beta2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         301 ctctccaacatggtggtgaagtcttgtaaatgtagc 336
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 29, Application US/08470837
Patent No. 5800811
GENERAL INFORMATION:
APPLICANT: Nimni, Marcel E.
APPLICANT: Hall, Frederick L.
APPLICANT: Tuan, Tai-Lan
APPLICANT: Cheung, David T.
TITLE OF INVENTION: Transforming Gr
TITLE OF INVENTION: AND TITLE OF INVENTION: A THEIR OF INVENTION: Their Use in WO
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 336 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                              NAME/KEY: mat_peptide
LOCATION: 1..132
                                                                                                                                                                                                                                                                                                   NAME/KEY: mat_peptide
LOCATION: 133..336
                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY:
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                                                                                                                                                                                                                                                                                   FEATURE:
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241 caggacctggagcccttgaccatcctgtactatgttgggaggacccccaaagtggagcag 300
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,837
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Pred. No. 9.7e-50;
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181 gigcigggacigiacaacacicigaacccigaagcaicigccicgcciigcigcgigcc 240
                                                                                                               181 GTCCTGGCCCTGTACAACCAGCATAACCCGGCGCGCCTCGGCGCGCCGTGCTGCGGCG 240
                                                                                                                                                          241 caggacctggagccctgaccatcctgtactatgttgggaggaccccaaagtggagcag 300
                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Cerletti, Nico
APPLICANT: Cox, David
APPLICANT: Cox, David
APPLICANT: Cox, David
APPLICANT: Schmitz, Albert
APPLICANT: Meyhack, Bernd
TITLE OF INVENTION: Process for Refolding Recombinantly
TITLE OF INVENTION: Produced TGF-beta-like Proteins
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/789,588 FILING DATE:
                                                                                                                                                                                                                                                                       301 ctctccaacatggtggtgaagtcttgtaaatgtagctga 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3: Henry P. No. 5922846ak
520 White Plains Road, P.O. Box 2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4-17861/+/Cont3
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APPLICATION NUMBER: US 08/486,057
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/201,703
FILING DATE: 25-FEB-1994
APPLICATION DATA:
APPLICATION NUMBER: GB 8927546.5
FILING DATE: 06-DEC-1989
ATTORNEY/AGGNT INFORMATION:
NAMME: NO. 5922846ak, Henry P.
REGISTATION NUMBER: 33200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                          RESULT 14
US-08-789-588-1
; Sequence 1, Application US/08789588
; Patent No. 5922846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (908) 277-5110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (908) 277-4306
INFORMATION FOR SEQ ID NO: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 339 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: U.S.A.
ZIP: 10591-9005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 520 WILL
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                                                                             APPLICANT: Schmitz, Albert
APPLICANT: Meyhack, Bernd
TITLE OF INVENTION: Process for Refolding Recombinantly
TITLE OF INVENTION: Produced TGF-beta-like Proteins
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                      COUPUTRY: U.S.A.
ZIP: 10591-9005
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFWWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                       ADDRESSEE: Henry P. No. 5650494ak
STREET: 520 White Plains Road, P.O. Box 2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4-17861/+/Cont3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/486,057B FILING DATE: 07-JUN-1995 CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 03-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08 8927546.5
FILING DATE: 06-DEC-1989
ATTORNEY/AGENT INCPORATION:
NAME: NO. 5656494ak, Henry P.
REGISTRATION NUMBER: 33200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 07/960,309 FILING DATE: 13-OCT-1992 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/621,502 FILING DATE: 03-DEC-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/201,703
FILING DATE: 25-FPB-1994
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 4-17(
TELECOMUNICATION INCORMATION:
TELEPHONE: (908) 277-5110
TELEFAX: (908) 277-4306
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 339 base pairs
TYRE: nucleic acid
STRANDENESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: DNA (genomic)
                                             McMaster, Gary K.
                      Cerletti, Nico
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 60.4
Best Local Similarity 75.2
Matches 255; Conservative
                                      APPLICANT: MCMASter,
APPLICANT: COX, Davic
APPLICANT: Schmitz,
APPLICANT: Meyhack,
TITLE OF INVENTION: I
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                                                                                                                                                                                                                                                                CITY: Tarrytown
STATE: New York
GENERAL INFORMATION:
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LOCATION:
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US-08-486-057B-1
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AUDRESSEE: PENNIE & EDMONDS
STREET: 1155 AVENUE OF THE AMERICAS
CITY: NEW YORK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 1, Application US/07669171; Patent No. 5304541; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA (genomic)
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                                Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
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10036
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                 Best Local Similarity
Matches 255; Conserv
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MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 16
US-07-669-171-1
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    Query Match
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                                                                                                                                                                                                                                                                        61 TACATTGACTTCCGCAAGGACCTCGGCTGGAAGTGGATCCACGAGCGCCAAGGGCTACCAT 120
                                                                                                                                                                                                                                                                                                                  121 gecaacttetgeteaggecettgeceataceteegeagtgeagacacacacageaeg 180
                                                                                                                                                                                                                                                                                                                                     tacattgacttccgacaggatctgggctggaagtgggtccatgaacctaagggctactat 120
                                                                                                                                                                                                                                                                                                                                                                                                                                            caggacctggagccctgaccatcctgtactatgttgggaggacccccaaagtggagcag 300
                                                                                                                                                                                                              Gaps
                                                                                                                                                                                             1 gotttggacaccaattactgcttccgcaacttggaggagaactgctgtgtgcgcccctc 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        No. 6057430el process for the production of biologically active dimeric protein
                                                                                                                                                                    ;
;
                                                                                                                                   Length 339;
                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO) CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IMMEDIATE SOURCE:
CLONE: E. coli LC137/pPLMu.hTGF-betal (DSM 5656)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COCATION: 1..336
CTHER INFORMATION: /product- "human TGF-betal"
US-09-123-233-1
                                                                                                                                     DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     301 ctctccaacatggtggtgaagtcttgtaaatgtagctga 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 204.6; DB 2
Pred. No. 2.7e-49;
                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: No. 6057430el pi
TITLE OF INVENTION: biologically act
NUMBER OF SEQUENCES: 14
COMPUTER READBLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/09/123,233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1, Application US/09123233 Patent No. 6057430
                                                                                                                                     60.4%;
75.2%;
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 339 base pairs
TYPE: nucleic acid
                                                                                                                                            Best Local Similarity 75.2
Matches 255; Conservative
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APPLICANT:
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            NAME/KEY:
LOCATION:
FEATURE:
                                                                        ; LOCATION:
US-08-789-588-1
                                                           NAME/KEY:
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                                                                                                                                     Query Match
FEATURE:
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gccaacttctgctcaggcccttgcccatacctccgcagtgcagacacaacccacagcacg 180
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                                   Gaps
                                                                                        1 gctttggacaccaattactgcttccgcaacttggaggagaaactgctgtgtgcgcccctc 60
                                                                                                                                                                                                                                                                               APPLICANT: MADISEN, LINDA
APPLICANT: MADISEN, LINDA
APPLICANT: MENMIN, JUNB RAE
TITLE OF INVENTION: GROWTH FACTOR-BETA
NUMBER OF SEQUENCES:
ADDRESSE: PENNE & EDMONDS
STREET: 1155 AVENUE OF THE AMERICAS
Length 339;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                            60.4%; Score 204.6; DB 3 75.2%; Pred. No. 2.7e-49;
                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY AGENT INFORMATION:
NAME: MISROCK, S. LESLIE
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 5624-159-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
TELEFAX: 212-869-9741
TELES. 66141 PENNIE
INFORMATION FOR SEQ ID NO: 1:
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                                                                     Gaps
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                                             Length 1560;
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Pred. No. 5e-49;
0; Mismatches 84; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                      RESULT 17
5168051-1
; PATENT NO. 5168051
; PATENT NO. 5168051
; TITLE OF INVENTION: NUCLEIC ACID ENCODING TGF-B ITS USES
NUMBER OF SEQUENCES: 21
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/389,929
; FILING DATE: 04-AUG-1989
                                                                     Indels
                                                                     84;
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                                           Score 204.6; DB Pred. No. 4.3e-49
                                    60.4%; Sco...
75.2%; Pred. No. 4...
0; Mismatches
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Best Local Similarity 75.2%;
Matches 255; Conservative (
                                                                 Matches 255; Conservative
261..1430
                                                       Local Similarity
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; LOCATION:
US-07-669-171-1
                                             Query Match
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1976 ctgtccaacatgatcgtgcgctcctgcaagtgcagctga 2014
                                                                                                                                       APPLICANT: Mu-En Lee
APPLICANT: Mark A. Perrella
TITLE OF INVENTION: FACTOR- INHIBITS
TITLE OF INVENTION: INDUCTBLE NITRIC OXIDE
TITLE OF INVENTION: SYNTHASE GENE
TITLE OF INVENTION: SYNTHASE GENE
TITLE OF INVENTION: TRANSCRIPTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Janis K. Fraser
REGISTRATION NUMBER: Reg. NO. 34,819
REFERENCE/DOCKET NUMBER: 05433/007001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
RITTLE APPLICATION NUMBER: PCT/HSQ4/N1710F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 5 April 1994
CLASSIFICATION:
PRIOR APPLICATION DATA:
PILLING DATE:
FILLING DATE:
                                                                                                   Sequence 3, Application PC/TUS9403705 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                             Richardson
                                                                                                                                                                                                                                                                                                                          E: Fish & Richardso
225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 75.2
Matches 255; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEX: 200154
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
LENGTH: 2745
                                                                                                                                                                                                                                                                                                                                                                                          Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Di
                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: doub
                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                     Boston
                                                                                                                                                                                                                                                                                                                               ADDRESSEE:
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CURRENT APPLICATION DATA:
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Best Local Similarity 71.1
Matches 241; Conservative
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tarrytown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: 11
MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY:
                                                                                                                                                         RESULT 20
US-08-486-057B-2
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US-08-486-057B-2
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1919 CAGGCGCTGGAGCCGCTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAG 1978
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                                                                                                                                                                                                                                                            APPLICANT: MERMIN, JUNE RAE
TITLE OF INVENTION: TGF-b1/b2: A NOVEL CHIMERIC TRANSFORMING
TITLE OF INVENTION: GROWTH FACTOR-BETA
UNMBER OF SEQUENCES: 3
CORRESPONDENCE ADMINESS:
ADDRESSEE: PENNIE & EDMONDS
STREET: 1155 AVENUE OF THE AMERICAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 1569;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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                                                          DB 1;
                                    301 ctctccaacatggtggtgaagtcttgtaaatgtagctga 339
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Pred. No. 7.9e-47
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/07/669,171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PC-DOS/MS-DOS
                                                                                                                                                                 Sequence 3, Application US/07669171
Patent No. 5304541
GENERAL INFORMATION:
APPLICANT: PURCHIO, ANTHONY F.
APPLICANT: MADISEN, LINDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE:
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18,872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 56
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; MOLECULE TYPE: DNA (genomic) US-07-669-171-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 212-869-9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 3:
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73.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MISROCK, S. LESLIE
REGISTRATION NUMBER: 18,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1569 base pairs
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STRANDEDNESS: single
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Best Local Similarity
Matches 250; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: U.S.A. ZIP: 10036
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                                                                                                                                                 US-07-669-171-3
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                                                                                                                                                                                                                                                                                                                                                                                                      Process for Refolding Recombinantly
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                                                                                                                                                                                                                                                                                                                                                                                                                             Produced TGF-beta-like Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                            DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E: Henry P. No. 5650494ak
520 White Plains Road, P.O. Box 2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            53.7%; Score 182.2; DB 1
71.1%; Pred. No. 5.9e-43;
iive 0; Mismatches 98
                                                                301 ctctccaacatggtggtgaagtcttgtaaatgtagctga
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TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/486,057B FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/201,703
FILING DATE: 25-FEB-1994
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/621,502
FILING DATE: 03-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 8927546.5
FILING DATE: 06-DEC-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 07/960,309 FILING DATE: 13-OCT-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                      Sequence 2, Application US/08486057B
Patent No. 5650494
GENERAL INFORMATION:
APPLICANT: Cerletti, Nico
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: NO. 5650494ak, Henry P. REGISTRATION NUMBER: 33200
                                                                                                                                                                                                                                                                                                              APPLICANT: McMaster, Gary K. APPLICANT: Cox, David APPLICANT: Schmitz, Albert APPLICANT: Meyhack, Bernd TITLE OF INVENTION: Process TITLE OF INVENTION: Produced
                                                                                                                                                                                                                                                                                                                   Gary K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA (genomic)
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TELEFAX: (908) 277-4306
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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GCTTTGGATGCGGCCTATTGCTTTAGAAATGTGCAGGATAATTGCTGCCTACGTCCACTT
                                                          tacattgacttccgacaggatctgggctggaagtgggtccatgaacctaagggctactat
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                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 31, Application US/08470837

Sequence 31, Application US/08470837

Patent No. 5800811

GENERAL INFORMATION:
APPLICANT: Nimni, Marcel E.
APPLICANT: Tuan, Tai-Lan
APPLICANT: Tuan, Tai-Lan
APPLICANT: Cheung, David T.
TITLE OF INVENTION: Transforming Growth Factor B Fusion
TITLE OF INVENTION: Their Use in Wound Healing
TITLE OF INVENTION: Their Use in Wound Healing
MUMBER OF SEQUENCES: 34

CORRESPONDENCE ADDRESS:
ADDRESSEE: Merchant & Gould
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E: Merchant & Gould
11150 Santa Monica Boulevard, Suite 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                      301 ctctccaacatggtggtgaagtcttgtaaatgtagctga 339
                                                                                                                                                                                                                                                                                                                         30630-1US01
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Sharp, Janice A.
REGISTRATION NUMBER: 34,051
REFERENCE/POCKET UNMBER: 3663
TELECOMMUNICATION INFORMATION:
TELEPHONE: 310-445-1140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 90025-3395
COMPUTER READABLE FORM:
MEDUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 339 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 310-445-9031
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: CDNA
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LOCATION:
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                                                                                                    DB 1; Length 339;
                                                                                                Score 182.2; DB 1; Length
Pred. No. 5.9e-43;
0; Mismatches 98; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2, Application US/08789588
Patent No. 5922846
GENERAL INFORMATION:
APPLICANT: Corletti, Nico
APPLICANT: Cox, David
APPLICANT: Schmitz, Albert
APPLICANT: Schmitz, Albert
APPLICANT: Meyhack, Bernd
TITLE OF INVENTION: Process for Refolding Recombinantly
TITLE OF INVENTION: Produced TGF-beta-like Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/789,588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  301 ctctccaacatggtggtgaagtcttgtaaatgtagctga 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AUDRESSEE: Henry P. No. 5922846ak
STRRET: 520 White Plains Road, P.O. Box 2005
CITY: Tarrytown
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/486,057
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/201,703
FILING DATE: 25-FEB-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/960,309
FILING DATE: 13-0CT-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/621,502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MBER: US 08/201,703
25-FEB-1994
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                  53.78;
71.18;
                                                                                                  Query Match 53.7
Best Local Similarity 71.1
Matches 241; Conservative
mat_peptide
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ZIP: 10591-9005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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; NAME/KEY:
; LOCATION:
US-08-470-837-31
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339 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 339;
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/123,233
FILING DATE: 03-DEC-15>C
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 8927546.5
FILING DATE: 06-DEC-1989
ATTORNEY/AGENT INFORMATION:
NAME: NO. 5922846ak, Henry P.
REGIESTRATION NUMBER: 33200
REFERENCE/DOCKET NUMBER: 4-17861/+/Cont3
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 277-5110
TELEFAX: (908) 277-5110
TELEFAX: (908) 277-5110
TELEFAX: (908) 277-5110
TELEFAX: (308) 277-5110
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Pred. No. 5.9e-43;
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Patent No. 6057430
GENERAL INFORMATION:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 530
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 53.7%;
Best Local Similarity 71.1%;
Matches 241; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                       ; NAME/KEY:
; LOCATION:
US-08-789-588-2
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61 tacattgacttccgacaggatctgggctggaagtgggtccatgaacctaagggctactat 120
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                                                                                                                                                                                                                                                                       Length 339;
                                                                                                                                                                                                                                                                                                                   Indels
                                                         MOLECULE TYPE: CDNA to mRNA
IMMEDIATE SOURCE:
CLONE: E. COLI LC137/PPLMu.hTGF-beta2 (DSM5657)
FEATURE:
                                                                                                                                                                                                                                                                         DB 3;
                                                                                                                                                                LOCATION: 1..336
OTHER INFORMATION: /product= "human TGF-beta2"
                                                                                                                                                                                                                                                                       Query Match 53.7%; Score 182.2; DB 3; Best Local Similarity 71.1%; Pred. No. 5.9e-43; Matches 241; Conservative 0; Mismatches 98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          301 CTTTCTAATATGATTGTAAAGTCTTGCAAATGCAGCTAA 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Mu-En Lee
APPLICANT: Mark A. Perrella
TITLE OF INVENTION: TRANSFORMING GROWTH
TITLE OF INVENTION: FACTOR- INHIBITS
TITLE OF INVENTION: SYNTHASE GENE
TITLE OF INVENTION: TRANSCRIPTION
NUMBER OF INVENTION: TRANSCRIPTION
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 558X
OPENATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 5 April 1994
CLASSFFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 4, Application PC/TUS9403705 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Fish & Richardson STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
nucleic acid
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                                         linear
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ZIP: 02110-2804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Boston
STATE: Massac
               STRANDEDNESS:
                                                                                                                                              NAME/KEY:
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PCT-US94-03705-4
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Conservative
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  241;
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5221620-3
    Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: PURCHIO, ANTHONY F.; MADISEN, LINDA; WEBB, NANCY TITLE OF INVENTION: CLONING AND EXPRESSION OF TRANSFORMING
                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                            98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 6;
                                                                                                                                                                                                                                                   DB 5;
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Pred. No. 1.1e-42;
                                                                                                                                                                                                                                                53.7%; Score 182.2; DB 571.1%; Pred. No. 9.6e-43; Live 0; Mismatches 98
                   NAME: Janis K. Fraser
REGISTRATION NUMBER: Reg. No. 34,819
REFERENCE/DOCKET NUMBER: 05433/007001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/446,020
FILING DATE: 05-DEC-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 285,140
FILING DATE: 16-DEC-1988
APPLICATION NUMBER: 234,065
FILING DATE: 18-AUG-1988
APPLICATION NUMBER: 234,065
FILING DATE: 25-AM-1988
APPLICATION NUMBER: 116,267
FILING DATE: 25-AM-1988
APPLICATION NUMBER: 106,752
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71.1%;
FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                      TELEX: 200154
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                             Best Local Similarity 71.1
Matches 241; Conservative
                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GROWTH FACTOR BETA-2
NUMBER OF SEQUENCES: 16
                                                                                                                                                                                           linear
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Best Local Similarity
                                                                                                                                               LENGTH: 1695
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;Patent No. 5221620
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LENGTH: 2569
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; Patent Po. 5221620
; APPLICANT: PURCHIO, ANTHONY F.; MADISEN, LINDA; WEBB, NANCY
; TITLE OF INVENTION: CLONING AND EXPRESSION OF TRANSFORMING
   Indels
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 98;
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 Mismatches
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FILING DATE: 05-DEC-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 285,140
FILING DATE: 16-DEC-1988
APPLICATION NUMBER: 234,065
FILING DATE: 18-AUG-1988
APPLICATION NUMBER: 148,267
FILING DATE: 25-JAN-1988
APPLICATION NUMBER: 106,752
FILING DATE: 06-OCT-1987
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CURRENT APPLICATION DATA:
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Matches 240; Conservative
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Best Local Similarity 51.9
Matches 179; Conservative
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250..666
             NUCLEIC ACID
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POSITION IN GENOME:
                                                                                 HYPOTHETICAL: NO FRAGMENT TYPE: C-ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                       mRNA
                    TYPE: NUCLEIC STRANDEDNESS:
                                                                                                                                   ORGANISM: BC
TISSUE TYPE:
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5187076-3
;Patent No. 5187076
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FEATURE:
NAME/KEY:
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LOCATION:
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FEATURE:
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US-07-764-731B-3
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                                                                                                      FESULT 27
5168051-3
5168051-3
; Patent No. 5168051
; APPLICANT: DERYNCK, RIK M.A.; GOEDDEL, DAVID V.
; APPLICANT: DIVENTION: NUCLEIC ACID ENCODING TGF-B ITS USES; UMMBER OF SEQUENCES: 21
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/389,929
; FILING DATE: 04-AUG-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Rosen, Vicki A.
APPLICANT: Wang, Elizabeth A.
APPLICANT: Warney, John M.
TITLE OF INVENTION: Methods for Producing BMP-7 Proteins NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSE: Legal Affairs, Genetics Institute, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        141 ttgcccatacctccgcagtgcagacacaacccacagcacggtgc 184
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/764,731B
                             GI5159B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Kapinos, Ellen J.
REGISTRATION NUMBER: 32,245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: GI:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-876-1170
TELEFAX: 617-876-5851
                                                                                                                                                                                                                                                                                                                                                  Query Match 28.1%;
Best Local Similarity 73.8%;
Matches 121; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                USA
                                                                                                                                                                                                                                                                ; SEQ ID NO:3;
; LENGTH: 975
5168051-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 894;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 54.6; DB 1; Length 8' Pred. No. 9.1e-07; 0; Mismatches 154; Indels
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APPLICATION NUMBER: US/07/490,033
FILING DATE: 07-MAR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 370,544
FILING DATE: 23-JUN-1989
APPLICATION NUMBER: 347,559
FILING DATE: 04-MAY-1989
APPLICATION NUMBER: 329,610
FILING DATE: 28-MAR-1989
                                                                                                                                                                             IMMEDIATE SOURCE:
LIBRARY: Bovine bone cDNA library
                                                                                                                             Bos taurus
3: Fetal long bone
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51.9%;
TOPOLOGY: circular MOLECULE TYPE: CDNA to mRNA
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COUNTRY:
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US-08-795-671-3
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                                                                                                                                                                                                                                                                                                                                           Length 894;
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Patent No. 5914234
GENERAL INFORMATION:
APPLICANT: LEE, SE-JIN
APPLICANT: LEE, SE-JIN
APPLICANT: MCPHERRON, ALEXANDRA C.
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-11
NUMBER OF SEQUENCES: 9
CORRESPONDENE: 9
CORRESPONDENE: SPENSLEY HORN JUBAS & LUBITZ
STREET: 1880 CENTURY PARK EAST, FIFTH FLOOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PatentIn Release #1.0, Version #1.25
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JHESSEE: SPENSLEY HORN JUBAS & LUBITZ
TET: 1880 CENTURY PARK EAST, FIFTH FLOOR
"E: CALIFORNIA
TRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/765,875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 90067
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
            FILING DATE: 08-APR-1988
APPLICATION UNDBER: 179,101
FILING DATE: 08-APR-1988
APPLICATION NUMBER: 179,197
FILING DATE: 08-ARR-1988
APPLICATION NUMBER: 28,285
FILING DATE: 20-MAR-1987
APPLICATION NUMBER: 31,346
FILING DATE: 26-MAR-1987
APPLICATION NUMBER: 943,322
FILING DATE: 17-DEC-1986
                                                                                                                                                                                                             APPLICATION NUMBER: 880,776
FILING DATE: 01-JUL-1986
APPLICATION NUMBER: 179,100
                                                                                                                                                                                                                                                                                                                                                         51.9%;
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                                                                                                                                                                                                                                                                  LENGTH: 894
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Best Local 3
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gcccttgcccatacctccgcagtgcagacacaccacagcacggtgctgggactgtaca 196
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/795,671
FILING DATE: February 6, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 52.8; DB 2;
Pred. No. 2.6e-06;
0; Mismatches 82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Se-Jin Lee and Alexandra McPherron
TITLE OF INVENTON: GROWTH DIFFERENTIATION FA
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
APPLICATION NUMBER: US/08/706,958
                                          US/08/272,763
                                                               FILING DATE: 08-JUL-1994
ATTORDEY/AGENT INFORMATION
NAME: TUMARKIN PH.D. LISA A.
REGISTRATION NUMBER: P-38,347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 3, Application US/08795671 Patent No. 6008434
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
                                                                                                                                                  REFERENCE/DOCKET NUMBER: PD
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/455-5100
TELEFAX: 619/455-5110
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: DNA (genomic)
IMMEDIATE SOURCE:
CLONE: MOUSE GDF-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15.6%;
55.4%;
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                                                                                                                                                                                                                                                                                   LENGTH: 630 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 15.6
Best Local Similarity 55.4
Matches 102; Conservative
                                             APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 4225 ExecucITY: La Jolla STATE: California
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TOPOLOGY: lir
                        FILING DATE:
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US-08-765-875-3
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Sequence 1, Application US/08452772 Patent No. 5700911 GENERAL INFORMATION:
                                                                                                                       DNA (genomic)
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54.9%;
                                                                                                                                                                       STRAIN: Bovine Activin WC
                                                                                                                                                                                                                             FEATURE:
NAME/KEY: misc_feature
                    INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 789 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 54.9
Matches 129; Conservative
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375..701
        617 876-5851
                                                                                                                                                      Bos Taurus
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324..704
                                                                                                                                                                                                                                                                    LOCATION: 322. 323
OTHER INFORMATION:
                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: DNA
ORIGINAL SOURCE:
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STATE: MA
COUNTRY: USA
.rp. 02140
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LOCATION:
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LOCATION:
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US-08-452-772-1
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFWWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
NAME: HAILE, PH.D., LISA A.
REGISTRATION NUMBER: 38.347
REFERENCETORET NUMBER: 07265/106001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5099
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 630 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/08247907A
Patent No. 5639638
GENERAL INFORMATION:
APPLICANT: WOZNEY, John
APPLICANT: CELESTE, Anthony J
TILLE OF INVENTION: BMP-11 COMPOSITIONS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: GENETICS INSTITUTE, INC. STREET: 87 CambridgePark Drive CITY: Cambridge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/247,907A FILING DATE: May 20, 1994 CLASSIFICATION: 435
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NAME: LAZAR, Steven R.
REGISTRATION NUMBER: 32,618
REFERENCE/DOCKET NUMBER: G152
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617 876-1170
                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 55.4 Matches 102; Conservative
                                                                                                                                                                                                                                    CLONE: MOUSE GDF-11
                                                                                                                                                                                                                                                                 ; NAME/KEY: CDS
; LOCATION: 198..575
US-08-795-671-3
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97 giccaigaacciaagggciaciaigccaacticigcicaggcccitgcccaiacciccgc 156
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                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     217 tctgcctcgccttgctgcgtgccccaggacctggagcccctgaccatcctgtact 271
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/note= "putative 3' end of intron"
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APPLICATION NUMBER: US/08/452,772
FILING DATE: 30-MAY-1995
                                                                                                                                                                               Score 51.8; DB 1;
Pred. No. 5.4e-06;
0; Mismatches 97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: WOZNEY, John
APPLICANT: CELESTE, Anthony J.
TITLE OF INVENTION: BMP-11 COMPOSITIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: BMP-11 COMPOSITIC
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENETICS INSTITUTE, INC.
STREET: 87 CambridgePark Drive
CITY: Cambridge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION: 30-MAY-122.
FILLING DATE: 30-MAY-122.
CLASSIFICATION: 530
PRIOR APPLICATION NUMBER: US 08/247,907
APPLICATION NUMBER: US 08/247,907
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPATING SYSTEM: PC-POS/MS-POS
OPERATING SYSTEM:
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Gaps

6

97; Indels

Length 789;

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97 giccaigaacciaagggciactaigccaacticigcicaggccciigcccaiacciccgc 156
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                                                                                                                                                                     NAME/KEY: misc_feature
LOCATION: 322..323
OTHER INFORMATION: /note= "putative 3' end of intron"
                                                                                                                                                                                                                                                                                                                                                            Score 51.8; DB 5;
Pred. No. 5.4e-06;
                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
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STREET: 53 STATE STREET
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ver
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/841,646
FILING DATE: 19920221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 33, Application US/07841646
Patent No. 5266683
GENERAL INFORMATION:
APPLICANT: OPPERMANN, HERNANN
APPLICANT: OZKAYNAK, ENGIN
APPLICANT: KUBERASAMPATH, THANGAVEL
APPLICANT: KUBERASAMPATH, THANGAVEL
APPLICANT: PANG, ROY H.L.
TITLE OF INVENTION: OSTEOGENIC DEVICES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 20-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 827,052
FILING DATE: 28-JAN-1992
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 810,560
FILING DATE: 20-DEC-1991
        DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                              15.3%;
54.9%;
                                                                    STRAIN: Bovine Activin WC
                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 54.9 Matches 129; Conservative
                                                                                                                                                                                                                                                       ) NAME/KEY: mat_peptide
) LOCATION: 375..701
PCT-US94-05288-1
                                               Bos Taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: BOSTON
STATE: MASSACHUSETTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS
                                                                                                             CDS
324..704
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    MOLECULE TYPE: I
ORIGINAL SOURCE:
                                                                                                           NAME/KEY:
LOCATION:
                                               ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 35
US-07-841-646-33
                                                                                                                                                      FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       157 agtgcagacacaacccacagcacggtgctgggactgtacaacactctgaacctgaagca 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            528 ATGCAAAAGTATCCGCACACCCTTGGTGCAACAGGCT------AACCCAAGAGGC 578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                37 gagaactgctgtgtgcgcccctctacattgacttccgacaggatctgggctggaagtgg 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   217 tetgcetegcettgetgegtgeeceaggacetggagecetgaceatectgtact 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 789;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: 322..323
OTHER INFORMATION: /note= "putative 3' end of intron"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO) CURRENT APPLICATION DATA: APPLICATION NUMBER: PCT/US94/05288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15.3%; Score 51.8; DB 1; 54.9%; Pred. No. 5.4e-06; tive 0; Mismatches 97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
TITLE OF INVENTION: BMP-11 COMPOSITIONS
UNMBER OF SEQUENCES: 11
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-CDOS/MSO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application PC/TUS9405288 GENERAL INFORMATION:
            NAME: LAZAR, Steven R.
REGISTRATION NUMBER: 32,618
REFERENCE/DOCKET NUMBER: GIS,
TELECOMMUNICATION INFORMATION:
TELEFHONE: 617 876-1170
TELEFHONE: 617 876-1851
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 789 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                           32,618
                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                      STRAIN: Bovine Activin WC
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 789 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
NAME/KEY: misc_feature
LOCATION: 322..323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 54.9
Matches 129; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mat_peptide 375..701
                                                                                                                                                                                                                                                                                                                   Bos Taurus
                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: CDS
LOCATION: 324..704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; NAME/KEY:
; LOCATION:
US-08-452-772-1
                                                                                                                                                                                                                                                                                                                 ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 34
PCT-US94-05288-1
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a ò Version #1.25

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166 acaacccacagcacggtgctgggactgtacaacactctgaaccctgaagcatctgcctcg 225
                                                    133 ACCAACCACGCCGTGGTGCAGACCTGGAACAACATGAACCCCGGCAAGGTACCCAAG 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy also COMPUTER: Floppy also COMPUTER: IEBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/147,023 FLING DATE: 21-FEB-1992
CLASSIFICATION 530
PRIOR APPLICATION DATA: APPLICATION NUMBER: US 810,560
FLING DATE: 20-DEC-1991
PRIOR APPLICATION DATA: APPLICATION NUMBER: US 660,162
FILING DATE: 28-JAN-1992
PRIOR APPLICATION DATA: US 621,988
FILING DATE: 22-FEB-1991
PRIOR APPLICATION NUMBER: US 621,849
FILING DATE: 04-DEC-1990
PRIOR APPLICATION NUMBER: US 616,374
APPLICATION NUMBER: US 616,374
FILING DATE: 21-NOV-1990
PRIOR APPLICATION DATA: APPLICATION NUMBER: US 616,374
FILING DATE: 21-NOV-1990
PRIOR APPLICATION DATA: APPLICATION NUMBER: US 616,374
FILING DATE: 21-NOV-1990
PRIOR APPLICATION NUMBER: US 616,374
FILING DATE: 21-NOV-1990
PRIOR APPLICATION NUMBER: US 610,024
FILING DATE: 21-NOV-1990
PRIOR APPLICATION NUMBER: US 610,024
FILING DATE: 21-NOV-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: OPPERANN, HERMANN
APPLICANT: OZKATNAK, ENGIN
APPLICANT: OZKATNAK, ENGIN
APPLICANT: RUBERSAMPATH, THANGAVEL
APPLICANT: RUGGER, DAVID C.
APPLICANT: PANG, ROY H.L.
TITLE OF INVENTION: OSTEOGENIC DEVICES
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: TESTA, HURMITZ & THIBEAULT
STREET: 53 STATE STREET
                                                                                                                                                                                                            286 cccaaagtggagcagctctccaacatggtg 315
                                                                                                                                                                                                                                                              253 ACCGTGGTGCTGAAGAACTACCAGGAGATG 282
                                                                                                                                                                                                                                                                                                                                                                                        Sequence 33, Application US/08147023 Patent No. 5468845 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 599,543
FILING DATE: 18-0CT-1990
PRIOR APPLICATION DATA: APPLICATION NUMBER: US 579,865
FILING DATE: 07-SEP-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 56
FILING DATE: 20-AUG-1990
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 53 STATE STREE CITY: BOSTON STATE: MASSACHUSETTS COUNTRY: U.S.A. ZIP: 02109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 15.2%; Score 51.6; DB 1; Length 314;
Best Local Similarity 55.2%; Pred. No. 4.7e-06;
Matches 149; Conservative 0; Mismatches 109; Indels 12; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13 CTGTACGTGGACTTCCAGCGCGACGTGGGACGACTGGATCATCGCCCCCGTCGAC 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : NAME/KEY: misc_feature
: LOCATION: 1..314
: OTHER INFORMATION: /note= "CONSENSUS PROBE"
US-07-841-646-33
                                                                                                                                                                                                                                                                                                                                             PRIOR DATE: 18-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 599,543
FILING DATE: 18-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 579,865
FILING DATE: 07-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 569,920
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 569,920
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 483,913
FILING DATE: 22-FEB-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 422,613
FILING DATE: 17-0CT-1989
FILING DATE: 17-0CT-1989
FILING DATE: 3315,342
FILING DATE: 23-FEB-1989
FILING DATE: 23-FEB-1989
FILING DATE: 15-AUG-1988
FILING DATE: 15-AUG-1988
FILING DATE: 15-AUG-1988
FILING DATE: 16-AUG-1988
FILING DATE: 16-AUG-1988
FILING DATE: 18-AUG-1988
FILING DATE: 18-AUG-1988
FILING DATE: 08-APR-1988
ATTORNEY/AGGNTT INFORMATION:
                                                                                          FILING DATE: 04-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 621,849
FILING DATE: 04-DEC-1990
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                      APPLICATION NUMBER: US 616,374
FILING DATE: 21-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 600,024
FILING DATE: 18-OCT-1990
US 660,162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: PITCHER, EDMUND R.
REGISTRATION NUMBER: 27,829
REFRENCE/DOCKET NUMBER: CRP-
TELECOMMUNICATION INFORMATION:
TELEPAN: 617/248-7000
INFORMATION FOR SEQ. ID NO: 33:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27,829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: YES
ANTI-SENSE: NO
                          22-FEB-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          314 base pairs
                     FILING DATE: 22-FEB-:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: NUCLEIC ACID
STRANDEDNESS: single
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
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US 483,913

APPLICATION NUMBER:

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OURTHAING STSTEM: PC-UOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/447,570
FILING DATE: 21-FEB-1992
CLASSITCATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 810,560
FILING DATE: 20-DEC-1991
APPLICATION NUMBER: US 827,052
FILING DATE: 20-DEC-1991
APPLICATION NUMBER: US 60,162
FILING DATE: 22-FEB-1991
APPLICATION NUMBER: US 60,162
FILING DATE: 22-FEB-1991
APPLICATION NUMBER: US 621,988
FILING DATE: 04-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 621,849
FILING DATE: 12-FEB-1991
PRIOR APPLICATION NUMBER: US 616,374
FILING DATE: 12-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 616,374
FILING DATE: 11-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 600,024
FILING DATE: 18-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 599,543
FILING DATE: 18-OCT-1990
PRIOR APPLICATION NUMBER: US 599,543
FILING DATE: 18-OCT-1990
PRIOR APPLICATION NUMBER: US 579,865
                                  ADDRESSEE: TESTA, HURWITZ & THIBEAULT STREET: 53 STATE STREET
                                                                                                       STATE: MASSACHUSETTS
COUNTRY: U.S.A.
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 422,613
FILING DATE: 17-0C1-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 315,342
FILING DATE: 23-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 232,630
FILING DATE: 15-AUG-1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICALOR ONTE: 07-SEP-1000
FILING DATE: 07-SEP-1000
PRIOR APPLICATION NUMBER: US 569,920
TOTAL NATE: 20-AUG-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 20-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 483,913
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 179,460 FILING DATE: 08-APR-1988 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: PITCHER, EDMUND R. REGISTRATION NUMBER: 27,829 REFERENCE/DOCKET NUMBER: CRITELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 617/248-7100
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 314 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 15-AUG-: PRIOR APPLICATION DATA:
          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nucleic acid
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STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          73 TICGACGCCTACTACTGCTCCGGAGCCTGCCAGTTCCCCTCTGCGGATCACTTCAACAGC 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               166 acaacccacagcacggtgctgggactgtacaacatttgaaccctgaagcatctgcctcg 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              133 ACCAACCACGCCGTGGTGCAGACCCTGGTGAACAACATGAACCCCGGCAAGGTACCCAAG 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ccttgctgctgccccaggacctggagccctgaccatcctgtactatgttgggaggacc 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             193 cecrecrecereceacererececareaceareacarecreraceresaceasaarree 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13 CTGTACGTGGACTTCCAGCGCGACGACGACGACGACGATCATCGCCCCCGTCGAC 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 314;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 15.2%; Score 51.6; DB 1; Length 3 Best Local Similarity 55.2%; Pred. No. 4.7e-06; Matches 149; Conservative 0; Mismatches 109; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ) NAME/KEY: misc_feature

) LOCATION: 1..314

); OTHER INFORMATION: /note= "CONSENSUS PROBE"

US-08-147-023-33
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: OPPERMANN, HERMANN
PAPLICANT: OZKAYNAK, ENGIN
APPLICANT: OZKAYNAK, ENGIN
APPLICANT: RUBERASAMPATH, THANGAVEL
APPLICANT: RUBGER, DAVID C.
APPLICANT: PANG, ROY H.L.
TITLE OF INVENTION: OSTEOGENIC DEVICES
NUMBER OF SEQUENCES: 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    253 ACCGTGGTGCTGAAGAACTACCAGGAGATG 282
                                                                                                                                                                                                                                                                                                                                                                                                                    CRP-001CP6
                                                                                         PELLING DATA: 17, CLT 1289
PELLING DATA: 17, CLT 1289
FILING DATE: 23-FEB-1989
FILING DATE: 32-FEB-1989
FILING DATE: 15-AUG-1988
FILING DATE: 15-AUG-1988
FILING DATE: 15-AUG-1988
ATDORNEY/AGENT INFORMATION:
NAME: PITCHEN, EDMUND.:
REGISTRATION NUMBER: 27, 829
RECISTRATION NUMBER: 27, 829
RECISTRATION NUMBER: 27, 829
RECISTRATION NUMBER: 27, 829
TELEPHONE: 617/248-7000
                                    17-OCT-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 33, Application US/08447570 Patent No. 5714589 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 314 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: YES
22-FEB-1990
                                                  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ANTI-SENSE: NO FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-447-570-33
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APPLICATION NUMBER: US 62 FILING DATE: 04-DEC-1990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  58 ctctacattgacttccgacaggatctgggctgg---aagtgggtccatgaacctaagggc 114
                                                                                                                                                                                                                                                                                                                                                                                                                                          73 ITCGACGCCTACTACTGCTCCGGAGCCTGCCAGTTCCCCTCTGCGGATCACTTCAACAGC 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         133 ACCAACCACGCCGTGGTGCAGACCCTGGTGAACAACATGAACCCCGGCAAGGTACCCAAG 192
                                                                                                                                                                                                                                                                                                                                                         13 CTGTACGTGGACTTCCAGCGGGACGTGGGACGACGACTGGATCATCGCCCCCGTCGAC 72
                                                                                                                                                                                                                                                                           12;
                                                                                                                                                                                                                                     Length 314;
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                              Score 51.6; DB 1;
Pred. No. 4.7e-06;
0; Mismatches 109;
                                                                                                             | LOCATION: 1..314
| OTHER INFORMATION: /note= "CONSENSUS PROBE"
US-08-447-570-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INCORNATION:

APPLICANT: OPPERMANN, HERMANN
APPLICANT: OPFERMANN, HERMANN
APPLICANT: OFFERASAMPATH, THANGAVEL
APPLICANT: RUBERASAMPATH, THANGAVEL
APPLICANT: RUBERASAMPATH, THANGAVEL
APPLICANT: RUBERASAMPATH, THANGAVEL
APPLICANT: PANG, ROY H.L.
TITLE OF INVENTION: OSTEOGENIC DEVICES
INVENER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: TESTA, HURWITZ & THIBEAULT
STREET: 53 STATE STREET
CITY: BOSTON
CITY: BOSTON
CITY: MASSACHUSETTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   286 cccaaagtggagcagctctccaacatggtg 315
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PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 827,052
FILING DATE: 28-JAN-1992
PRIOR APPLICATION NUMBER: US 660,162
FILING DATE: 22-FEB-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 810,560
FILING DATE: 20-DEC-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 33, Application US/08449700 Patent No. 5863758
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: YES
ANTI-SENSE: NO
                                                                                                                                                                                                                              Query Match
Best Local Similarity 55.2%;
Matches 149; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08
FILING DATE: 21-FEB-1992
                                                                                                  misc_feature
1..314
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                                                                                                      NAME/KEY:
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US-08-449-700-33
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58 ctctacattgacttccgacaggatctgggctgg---aagtgggtccatgaacctaagggc 114 Gaps 13 CIGIACGIGGACTICCAGCGCGACGIGGGCTGGGACGACIGGATCATCGCCCCCGTCGAC 72 166 acaacccacagcacggtgctgggactgtacaacactctgaaccctgaagcatctgcctcg 12; Length 314; Score 51.6; DB 2; Length 31 Pred. No. 4.7e-06; 0; Mismatches 109; Indels NAME/KEY: misc\_feature
LOCATION: 1..314
CTHER INFORMATION: /note= "CONSENSUS PROBE"
US-08-449-700-33 NAME: PITCHER, EDMUND R.
REGISTRATION NUMBER: 27 829
REFERENCE/DOCKET NUMBER: CRP-001CP6
TELECOMMUNICATION INFORMATION: PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 315,342
FILING DATE: 23-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 232,630
FILING DATE: 15-AUG-1988
PRIOR APPLICATION NUMBER: US 212,630
PRIOR APPLICATION DATA: PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 621,849
FILING DATE: 04-DEC-1990 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 616,374
FILING DATE: 21-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 600,024 FILING DATE: 18-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 599,543 US 579,865 FILING DATE: 22-FEB-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 422,613 us 569,920 US 483,913 TOPOLOGY: linear MOLECULE TYPE: DNA (genomic) 15.2%; 55.2%; APPLICATION NUMBER: US 57 FILING DATE: 07-SEP-1990 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 56 FILING DATE: 18-OCT-1990 PRIOR APPLICATION DATA: 18-OCT-1990 FILING DATE: 08-APR-1988 ATTORNEY/AGENT INFORMATION: 20-AUG-1990 : 617/248-7000 617/248-7100 SEQUENCE CHARACTERISTICS: LENGTH: 314 base pairs TYPE: nucleic acid STRANDEDNESS: single Query Match
Best Local Similarity 55.2
Matches 149; Conservative TELEFAX: 617/248-7100 INFORMATION FOR SEQ ID NO: PRIOR APPLICATION DATA:
APPLICATION NUMBER: ANTI-SENSE: NO FILING DATE: HYPOTHETICAL: TELEPHONE:

22

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----cgcagtgcagac 165
                                                                                                                    133 ACCAACCACGCCGTGGTGCAGACCCTGGTGAACAACATGAACCCCGGCAAGGTACCCAAG 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  166 acaacccacagcacggtgctgggactgtacaacactctgaaccctgaagcatctgcctcg 225
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                                           73 TrcGacccracracrecreceGaccreccagrrececrreceGarcacrreaacage
                                                                                       acaacccacaggcacggtgctgggactgtacaacactctgaaccctgaagcatctgcctcg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 51.6; DB 6; Length 31 Pred. No. 4.7e-06; 0; Mismatches 109; Indels
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APPLICANT: KUBERASAMPATH, THANGAVEL; RUEGER, DAVID

; TITLE OF INVENTION:OSTEOGENIC DEVICES
        115 tactatgccaacttctgctcaggcccttgcccatacctc-
                                                                                                                                                                                                                                                      286 cccaaagtggagcagctctccaacatggtg 315
                                                                                                                                                                                                                                                                                         253 ACCGTGGTGCTGAAGAACTACCAGGAGATG 282
                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF INVENTION: OLD GGGALLO. BEVILES.
NUMBER OF SEQUENCES: 25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/268,252
FILING DATE: 29-UNN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 103,604
FILING DATE: 06-AGG-1993
APPLICATION NUMBER: 827,052
FILING DATE: 28-JAN-1992
APPLICATION NUMBER: 579,865
FILING DATE: 07-SEP-1990
APPLICATION NUMBER: 179,406
FILING DATE: 08-APR-1988
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US-07-718-274A-1
Sequence 1, Application US/07718274A
Patent No. 5284756
GENERAL INFORMATION:
APPLICANT: Grinna, Lynn
APPLICANT: Parsons, Thomas F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              286 cccaaagtggagcagctctccaacatggtg
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55.2%;
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Matches 149; Conservative
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5496552-1
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133 ACCAACCACGCCGTGGTGCAGACCCTGGTGAACAACATGAACCCCGGGAAGGTACCCAAG 192
                                                                         193 cccrecrecereceacceaecrerececearcaecarecreraceresaceaeaarrec 252
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Pred. No. 4.7e-06;
0; Mismatches 109; Indels
                                                                                                                                                                                                                                                                                                                      APPLICANT: OPPERMANN, HERMANN
APPLICANT: OZKAYNAK, ENOIN
APPLICANT: OZKAYNAK, ENOIN
APPLICANT: RUBERASAMPATH, THANGAVEL
APPLICANT: RUBGER, DAVID C.
APPLICANT: PANG, ROY H.L.
TITLE OF INVENTION: ANTIBODIES TO OSTEOGENIC PROTEINS
NUMBER OF SEQUENCES: 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER REAABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/449,699A
FILING DATE: 24-MAY-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/147,023
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: 1.314
OTHER INFORMATION: /note= "CONSENSUS PROBE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: TESTA, HURWITZ & THIBEAULT
STREET: 125 HIGH STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STK-001CP6CN
                                                                                                                        315
                                                                                                                                                          253 ACCGTGGTGCTGAAGAACTACCAGGAGATG 282
                                                                                                                  286 cccaaagtggagcagctctccaacatggtg
                                                                                                                                                                                                                                                            Sequence 33, Application US/08449699A
Patent No. 5958441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 617/248-7100
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 314 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: PITCHER, EDMUND R.
REGISTRATION NUMBER: 27,829
REFERENCE/DOCKET NUMBER: STI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/248-7000
TELEFAX: 617/248-7100
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ilarity 55.2%;
Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MASSACHUSETTS: U.S.A.
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                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ANTI-SENSE: NO FEATURE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE:
                                                                                                                                                                                                                      RESULT 39
US-08-449-699A-33
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 149;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE:
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Gaps

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77 aggatctgggctggaagtgggtccatgaacctaagggctactatgccaacttctgctcag 136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17 actgcttccgcaacttggaggagaactgctgtgtgcgcccctctacattgacttccgac 76
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15.0%; Score 51; DB 1; Length 417; 50.5%; Pred. No. 7.5e-06;
                                                                                                                                                                     APPLICANT: McCoy, John
APPLICANT: Murray, Beth
APPLICANT: Wolfman, Neil
TITLE OF INVENTION: MUTANTS OF BONE MORPHOGENIC PROTEINS
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                     ADDRESSEE: Genetics Institute, Inc - Legal Affairs STREET: 87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM: PC_DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/163,877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches 145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
CLASSIFICATION: 435
ATONEY/AGAIT INFORMATION:
NAME: Lazar, Steven R.
REGISTRATION NUMBER: 32,618
REFERENCE/DOCKET NUMBER: GI 5219
TELEPHONE: 617 876 1170 x 8260
TELEPHONE: 617 876 -5851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GI 5219
                                                                  RESULT 42
US-08-163-877-9
: Sequence 9, Application US/08163877
: Patent No. 5399677
                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: DNA (genomic) ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 417 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 50.5
Matches 157; Conservative
                                                                                                                                                                                                                                                                                                                                             CITY: Cambridge
STATE: Massachusetts
      386 GAAACATGGTG 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM:
SOFTWARE: PatentI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1..417
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                                                                                                                                                      GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                             02140
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US-08-163-877-9
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Pred. No. 7.5e-06;
0; Mismatches 145; Indels
                                                                                                                                                                                                                                        COMPUTER KEADABLE FURM:

MEDIUM TYRE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/718,274A
FILING DATE: 19910620
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/415,555
FILING DATE: 04-0CT-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/256,034
FILING DATE: 11-0CT-1988
ATTORNEY/AGENT INFORMATION:
NAME: Sharp, Jeffrey S:
REGISTRATION: NUMBER: 31,879
REGISTRATION: NUMBER: 31,879
REGISTRATION: NUMBER: 31,879
                                                             ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & ADDRESSEE: Bicknell
                                                                                                     STREET: Two First National Plaza, 20 South Clark STREET: Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 27129/9430 TELECOMMUNICATION INFORMATION: TELEPHONE: (312) 346-5750 TELEX: 25-3856 INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
TITLE OF INVENTION: Osteogenic Factor
NUMBER OF SEQUENCES: 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15.0%;
50.5%;
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TYPE: NUCLEIC ACID
STRANDEDNESS: single
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Best Local Similarity 50.5
Matches 157; Conservative
                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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COUNTRY: USA
                                                                                                                                             CITY: Chicago
STATE: Illino
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                            137 gcccttgcccat----acctccgcagtgcagacacaacccacagacgtgctgg 187
                                                                                                                                                                 266 CGCTGGTCCACTTCATCAACCGGAAACGGTGCCCAAGCCCTGCTGTGCGCCCACGCAGC 325
                                                                                                                      188 gactgtacaacactctgaaccctgaagcatctgcctcgccttgctgcgtgccccaggacc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Grinna, Lynn
APPLICANT: Parsons, Thomas F.
APPLICANT: Parsons, Theofan, Georgia
APPLICANT: Theofan, Heterodimeric Osteogenic Factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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APPLICATION NUMBER: US 07/415,555
FILING DATE: 04-00T-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/256,034
FILING DATE: 11-00T-1988
ATTORNEY/AGENT INFORMATION:
NAME: Sharp, Jeffrey S.
REGISTRATION NUMBER: 31,879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-64023
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APPLICATION NUMBER: US 08/149,106
FILING DATE: 11-0CT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/718,274
FILING DATE: 20-JUN-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/298,021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1, Application US/08298021
Patent No. 5508263
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 417 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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CITY: Chicago
STATE: Illinoi:
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US-08-298-021-1
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Pred. No. 7.5e-06;
0; Mismatches 145; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: Two First National Plaza, 20 South Clark
STREET: Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/415,555
FILING DATE: 04-0CT-1989
PRIOR APPLICATION NUMBER: US 07/256,034
APPLICATION NUMBER: US 07/256,034
FILING DATE: 11-0CT-1988
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Grinna, Lynn
APPLICANT: Parsons, Thomas F.
APPLICANT: Theofan, Georgia
TITLE OF INVENTION: Osteogenic Factor
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27129/9430
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                          Sequence 1, Application US/08149106
Patent No. 5411941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Sharp, Jeffrey S. REGISTRATION NUMBER: 31,879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 27
TELECOMMUNICATION INFORMATION:
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TELEFAX: (312) 984-9740
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 50.5%;
Matches 157; Conservative (
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TYPE: nucleic acid
STRANDEDNESS: single
                                             308 acatggtggtg 318
                                                                                          386 GAAACATGGTG 396
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CITY: Chicago
STATE: Illinois
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; LOCATION:
US-08-149-106-1
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US-08-149-106-1
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MOLECULE TYPE:
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                                                                                                                                                                                86 ACAGCAGCAGCGACCAGAGGCAGGCCTGTAAGAAGCACGAGCTGTATGTCAGCTTCCGAG 145
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                                                                                                                                                                                                                                                                                                                                                                                                                                           248 tggagccctgaccatcctgtactatgttgggaggacccccaaagtggagcagctctcca
                                                                                                              6
                                                                           Length 417;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 9, Application US/08360914B
Patent No. 5756308
GENERAL INFORMATION:
APPLICANT: Neil M. WOLFMAN and John MCCOY
TITLE OF INVENTION: MUTANTS OF BONE MORPHOGENIC PROTEINS
UNMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
                                                                        Score 51; DB 1; Length 417
Pred. No. 7.5e-06;
0; Mismatches 145; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Genetics Institute, Inc - Legal Affairs STREET: 87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPOSITION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
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PRICE APPLICATION DATA:
APPLICATION NUMBER: US 08/163,877
FILING DATE: December 7, 1993
ATTORNEY/AGENT INFORMATION:
NAME: LAZAR, SLEVEN R.
REGISTRATION NUMBER: 32,618
REFERENCE/DCCKET NUMBER: GI 5219B
TELECHONE: 617 498-8260
TELEFAX: 617 876-5851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/360,914B
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIBLE
                                                                        15.0%;
50.5%;
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SEQUENCE CHARACTERISTICS:
LENGTH: 417 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                      Query Match 15.0 Best Local Similarity 50.5 Matches 157; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Cambridge
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 308 acatggtggtg 318
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; LOCATION:
US-08-298-021-1
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86 ACAGCAGCAGCGACCAGAGGCAGGCCTGTAAGAAGCACGAGCTGTATGTCAGCTTCCGAG 145
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                                                                                                                                                                                                                                                                                                                                                                                                                                          137 gecettgcccat----acctecgcagtgcagacacaacccacaggcaggtgctgg 187
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                                                                                                                                                                                                                                                              17 actgcttccgcaacttggaggagaactgctgtgtgcgccccctctacattgacttccgac
                                                                                                                                                                                                                                                                                                                                                                          146 ACCTGGGCTGGCAGGACTGGATCATCGCCCCCTACGCCGCCTACTACTGTGAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      248 tggagcccctgaccatcctgtactatgttgggaggacccccaaagtggagcagctctcca
                                                                                                                                                                                                                       6
                                                                                                                                                                           Length 417;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 9, Application US/08741589A
Patent No. 5804416
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Neil M. WOLFMAN and John MCCOX
TITLE OF INVENTION: MUTANTS OF BONE MORPHOGENIC PROTEINS
                                                                                                                                                                       Score 51; DB 1; Length 417
Pred. No. 7.5e-06;
0; Mismatches 145; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Genetics Institute, Inc - Legal Affairs STREET: 87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CUCRRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/741,589A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5219B-DIV
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APPLICATION NUMBER: US 08/163,877
FILING DATE: December 7, 1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-ncc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          32,618
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 617 498-8260
                                                                                                                                                                         15.0%;
50.5%;
                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Lazar, Steven R. REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 617 876-5851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                       Query Match
Best Local Similarity
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                                                                                  1..417
ORIGINAL SOURCE:
ORGANISM: bmp-7
                                                             NAME/KEY: CDS
                                                                                  ; LOCATION:
US-08-360-914B-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 46
US-08-741-589A-9
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TOPOLOGY: line
MOLECULE TYPE: D
ORIGINAL SOURCE:
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US-08-621-803-248
                                                                                                                                                                                                    NAME/KEY:
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PCT-US94-13181-9
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                                                                                                                                                                                                               Length 417;
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GENERAL INFORMATION:
APPLICANT: GENETICS INSTITUTE, INC.
TITLE OF INVENTION: MUTANTS OF BONE MORPHOGENIC PROTEINS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc - Legal Affairs
                                                                                                                                                                                                           15.0%; Score 51; DB 1; Length 417 50.5%; Pred. No. 7.5e-06; ive 0; Mismatches 145; Indels
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ZIP: 02140

MEDIUM TYPE: Floppy disk
COMPUTER: EM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/13181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Lazar, Steven R.
REGISTRATION NUMBER: 32,618
REFERENCE/DOCKET NUMBER: GI 5219-PCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/163,877
FILING DATE: December 7, 1993.
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 87 CambridgePark Drive
            LENGTH: 417 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                        Best Local Similarity 50.5
Matches 157; Conservative
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: Massachusetts
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       308 acatggtggtg 318
                                                                    MOLECULE TYPE: DNA
ORIGINAL SOURCE:
ORGANISM: bmp-7
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                                                          linear
                                                                                                                                                 1..417
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                           TYPE: nucleic STRANDEDNESS:
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                                                         TOPOLOGY:
                                                                                                                                ; NAME/KEY:
; LOCATION:
US-08-741-589A-9
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                                                                                                                     FEATURE:
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77 aggatotgggactggaagtgggtccatgaacctaagggctactatgccaacttctgctcag 136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         137 gcccttgcccat...-acctccgcagtgcagacacaacccacagcacggtgctgg 187
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 266 CGCTGGTCCACTTCATCAACCCGGAAACGGTGCCCAAGCCCTGCTGTGCGCCCACGCAGC 325
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Methods for Recombinant Microbial Production of TITLE OF INVENTION: Fusion Proteins and BPI-Derived Peptides
                                                                                                                                                                                                                                                                                                                                                                                                                       6
                                                                                                                                                                                                                                                                                                                                                                          15.0%; Score 51; DB 5; Length 417
50.5%; Pred. No. 7.5e-06;
ive 0; Mismatches 145; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AUDRESSEE: Marshall, O'Toole, Gerstein, Murray & STRRET: 6300 Sears Tower, 233 South Wacker Drive CITY: Chicago STATE: Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 248, Application US/08621803; Patent No. 5851802; GENERAL INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617 498-8260
TELEFFAX: 617 876-5851
                                                             INFORMATION FOR SEQ ID NO: 9: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Better, Marc D.
                                                                                                    LENGTH: 417 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  265
                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 157; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                386 GAAACATGGTG 396
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Best Local Similarity
                                                                                                                                                                    linear
                                                                                                                                                                                                                               ORGANISM: bmp-7
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NAME/KEY: misc_feature
LOCATION: (23)...(161)
COTHER INFORMATION: /label="Bone D" /note="Bone D is the subunit of
OTHER INFORMATION: /label="Bone D" /note="Bone D is the subunit of
OTHER INFORMATION: /label="Bone D" /note="Bone D is the subunit of
OTHER INFORMATION: 5,284,756 e.g., Fig. 6, Example 9, Seq ID No. 6242219: 1
OTHER INFORMATION: and 2."
FERTURE:
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                                                                                                                   GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Better, Marc D.
TITLE OF INVENTION: Improved Methods for Recombinant Peptide Production
FILE REFERENCE: 1103/11041US01
CURRENT APPLICATION NUMBER: US/09/271,970
CURRENT FILING DATE: 1999-03-18
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Patentin Ver. 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: (1). (65)
OTHER INFORMATION: /label= EcoRI /note="residues 1-65 comprise EcoRI OTHER INFORMATION: site to beginning of pel B."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: (549)...(557)
COTHER INFORMATION: /label=XHOI /note="residues 549-557 comprise stop contex INFORMATION: codon and XhoI site."
US-09-271-970-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION: (1)..(22)
OTHER INFORMATION: Jabel-pel B /note-"pel B is the leader sequence
OTHER INFORMATION: from the pectate lyase gene of Erwinia
OTHER INFORMATION: carotovora."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gactgtacaacactctgaaccctgaagcatctgcctcgccttgctgcggcgcccaggacc
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                                                                           ; Sequence 1, Application US/09271970 ; Patent No. 6242219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 50.5
Matches 157; Conservative
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LOCATION: (1)..(65)
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                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                  SEQ ID NO 1
                                                     US-09-271-970-1
                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
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Best Local S
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FRATURE:

INAME/KET: misc_feature

LOCATION: residues 549-557

OTHER INFORMATION: /label= Xhor

OTHER INFORMATION: /note="residues 549-557 comprise stop codon and XhoI site."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: residues 1-65
OTHER INFORMATION: /Label= ECORI
OTHER INFORMATION: /Anote="residues 1-65 comprise EcoRI site to begining of pel
OTHER INFORMATION: B."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /label= "Bone D" // Anote="Bone D is the subunit of human osteogenic protein (s U.S. Patent No. 5851802 5,284,756 e.g., Fig. 6, Example 9, ID Nos: 1 and 2."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="pel B is the leader sequence from the pectate lyase gene of Erwinia carotovora."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        248 tggagcccctgaccatcctgtactatgttgggaggaccccaaagtggagcagctctcca 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17 actgcttccgcaacttggaggagaactgctgtgtgcgcccctctacattgacttccgac 76
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 557;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15.0%; Score 51; DB 2; Length 557 50.5%; Pred. No. 8.2e-06; ive 0; Mismatches 145; Indels
REGISTRATION NUMBER: 25,447
REFERENCE/DOCKET NUMBER: 27129/33199
FELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /label= pel B
                                                                                                                                                248:
                                                                                     TELERA: 312.1474-0448
TELERA: 25-3856
INFORMATION FOR SEQ ID NO: 24
SEQUENCE CHARACTERISTICS:
LENGTH: 557 base pairs
TEPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc_feature
LOCATION: AA 23-161
OTHER INFORMATION: /lab
OTHER INFORMATION: /not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc_feature
LOCATION: AA 1-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 15.0
Best Local Similarity 50.5
Matches 157; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: /
OTHER INFORMATION: /
OTHER INFORMATION: 9
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LOCATION: 66..548
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/note="pel B is the leader sequence from the pectate lyase gene of Erwinia caratovora." /label= EcoRI /note="residues 1-65 comprise EcoRI site to beginning of B." 248 tggagcccctgaccatcctgtactatgttgggaggacccccaaagtggagcagctctcca 307 GENERAL INFORMATION:
APPLICANT: Better, Marc D.
TITLE OF INVENTION: Methods for Recombinant Microbial Production of
TITLE OF INVENTION: Fusion Proteins and BPI-Derived Peptides
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS: 188 gactgtacaacactctgaaccctgaagcatctgcctcgccttgctgcgtgccccaggacc E: Marshall, O'Toole, Gerstein, Murray & Borun 6300 Sears Tower, 233 South Wacker Drive STATE: CILLIANGE
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/621,803
FILING DATE: J2-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: BOTON, MICHBER: 25,447
REGISTRATION NUMBER: 25,447
REFERENCE/DOCKET NUMBER: 27129/33199 NAME/KEY: misc\_feature LOCATION: AA 23-161 OTHER INFORMATION: /label= "Bone D" /label= pel B Sequence 256, Application US/08621803 Patent No. 5851802 256: TELEPHONE: 312/474-6300 TELEFAX: 312/474-0448 residues 1-65 LENGTH: 613 base pairs TYPE: nucleic acid STRANDEDNESS: single NAME/KEY: misc\_feature LOCATION: AA 1-22 TELEKAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS: NAME/KEY: misc\_feature MOLECULE TYPE: protein LOCATION: residues OTHER INFORMATION: OTHER INFORMATION: OTHER INFORMATION: OTHER INFORMATION: 308 acatggtggtg 318 OTHER INFORMATION: OTHER INFORMATION: 517 gaaacatggtg 527 66..602

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/note="pel B is the leader sequence from the pectate lyase gene of Erwinia caratovora."
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CCATION: residues 603-613
O'THER INFORMATION: /label= XhoI
O'THER INFORMATION: /note="residues 603-613 comprise stop codon and XhoI site.
US-08-621-803-260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           to beginning
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          /label= EcoRI
/note="residues 1-65 comprise EcoRI site
B."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: /label= peptide sequence
OTHER INFORMATION: /note="BPI-derived peptide.
                                                                                                         27129/33199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /label= pel B
                      FILING DATE: 22-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: BOTUN, Michael F.
REGISTRATION NUMBER: 25.447
REFERENCE/DOCKET NUMBER: 2712?
TELECOMUNICATION INFORMATION:
TELECHONE: 312/474-6300
TELEPHONE: 312/474-6448
                                                                                                                                                                                                           260:
                                                                                                                                                             TELERA: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 26
SEQUENCE CHARACTERISTICS:
LENOTH: 613 base pairs
TYPE: nucleic acid
STRANDENESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc_feature
LOCATION: AA 1-22
OTHER INFORMATION: /labe
OTHER INFORMATION: gene of
                                                                                                                                                                                                                                                                                                                                                                                                                                                        residues 1-65
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LOCATION: residues 1-65
OTHER INFORMATION: /lak
OTHER INFORMATION: /not
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AA 23-161
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                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: protein
        APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                       CDS
66..602
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Matches 157; Conserv
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NAME/KEY:
LOCATION:
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LOCATION:
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        (see
                                                                                                   /note="Bone D is the subunit of human osteogenic protein (s U.S. Patent No. 5851802 5,284,756 e.g., Fig. 6, Example 9, ID NOs: 1 and 2."
                                                                                                                                                                                                                                                                                                  NAME/KEY: misc_feature; Indextrown: residues 603-613
COTHER INFORMATION: /label= XhoI
COTHER INFORMATION: /note="residues 603-613 comprise stop codon and XhoI site.
US-08-621-803-256
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  217 ACAGCAGCAGCAGCAGGCAGGCCTGTAAGAAGCACGAGCTGTATGTCAGCTTCCGAG 276
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 260, Application US/08621803
Patent No. 5851802
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
TITLE OF INVENTION: Methods for Recombinant Microbial Production of TITLE OF INVENTION: Fusion Proteins and BPI-Derived Peptides NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 51; DB 2; Length 613
Pred. No. 8.5e-06;
0; Mismatches 145; Indels
                                                                                                                                                                                                 NAME/KEY: misc_feature
LOCATION: AA 166-179
OTHER INFORMATION: /label= peptide sequence
OTHER INFORMATION: /note="BPI-derived peptide."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: Illinois
COUNTRY: United States of America
COUNTRY: United States of America
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 15.0%;
Best Local Similarity 50.5%;
Matches 157; Conservative
                                                                          NAME/KEY: misc_feature
LOCATION: AA 162-165
OTHER INFORMATION: /labe
OTHER INFORMATION: /note
OTHER INFORMATION: site.
FEATURE:
OTHER INFORMATION:
OTHER INFORMATION:
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CITY: Chicago
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Query Match 15.0%; Score 51; DB 4; Length 646; Best Local Similarity 50.5%; Pred. No. 8.6e-06; Matches 157; Conservative 0; Mismatches 145; Indels

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NAME/KEY: misc_feature
COGATION: residues 1-65
OTHER INFORMATION: /label= ECORI
OTHER INFORMATION: /note="residues 1-65 comprise ECORI site to beginning of p
                                                                                                                   aggatetggggetggaagtgggteeatgaacetaagggetactatgeeaaettetgeteag 136
                                                                                                                                                                                                                                   397 cgctggtccacttcatcaacccggaaacggtgcccaagccctgctgtgcgcccacgcagc 456
                                                                                                                                                                                      137 gecettgeceat-----aceteegeagtgeagacacaaceacageacggtgetgg 187
                                                                                                                                                                                                                                                                                                                                                                         248 tggagcccctgaccatcctgtactatgttgggaggacccccaaagtggagcagctctcca 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 254, Application US/08621803
Patent No. 5831802
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
TITLE OF INVENTION: Methods for Recombinant Microbial Production of TITLE OF INVENTION: Fusion Proteins and BPI-Derived Peptides NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                 188 gactgtacaacactctgaaccctgaagcatctgcctcgccttgctgcgtgccccaggacc
    actgcttccgcaacttggaggagaactgctgtgtgcgccccctctacattgacttccgac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3: Marshall, O'Toole, Gerstein, Murray & Borun 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: BOTUN, Michael F.
REGISTRATION NUMBER: 25,447
REFERENCE/DOCKET NUMBER: 27129/33199
TELECOMMUNICATION: INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Illinois
: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/621,803 FILING DATE: 22-MAR-1996 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            : 658 base pairs
nucleic acid
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TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 658 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 single
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    308 acatggtggtg 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  517 gaaacatggtg 527
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: United ZIP: 60606-6402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: CDS
LOCATION: 66.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 54
US-08-621-803-254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
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17
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/label= pel B /note="pel B is the leader sequence from the pectate lyase gene of Erwinia caratovora."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note-"Bone D is the subunit of human osteogenic protein (U.S. Patent No. 5851802 5,284,756 e.g., Fig. 6, Example 9, ID Nos: 1 and 2."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: AA 162-165
OTHER INFORMATION: /label= cleavage linker
OTHER INFORMATION: /note="Ala-Leu-Asp-Pro linking sequence with Asp-Pro cleav
OTHER INFORMATION: site."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               residues 651-661
RMATION: /label= XhoI
RMATION: /note="residues 651-661 comprise stop codon and XhoI site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label= EcoRI
/note="residues 1-65 comprise EcoRI site to beginning of
B."
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                                                                                     ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/621,803
FILING DATE: 22-MAR-1996
ATTORNEY/AGENT INFORMATION:
6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: /label= peptide sequence
OTHER INFORMATION: /note="BPI-derived peptide."
                                                                                                                                                                                                                                                                                                                                                                     27129/33199
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                                                                                                                                                                                                                                                                                                                   NAME: Borun, Michael F. REGISTRATION NUMBER: 25,447
                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 27
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
                                             : Illinois
RY: United States of
60606-6402
                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 312/.
TELEFAX: 312/.
TELEFAX: 35-3856
INFORMATION FOR SEGULD NO: 262.
SEQUENCE CHARACTERISTICS:
LENGTH: 661 base pairs
""PB: nucleic acid
""PB: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc_feature
LOCATION: AA 23-161
OTHER INFORMATION: /labe
OTHER INFORMATION: /note
OTHER INFORMATION: U.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  residues 1-65
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AA 166-195
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AA 1-22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION:
COTHER INFORMATION:
US-08-621-803-262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
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OTHER INFORMATION:
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                     Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: CDS
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LOCATION:
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LOCATION:
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                                          STATE: Il
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE
                                                                                                                                                                           NAME/KEY: misc_feature
LOCATION: AA 23-161
OTHER INFORMATION: /label= "Bone D"
OTHER INFORMATION: /note="Bone D is the subunit of human osteogenic protein (see OTHER INFORMATION: U.S. Patent No. 5851802 5,284,756 e.g., Fig. 6, Example 9, Se OTHER INFORMATION: ID NOS: 1 and 2."
                                                                                                                                                                                                                                                                                                                   FEATURE:
NAME/KEY: misc_feature
LOCATION: AA 162-165
OTHER INFORMATION: /label= cleavage linker
OTHER INFORMATION: /note="Ala-Leu-Asp-Pro linking sequence with Asp-Pro cleavage
OTHER INFORMATION: site."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | NAME/KEY: misc_feature | LOCATION: residues 648-658 | OTHER INFORMATION: /label= Xho! | OTHER INFORMATION: /note="residues 648-658 comprise stop codon and XhoI site." US-08-621-803-254 |
  NAME/KEY: misc_feature
LOCATION: AA 1-22
OTHER INFORMATION: /label= pel B
OTHER INFORMATION: /note="pel B is the leader sequence from the pectate lyase
OTHER INFORMATION: gene of Erwinia caratovora."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 137 gcccttgcccat----acctccgcagtgcagacacaacccacagcacggtgctgg 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         188 gactgtacaacactctgaaccctgaagcatctgcctcgccttgctgcgtgccccaggacc 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      248 tggagccctgaccatcctgtactatgttgggaggaccccaaagtggagcagctctcca 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              457 TCAATGCCATCTCCGTCCTCTACTTCGATGACAGCTCCAACGTCATCCTGAAGAAATACA 516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 262, Application US/08621803
Patent No. 5851802
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
TITLE OF INVENTION: Methods for Recombinant Microbial Production of TITLE OF INVENTION: Fusion Proteins and BPI-Derived Peptides NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17 actgettecgeaacttggaggagaactgetgtggggeeceetetacattgaetteegae 76
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc_feature
LOCATION: AA 166-194
OTHER INFORMATION: //abel= peptide sequence
OTHER INFORMATION: /note="BPI-derived peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 50.5
Matches 157; Conservative
OTHER INFORMATION: B."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-621-803-262
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ZIP: 02109

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/841,646
TITTING DATE: 1992021 ADDRESSEE: TESTA, HURWITZ & THIBEAULT STREET: 53 STATE STREET CITY: BOSTON STATE: MASSACHUSETTS APPLICANT: OZKAYNAK, ENGIN
APPLICANT: KUBERSAKAMPATH, THANGAVEL
APPLICANT: RUBGER, DAVID C.
APPLICANT: PANG, ROY H.L.
APPLICANT: PANG, ROY H.L.
TITLE OF INVENTION: OSTEOGENIC DEVICES
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS: FILING DATE: 19920221
CLASSIFICATION: 530
PRIOR APPLICATION 530
PRIOR APPLICATION DATA:
APPLICATION NURBER: US 810,560
FILING DATE: 20-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NURBER: US 827,052
PRIOR APPLICATION DATA:
APPLICATION NURBER: US 660,162
FILING APPLICATION DATA:
APPLICATION NURBER: US 660,162
FILING APPLICATION DATA:
APPLICATION NURBER: US 621,988
FILING APPLICATION DATA:
APPLICATION NURBER: US 621,988
FILING APPLICATION DATA:
APPLICATION NURBER: US 621,988
FILING APPLICATION NURBER: US 621,988
FILING APPLICATION DATA:
APPLICATION NURBER: US 621,988
FILING APPLICATION DATA:
APPLICATION NURBER: US 621,849 Sequence 10, Application US/07841646 Patent No. 5266683 APPLICATION NUMBER: US 616,374 FILING DATE: 21-NOV-1990 PRICA APPLICATION DATA: APPLICATION NUMBER: US 600,024 OPPERMANN, HERMANN COUNTRY: U.S. FILING DATE: 04-DEC-1 PRIOR APPLICATION DATA: acatggtggtg 318 517 GAAACATGGTG 527 GENERAL INFORMATION: US-07-841-646-10 APPLICANT: APPLICANT: 277 11 137

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77 aggatotggggctggaggtgggtccatgaacctaagggctactatgccaacttctgctcag 136 gcccttgcccat----acctccgcagtgcagacacaacccacagcacgtgctgg 187 Gaps 17 actgetteegeaacttggaggagaactgetgtgtgegeeeeetetacattgaetteegae 76 tggagcccctgaccatcctgtactatgttgggaggaccccaaagtggagcagctctcca 800 GCTGGTCCACTTCATCAACCGGAAACGGTGCCCAAGCCCTGCTGTGCGCCCACGCAGC 6 Score 51; DB 1; Length 1004; Pred. No. 9.8e-06; 0; Mismatches 145; Indels /function= "OSTEOGENIC PROTEIN" /product= "OP1B" /note= "OP1B - FUSION" CRP-001CP6 APPLICATION NUMBER: US 422,613
FILING DATE: 17-0CT-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 315,342
FILING DATE: 23-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 232,630
FILING DATE: 15-AUG-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 179,460
FILING DATE: 08-APR-1988
ATTORNEY AGENT INFORMATION: PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 579, 865
FILING DATE: 07-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 569, 920
PRIOR APPLICATION NUMBER: US 483, 913
FILING DATE: 22-FEB-1990
PRIOR APPLICATION NUMBER: US 483, 913
FILING DATE: 22-FEB-1990 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 599,543 27,829 REFERENCE/DOCKET NUMBER: CF TELECOMUNICATION INFORMATION: TELEPHONE: 617/248-7100 TELEFAX: 617/248-7100 INFORMATION FOR SEQ ID NO: 10: SEQUENCE CHARACTERISTICS: 15.0%; 50.5%; 18-OCT-1990 NAME: PITCHER, EDMUND R. REGISTRATION NUMBER: 27, 1004 base pairs Best Local Similarity 50.53 Matches 157; Conservative TYPE: NUCLEIC ACID
STRANDEDNESS: sinql LOCATION: 1.951 OTHER INFORMATION: OTHER INFORMATION: OTHER INFORMATION: TOPOLOGY: linear MOLECULE TYPE: cDNA HYPOTHETICAL: YES Similarity ANTI-SENSE: FEATURE: NAME/KEY: TELEFAX: US-07-841-646-10 LENGTH: Query Match 137

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COMPUTER READABLE FORM:
MEDTUM TYPE: Floppy disk
COMPUTER: IBM FO Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
APPLICATION NUMBER: US/08/147,023
FILING DATE: 21 FEB-1992
CLASSIFICATION: 530 CORRESPONDENCE ADDRESS:
ADDRESSEE: TESTA, HURWITZ & THIBEAULT
STREET: 53 STATE STREET APPLICANT: OPPERMANN, HERMANN
APPLICANT: OZKAYNAK, ENGIN
APPLICANT: KUBERASAMPATH, THANGAVEL
APPLICANT: RUBGER, DAVID C.
APPLICANT: PANG, ROY H.L.
TITLE OF INVENTION: OSTEOGENIC DEVICES
NUMBER OF SEQUENCES: 33 FILING DATE: 21-FEB 1992
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60,162
FILING DATE: 22-FEB-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 621,988
FILING DATE: 04-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 621,849
FILING DATE: 04-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 631,849
FILING DATE: 04-DEC-1990
PRIOR APPLICATION NUMBER: US 631,849
FILING DATE: APPLICATION DATA:
APPLICATION NUMBER: US 631,849 APPLICATION NUMBER: US 616,374
FILING DATE: 21-NOV-1990
RIOR APPLICATION DATA:
FILING DATE: 18-0CT-1990
PRIOR APPLICATION NUMBER: US 599,543
APPLICATION NUMBER: US 599,543
FILING DATE: 18-0CT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 599,543
APPLICATION NUMBER: US 579,865 ETLING DATE: 22-FEB-1990
PRICK APPLICATION DATA:
APPLICATION .....APPLICATION .....APPLICATION .....APPLICATION .....APPLICATION .....APPLICATION ......APPLICATION ...... FILING DATE: 07-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 569,920
FILING DATE: 20-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 483,913 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 315,342
FILING DATE: 23-FEB-1989 Sequence 10, Application US/08147023 Patent No. 5468845 GENERAL INFORMATION: JMBER: US 579,865 07-SEP-1990 APPLICATION NUMBER: US 422,613 FILING DATE: 17-OCT-1989 STREET: 53 STATE STREE CITY: BOSTON STATE: MASSACHUSETTS COUNTRY: U.S.A. 308 acatggtggtg 318 920 GAAACATGGTG 930 02109 RESULT 57 US-08-147-023-10 ò Dp

800 CGCTGGTCCACTTCATCAACCCGGAAACGGTGCCCAAGCCCTGCTGTGCGCCCACGCAGC 859 307 17 actgetteegeaacttggaggagaactgetgtgtgegeeeeetetacattgaetteegae 76 Gaps 137 gcccttgcccat-----acctccgcagtgcagacacaccacaggcaggtgctgg 248 tggagcccctgaccatcctgtactatgttgggaggacccccaaagtggagcagctctcca 6 Length 1004; 15.0%; Score 51; DB 1; Length 100 50.5%; Pred. No. 9.8e-06; ive 0; Mismatches 145; Indels /function= "OSTEOGENIC PROTEIN" /product= "OP1B" /note= "OP1B - FUSION" APPLICANT: OPPERMANN, HERMANN
APPLICANT: OZRAYNAK, ENGIN
APPLICANT: CZRAYNAK, ENGIN
APPLICANT: KUBERASAMPATH, THANGAVEL
APPLICANT: RUEGER, DAVID C.
TITLE OF INVENTION: OSTEOGENIC DEVICES
NUMBER OF SEQUENCES: 33 CRP-001CP6 us 232,630 US 179,460 Sequence 10, Application US/08447570 Patent No. 5714589 GENERAL INFORMATION: PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 179,460
FILING DATE: 08-APR-1988
ATTORNEY,AGENT INFORMATION:
NAME: PITCHER, EDMUND R.
REGISTRATION NUMBER: 27,829
REFERENCE,DOCKET NUMBER: CRP-0TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/248-7000
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS: 15-AUG-1988 LENGTH: 1004 base pairs TYPE: nucleic acid STRANDEDNESS: single Query Match 15.0 Best Local Similarity 50.5 Matches 157; Conservative PRIOR APPLICATION DATA: CORRESPONDENCE ADDRESS: ) NAME/KEY: CDS ; LOCATION: 1..951 ; OTHER INFORMATION: ; OTHER INFORMATION: US-08-147-023-10 APPLICATION NUMBER: FILING DATE: 15-AUG TOPOLOGY: linear MOLECULE TYPE: CDNA HYPOTHETICAL: YES 308 acatggtggtg 318 920 GAAACATGGTG 930 HYPOTHETICAL: Y ANTI-SENSE: NO FEATURE: RESULT 58 US-08-447-570-10 Db δλ 염 염 ŏ g ŏ OD δ

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;; 77 aggatotggggctggaagtgggtccatgaacctaagggctactatgccaacttctgctcag 136 800 CGCTGGTCCACTTCATCAACCCGGAAACGTGCCCAAGCCCTGCTGTGCGCCCACGCAGC 859 188 gactgtacaacactctgaaccctgaagcatctgcctcgccttgctgcgtgccccaggacc 247 620 ACAGCAGCAGCGACCAGAGGCAGGCCTGTAAGAAGCACGAGCTGTATGTCAGCTTCCGAG 679 248 tggagcccctgaccatcctgtactatgttgggaggacccccaaagtggagcagctctcca 307 Gaps 17 actgetteegeaacttggaggagaactgetgtgtgegeeecetetacattgaetteegae 76 137 gocottgocoat-----acotcogoagtgoagacacaacacacagoaggtgotgg 6 Score 51; DB 1; Length 1004; Pred. No. 9.8e-06; 0; Mismatches 145; Indels /function= "OSTEOGENIC PROTEIN" /product= "OP1B" /note= "OP1B - FUSION" SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA: ADDRESSEE: TESTA, HURWITZ & THIBEAULT STREET: 53 STATE STREET OSTEOGENIC DEVICES Sequence 10, Application US/08449700
Patent No. 5863758
GENERAL INFORMATION: HERMANN
APPLICANT: OPPERMANN, HERMANN
APPLICANT: NUBGER, DAVID C.
APPLICANT: RUBGER, DAVID C.
APPLICANT: PANG, ROY H.L.
TITLE OF INVENTION: OSTEOGENIC DEVICES;
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS: APPLICATION NUMBER: US/08/449,700 FILING DATE: 21-FEB-1992 CLASSIFICATION: 530 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 810,560 FILING DATE: 20-DEC-1991 COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS 15.0%; 50.5%; Floppy disk Query Match
Best Local Similarity 50.5
Matches 157; Conservative CITY: BOSTON STATE: MASSACHUSETTS COUNTRY: U.S.A. ZIP: 02109 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy FILING DATE: 20-DEC-PRIOR APPLICATION DATA: COCATION: 1.951
COCHER INFORMATION:
COTHER INFORMATION:
COTHER INFORMATION:
US-08-447-570-10 308 acatggtggtg 318 920 GAAACATGGTG 930 NAME/KEY: CDS HYPOTHETICAL: Y ANTI-SENSE: NO FEATURE: MOLECULE TYPE: RESULT 59 US-08-449-700-10 g g οy g g a δ õ

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140 GGGAGTGTCCCTCTGAACTCCTACATGAACGCCACCACCACCACCACCATGAGA 799
                                                                                                                                                                                                                                                                                                      860 TCAATGCCATCTCCTCTACTTCGATGACAGCTCCAACGTCATCCTGAAGAAATACA 919
                                                                                                        gcccttgcccat-----acctccgcagtgcagacacaaccacagcacggtgctgg 187
                                                                                                                                                                                                                                     248 tggagcccctgaccatcctgtactatgttgggaggacccccaaagtggagcagctctcca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: OPPERANN, HERMANN
APPLICANT: OPPERASAMPATH, THANGAVEL
APPLICANT: KUBERASAMPATH, THANGAVEL
APPLICANT: RUEGER, DAVID C.
APPLICANT: PAG, ROY H.L.
TITLE OF INVENTION: ANTIBODIES TO OSTEOGENIC PROTEINS
NUMBER OF SEQUENCES: 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: 1..951
OTHER INFORMATION: /function= "OSTEOGENIC PROTEIN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/449,699A
FILING DATE: 24-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER: 27,829
REFERENCE/DOCKET NUMBER: STK-001CPGCN
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/248-7100
TELEFAX: 617/248-7100
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE GRARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: TESTA, HURWITZ & THIBEAULT
STREET: 125 HIGH STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/147,023
FILING DATE: 01-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: PITCHER, EDWIND R.
REGISTRATION NUMBER: 27,829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 10, Application US/08449699A Patent No. 5958441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 1004 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MASSACHUSETTS: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                 308 acatggtggtg 318
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US-08-449-699A-10
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/product= "OP1B"
/note= "OP1B - FUSION"
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                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 621,849
FILING DATE: 0.4-DEC-1990
FILING DATE: 0.4-DEC-1990
FILING DATE: 1.NOV-1990
FILING DATE: 21-NOV-1990
FILING DATE: 18-OCT-1990
FILING APPLICATION NUMBER: US 599,543
FILING DATE: 18-OCT-1990
FILING APPLICATION DATA:
APPLICATION NUMBER: US 599,543
FILING DATE: 0.7-SEP-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 569,920
FILING DATE: 20-AUG-1990
PRIOR PAPLICATION DATA:
APPLICATION NUMBER: US 483,913
FILING DATE: 22-FEB-1990
PRIOR APPLICATION NUMBER: US 422,613
FILING DATE: 17-OCT-1989
PRIOR APPLICATION DATA:
                                                        APPLICATION NUMBER: US 660,162
FILING DATE: 22-FEB-1991
PRIOR APPLICATION DATA: APPLICATION NUMBER: US 621,988
FILING DATE: 04-DEC-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 315,342 FILING DATE: 23-FEB-1989
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APPLICATION NUMBER: US 232,630
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APPLICATION NUMBER: US 827,052
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 179,466
FILING DATE: 08-APR-1988
ATTORNEY/AGENT INFORMATION:
NAME: PITCHER, EDMUND R.
REGISTRATION NUMBER: 27,829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEFONE: 617/248-7000
TELEFAX: 617/248-7100
TELEFAX: 617/248-7100
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 1004 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                   28-JAN-1992
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Best Local Similarity 50.5°
Matches 157; Conservative
                   FILING DATE: 28-JAN-PRIOR APPLICATION DATA:
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OTHER INFORMATION:
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MOLECULE TYPE: CDNA
HYPOTHETICAL: YES
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OTHER TAME
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MOLECULE TYPE:
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                                                                                                                        Gaps
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                                                                                                                        6
                                                                                 15.0%; Score 51; DB 2; Length 1004; 50.5%; Pred. No. 9.8e-06; ive 0; Mismatches 145; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 9, Application US/07764731B
Patent No. 5366875
GENERAL INFORMATION:
APPLICANT: Rosen, Vicki A.
APPLICANT: Wang, Elizabeth A.
APPLICANT: Wang, John M.
TILLE OF INVENTION:
NUMBER OF SEQUENCES: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AUDRESSEE: Legal Affairs, Genetics Institute,
STREET: 87 CambridgePark Drive
CITY: Cambridee
/product= "OP1B"
/note= "OP1B - FUSION"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/764,731E
FILING DATE: 19910924
CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INCRMATION:
NAME: Kapinos, Ellen J.
REGISTRATION NUMBER: 32,245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: GI
TELECOMMUNICATION INFORMATION
TELEPHONE: 617-876-1170
TELEFAX: 617-876-5851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 1259 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 1259 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
TOPOLOGY: circular
                                                                                                                  Matches 157; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Legal Aff
; OTHER INFORMATION:
; OTHER INFORMATION:
US-08-449-699A-10
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                                                                                                      Similarity
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                                                                                   Query Match
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1049 CGCTGGTCCACTTCATCAACCCGGAAACGGTGCCCAAGCCCTGCTGTGCGCCCACGCAGGC 1108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17 actgcttccgcaacttggaggagaactgctgtgtgcgcccctctacattgacttccgac 76
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             6
                                                                                                                                                                                                                                                                                                                                                                                                                         Length 1259;
                                                                                                                   LIBRARY: U2-OS Human Osteosarcoma cDNA library CLONE: U2-5
                                                                                                                                                                                                                                                                                                                                                                                                                       15.0%; Score 51; DB 1; ilarity 50.5%; Pred. No. 1.1e-05; Conservative 0; Mismatches 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: TESTA, HURWITZ & THIBEAULT STREET: 53 STATE STREET CITY: BOSTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: OSTEOGENIC DEVICES NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: OPPERMANN, HERMANN
APPLICANT: OZKAYNAK, ENGIN
APPLICANT: KUBERSAMPATH, THANGAVEL
APPLICANT: RUGGER, DAVID C.
APPLICANT: PANG, ROY H.L.
TITLE OF INVENTION: OSTEOGENIC DEVIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 14, Application US/07841646
Patent No. 5266683
GENERAL INFORMATION:
                                                                        Homo sapiens
U2-0S Osteosarcoma
CDNA to mRNA
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MEDIUM TYPE: Floppy disk
                                    C-terminal
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783..1200
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Matches 157; Conserv
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                                                                                                        IMMEDIATE SOURCE:
                                                   ORIGINAL SOURCE:
             HYPOTHETICAL:
FRAGMENT TYPE:
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                                                                                       CELL LINE:
                                                                                                                                                                                                                    NAME/KEY:
                                                                    ORGANISM:
                                                                                                                                                                                                                                         LOCATION:
                                                                                                                                                                                                                                                                           NAME/KEY:
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/function= "OSTEOGENIC PROTEIN" /product= "OPID"
                                          SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/841,646
FILING DATE: 1992021
CLASSIFICATION 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 810,560
FILING DATE: 20-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 827,052
FILING DATE: 38-JAN-1992
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PALICATION UNDER: US 600,024
PRIOR APPLICATION UNDER: US 600,024
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 599,543
FILING DATE: 18-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 579,865
FILING DATE: 07-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 69,920
PRIOR APPLICATION NUMBER: US 483,913
FILING DATE: 22-FEB-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 483,913
FILING DATE: 17-OCT-1989
PRIOR APPLICATION NUMBER: US 422,613
FILING DATE: 37-OCT-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 315,342
FILING DATE: 37-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 315,342
FILING DATE: 23-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 312,630
                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 621,988
FILING DATE: 04-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 621,849
FILING DATE: 04-DEC-1990
PRIOR APPLICATION NUMBER: US 616,374
FILING DATE: 100V-1990
PRIOR APPLICATION NUMBER: US 616,374
FILING DATE: 21-NOV-1990
PRIOR APPLICATION NUMBER: US 600,024
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 660,162
FILING DATE: 22-FEB-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 179,460 FILING DATE: 08-APR-1988 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 27,829
REFERENCE/DOCKET NUMBER: CRE
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 14: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PITCHER, EDMUND R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: 617/248-7000
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TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: NUCLEIC ACID
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OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: CDNA HYPOTHETICAL: YES
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1; 1073 CGCTGGTCCACTTCATCAACCGGAAACGGTGCCCAAGCCCTGCTGTGCGCCCACGCAGC 1132 893 ACAGCAGCAGCGACCAGAGGCAGGCCTGTAAGAAGCACGAGCTGTATGTCAGCTTCCGAG 952 Gaps 17 actgcttccgcaacttggaggagaactgctgtgtgcgcccctctacattgacttccgac 76 188 gactgtacaacactctgaaccctgaagcatctgcctcgccttgctgcgtgccccaggacc 6 Length 1277; Score 51; DB 1; Length 127 Pred. No. 1.1e-05; 0; Mismatches 145; Indels SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/147,023
FILING DATE: 21-FEB.1992
CLASSIFICATION 1530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 810,560
FILING DATE: 20-DEC-1991
PRIOR APPLICATION NUMBER: US 827,052
FILING DATE: 28-JAN-1992 ; OTHER INFORMATION: /note= "OP1D - FUSION" US-07-841-646-14 Sequence 14, Application US/08147023
Sequence 14, Application US/08147023
Sequence 14, Application US/08147023
Sequence 14, Application US/08147023
September 10. S468845
September 10. FILING DATE: 28-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION UNBER: US 660,162
FILING DATE: 22-FEB-1991
PRIOR APPLICATION NUMBER: US 621,988
FILING DATE: 04-DEC-1990 ZIP: 02109 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS Query Match 15.0%; Best Local Similarity 50.5%; Matches 157; Conservative CITY: BOSTON STATE: MASSACHUSETTS 1193 GAAACATGGTG 1203 308 acatggtggtg 318 COUNTRY: U.S.A. ZIP: 02109 RESULT 63 US-08-147-023-14 Query Match Best Local S ò á q οy g δ qq ò a ŏ

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1133 TCAATGCCATCTCCGTCCTCTACTTCGATGACAGCTCCAACGTCATCCTGAAGAAATACA 1192
                                                                                                                                               248 tggagccctgaccatcctgtactatgttgggaggacccccaaagtggagcagctctcca 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
SOFTWARE PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/447,570
FILING DATE: 1992
CLASSIFICATION 336
PROOF APPLICATION NUMBER: US/08/10/20
FILING DATE: 20-DEC-1991
PROOR APPLICATION NUMBER: US 810,560
FILING DATE: 20-DEC-1991
PROOR APPLICATION NUMBER: US 827,052
FILING DATE: 28-JAN-1992
PROOR APPLICATION NUMBER: US 827,052
FILING DATE: 28-JAN-1992
PROOR APPLICATION NUMBER: US 827,052
FILING DATE: 22-FEB-1991
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APPLICANT: OZKAYNAK, ENGIN
APPLICANT: KUBERASAMPATH, THANGAVEL
APPLICANT: RUEGER, DAVID C.
APPLICANT: PANG, ROY H.L.
TITLE OF INVENTION: OSTEOGENIC DEVICES
NUMBER OF SEQUENCES: 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 621,988
FILING DATE: 04-026-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 621,849
FILING DATE: 04-026-1990
PRIOR APPLICATION NUMBER: US 616,374
FILING DATE: 17-026-1990
PRIOR APPLICATION NUMBER: US 616,374
FILING DATE: 21-007-1990
PRIOR APPLICATION NUMBER: US 610,024
APPLICATION NUMBER: US 600,024
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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PROPERTY APPLICATION NUMBER: US 599,543
FITTING DATE: 18-OCT-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 579,865
FILING DATE: 07-SEP-1990
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APPLICATION NUMBER: US 569,920
FILING DATE: 20-AUG-1990
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 14, Application US/08447570 Patent No. 5714589
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                     1193 GAAACATGGTG 1203
                                                                                                                                                                                                                                                              308 acatggtggtg 318
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gcccttgcccat----acctccgcagtgcagacacaacccacaggcacggtgctgg 187
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /function= "OSTEOGENIC PROTEIN"
/product= "OP1D"
/note= "OP1D - FUSION"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CRP-001CP6
                    APPLICATION NUMBER: US 621,849
FILING DATE: 04-DEC-1990
FILING APPLICATION DATA:
APPLICATION NUMBER: US 616,374
FILING APPLICATION DATA:
APPLICATION NUMBER: US 600,024
FILING APPLICATION DATA:
APPLICATION NUMBER: US 599,543
FILING APPLICATION DATA:
APPLICATION NUMBER: US 599,543
FILING APPLICATION DATA:
APPLICATION NUMBER: US 59,920
FILING APPLICATION DATA:
APPLICATION NUMBER: US 59,920
FILING APPLICATION NUMBER: US 483,913
FILING DATE: 20-AUG-1990
FILING APPLICATION NUMBER: US 483,913
FILING DATE: 17-OCT-1989
FILING DATE: 15-AUG-1988
FILING DATE: 108-APR-1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 1277 base pairs.
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 50.5
Matches 157; Conservative
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: , ; OTHER INFORMATION: , ; OTHER INFORMATION: , ; OTHER INFORMATION: /
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ANTI-SENSE: NO FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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CITY: BOSTON
STATE: MASSACHUSETTS
CONDITRY: U.S.A.
ZIP: 0.2109
COMPUTER READABLE FORM:
MEDIUM TYPE: F.LOPPY disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/449,700
FILING DATE: 21-FEB-1992
CLASSIFICATION DATA:
APPLICATION NUMBER: US 810,560
FILING DATE: 22-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 660,162
FILING DATE: 28-BEB-1991
PRIOR APPLICATION NUMBER: US 621,988
FILING DATE: 04-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 621,849
FILING DATE: 04-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 61,849
FILING DATE: 12-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 61,849
FILING DATE: 18-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 61,849
FILING DATE: 21-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 61,849
FILING DATE: 18-OCT-1990
PRIOR APPLICATION NUMBER: US 61,849
FILING DATE: 18-OCT-1990
PRIOR APPLICATION NUMBER: US 61,849
FILING DATE: 18-OCT-1990
PRIOR APPLICATION NUMBER: US 600,024
FILING DATE: 18-OCT-1990
PRIOR APPLICATION NUMBER: US 670,024
                                                                                                                                                                                                  ADDRESSEE: TESTA, HURWITZ & THIBEAULT STREET: 53 STATE STREET
                                                                                                                               OSTEOGENIC DEVICES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CRP-001CP6
    OPPERMANN, HERMANN
OZKÁYNAK, ENGIN
KUBERASAMPATH, THANGAVEL
RUEGER, DAVID C.
PANG, ROY H.L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 579,865
FILING DATE: 07-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 569,920
FILING DATE: 20-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 483,913
FILING DATE: 22-FEB-1990
PRIOR APPLICATION NUMBER: US 42,613
FILING DATE: 17-OCT-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-AUG-1988
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US 315,342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: PITCHER, EDMUND R. REGISTRATION NUMBER: 27,829 REFERENCE/DOCKET NUMBER: CRETELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 31
FILING DATE: 23-FEB-1989
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                                                                                                 APPLICANT: PANG, ROY H
TITLE OF INVENTION: OS
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
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FILING DATE: 15-AUG
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                                                                               APPLICANT:
                                                      APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                77 aggatotggggctggaagtgggtccatgaacctaagggctactatgccaacttctgctcag 136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /function= "OSTEOGENIC PROTEIN"
/product= "OP1D"
/note= "OP1D - FUSION"
                                                                                                                                                                                                                                                                                                                                                                                                                    CRP-001CP6
                                                                PRIOR APPLICATION NUMBER: US 422,613
FILING APPLICATION DATA:
APPLICATION NUMBER: US 315,342
FILING DATE: 23-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 232,630
FILING DATE: 15-AUG-1988
RROR APPLICATION NUMBER: US 179,460
FILING DATE: 08-APR-1988
APPLICATION NUMBER: US 179,460
FILING DATE: DATA:
APPLICATION NUMBER: 27,829
REGISTRATION NUMBER: 27,829
REGISTRATION NUMBER: 27,829
REFERENCE/DOCKET NUMBER: CRP-001C
TELECOMUNICATION INFORMATION:
TELEPHONE: 617/248-71000
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US-08-449-700-14
is Sequence 14, Application US/08449700
Patent No. 5863758
GENERAL INFORMATION:
  US 483,913
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 617/248-7100
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 1277 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
APPLICATION NUMBER: US 48 FILING DATE: 22-FEB-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match
Best Local Similarity 50.55
Matches 157; Conservative
                        FILING DATE: 22-FEB-1
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: CDS
LOCATION: 1.1224
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-447-570-14
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TOPOLOGY:
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US-07-539-756-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: OPPERMANN, HERMANN
APPLICANT: OZKAYNAK, ENGIN
APPLICANT: KUBERASAMPATH, THANGAVEL
APPLICANT: KUBERASAMPATH, THANGAVEL
APPLICANT: PANG, ROY H.L.
TITLE OF INVENTION: ANTIBODIES TO OSTEOGENIC PROTEINS
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: TESTA, HURWITZ & THIBEAULT
STREET: 125 HIGH STREET
                                                                                                                                                                                                                                                                   /function= "OSTEOGENIC PROTEIN"
/product= "OP1D"
/note= "OP1D - FUSION"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIALS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 14, Application US/08449699A Patent No. 5958441 GENERAL INFORMATION:
TELEPHONE: 617/248-7000
TELEFAX: 617/248-7100
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 1277 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: YES
                                                                                                                                                                                                                                                                                                                                                                                                             Matches 157; Conservative
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                                                                                                                                                                                                                                              LOCATION: 1.1224
CTHER INFORMATION:
COTHER INFORMATION:
CTHER INFORMATION:
US-08-449-700-14
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US-08-449-699A-14
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Pred. No. 1.1e-05;
0; Mismatches 145; Indels
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Patent No. 5364839
GENERAL INFORMATION:
APPLICANT: WANG, ELIZABETH A.
APPLICANT: WANG, ELIZABETH A.
APPLICANT: KRIZ, MARY JO
TITLE OF INVENTION: FORMULATIONS
NUMBER OF INVENTION: FORMULATIONS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product= "OP1D"
/note= "OP1D - FUSION"
             JMBER: US/08/449,699A
24-MAY-1995
                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/147,023
FILING DATE: 01-NOV-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                    NAME: PITCHER, EDMUND R.
REGISTRATION UNMBER: 27,829
REFRENCE/DOCKET NUMBER: STK-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/248-7000
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 50.5%;
Matches 157; Conservative
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CURRENT APPLICATION DATA:
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EDNESS: single
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                                                             CLASSIFICATION:
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LOCATION: 1..1
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STRANDEDNESS:
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                                    FILING DATE:
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308 acatggtggtg 318
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45239-8707
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                                                        Ohio
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                                                       STATE: O
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Sequence 7, Application US/08377292
Patent No. 5695615
GENERAL INFORMATION:
APPLICANT: STONE, ROGER L.
TITLE OF INVENTION: THERAPEUTIC FORMULAS FOR OSTEOINDUCTION
NUMBER OF SEQUENCES: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 15.0%; Score 51; DB 1; Length 1448; Best Local Similarity 50.5%; Pred. No. 1.1e-05; Matches 157; Conservative 0; Mismatches 145; Indels
GENETICS INSTITUTE, INC.
GAL AFFAIRS - 87 CAMBRIDGEPARK DRIVE
                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0, Version #1.25
CUBRENT APPLICATION DATA:
CALLCATION NUMBER: US/07/539,756
FILING DATE: 19900618
                                                                                                                                                                                                                          FILING DATE: 19900618
CLASSIFICATION: 514
ATTORNEY AGENT INFORMATION:
NAME: MCDANIELS, PATRICIA A.
REGISTRATION NUMBER: 33,194
REFERENCE/DOCKET NUMBER: 615172
TELEPHONE: (617) 876-1170 X405
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1448 base pairs
                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: DNA (genomic)
                  F: LEGAL AFFAIRS
CAMBRIDGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: NUCLEIC ACID
STRANDEDNESS: double
                                                       MASSACHUSETTS
USA
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; LOCATION:
US-07-539-756-3
                                  CITY: CAL
STATE: M.
COUNTRY:
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1298 TCAATGCCATCTCCGTCCTCTACTTCGATGACAGCTCCAACGTCATCCTGAAGAAATACA 1357
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; Patent No. 5866364
; GENERAL INFORMATION:
   APPLICANT: Israel, David
; APPLICANT: Wolfman, Nail M.
   TITLE OF INVENTION: Recombinant Bone Morphogenetic Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15.0%; Score 51; DB 1; Length 1448; 50.5%; Pred. No. 1.1e-05;
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                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
ADDRESSEE: The Procter & Gamble Company
STREET: 11810 East Miami River Road
CITY: Cincinnati
                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/243,435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
APPLICATION NUMBER: US/08/117,367
                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/377,292
FILING DATE: 23-JAN-1995
CLASSIFICATION: 514
                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MAME: COSEtanje, Brahm J.
REGISTRATION NUMBER: 34,804
TELECOMUNICATION INFORMATION:
TELEPHONE: 513-245-2858
TELEPRAX: 513-741-3012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1448 base pairs
TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 50.5
Matches 157; Conservative
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Heterodimers, Compositions and Methods of Use. ^{30}
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Pred. No. 1.1e-05;
0; Mismatches 145; Indels
                                                        ADDRESSEE: Legal Affairs, Genetics Institute, Inc
STREET: 87 CambridgePark Drive
                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/989,847
                                                                                                                                                                                                                                                                                                                                                                 GI-5192B
                                                                                                                                                                           MEDIUM TYPE: Tape
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: KAPINOS, Ellen J.
REGISTRATION NUMBER: 32,245
REFERENCE/DOCKET NUMBER: GI-5
TELEPHONE: 617-876-1170
TELEPHONE: 617-876-1170
TELEPHONE: 617-876-1870
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 5, Application US/08469411
Patent No. 6110880
GENERAL INFORMATION:
APPLICANT: Israel, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                1448 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 157; Conservative
                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Tape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       double
   TITLE OF INVENTION: HE NUMBER OF SEQUENCES: 3
                                                                                                                                                                                                                                                                                               CLASSIFICATION: 436
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97..1389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: doub.
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                                                                                                                        COUNTRY: USA
ZIP: 02140-2387
                                                                                       Cambridge
                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY:
LOCATION:
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                                                                                         CITY: C
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1058 ACAGCAGCAGCGACCAGAGGCAGGCCTGTAAGAAGCACGAGCTGTATGTCAGCTTCCGAG 1117
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Heterodimers, Compositions and Methods of Use.
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                                                                                                                        ADDRESSEE: Legal Affairs, Genetics Institute, Inc. STREET: 87 CambridgePark Drive CITY: Cambridge STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 1448;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 15.0%; Score 51; DB 4; Length 144 Best Local Similarity 50.5%; Pred. No. 1.1e-05; Matches 157; Conservative 0; Mismatches 145; Indels
                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GI-5192B-CON
                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: 97..1389
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Kapinos, Ellen J.
REGISTRATION NUMBER: 32,245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 06-Jun-1995
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-498-8622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 71
US-07-841-646-12
; Sequence 12, Application US/07841646
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MOLECULE TYPE: DNA (genomic)
Wolfman, Neil M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 617-876-5851
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS: double
                                                                                                                                                                                                                              COUNTRY: USA ZIP: 02140-2387 COMPUTER READABLE FORM: MEDIUM TYPE: Tape
                                                                            NUMBER OF SEQUENCES: 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
                                                                                                        CORRESPONDENCE ADDRESS:
                        TITLE OF INVENTION:
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1121 ACAGCAGCGACCAGAGGCAGGCCTGTAAGAAGCACGAGCTGTATGTCAGCTTCCGAG 1180 .1301 GGCTGGTCCACTTCATCAACCCGGAAACGGTGCCCAAGCCCTGCTGTGCGCCCACGCAGC 1360 77 aggatctgggatggaagtgggtccatgaacctaagggctactatgccaacttctgctcag 136 137 gecettgeceat----aceteegeagtgeagacacaaceacageacggtgetgg 187 188 gactgtacaacactctgaaccctgaagcatctgcctcgccttgctgctgctgcccaggacc 247 17 actgottocgcaacttggaggagaactgctgtgtgcgccccctctacattgacttccgac 76 Length 1505; Indels /function= "OSTEOGENIC PROTEIN" /product= "OP1C" /note= "OP1C - FUSION" 15.0%; Score 51; DB 1; Ler 50.5%; Pred. No. 1.1e-05; live 0; Mismatches 145; ADDRESSEE: TESTA, HURWITZ & THIBEAULT STREET: 53 STATE STREET
CITY: BOSTON
STATE: MASSACHUSETTS
COUNTRY: U.S.A.
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPAtible APPLICANT: OPPERMANN, HERMANN
APPLICANT: OZKAYNKK, ENGIN
APPLICANT: CZKAYNKK, ENGIN
APPLICANT: KUBERASAMPATH, THANGAVEL
APPLICANT: RUEGER, DAVID C.
APPLICANT: PANG, ROY H.L.
TITLE OF INVENTION: OSTEOGENIC DEVICES
CORRESPONDENCE ADDRESS: 33 CRP-001CP6 Sequence 12, Application US/08147023 Patent No. 5468845 GENERAL INFORMATION: INFORMATION FOR SEQ ID NO: 12: SEQUENCE CHARACTERISTICS: LENGTH: 1505 base pairs TYPE: NUCLEIC ACID STRANDEDNESS: Single TOPOLOGY: linear REFERENCE/DOCKET NUMBER: CR: TELECOMMUNICATION INFORMATION: TELEPHONE: 617/248-7000 TELEFAX: 617/248-7100 Best Local Similarity 50.5 Matches 157; Conservative NAME/KEY: CDS

LOCATION: 1..1452

COTHER INFORMATION: CTHER INFORMATION: CTHER INFORMATION: CTHER INFORMATION: US-07-841-646-12 | ||||| 1421 GAAACATGGTG 1431 MOLECULE TYPE: CDNA HYPOTHETICAL: YES 308 acatggtggtg 318 0 2 HYPOTHETICAL: ANTI-SENSE: FEATURE: RESULT 72 US-08-147-023-12 Query Match g g ŏ ŏ δ Óλ ò

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US-08-147-023-12

; 1301 cgcrggrccacurcarcaacccggaaacggrgcccaagcccrgcrgrgcgcccacgcagc 1360 1361 TCAATGCCATCTCCGTCCTCTACTTCGATGACAGCTCCAACGTCATCCTGAAGAAATACA 1420 77 aggatctgggatggaagtgggtccatgaacctaagggctactatgccaacttctgctcag 136 137 gocottgcccat-----acctccgcagtgcagacacaaacccacaggtgctgg 187 188 gactgtacaacactctgaaccctgaagcatctgcctcgccttgctgcgtgccccaggacc 247 248 tggagcccctgaccatcctgtactatgttgggaggacccccaaagtggagcagctctcca 307 Gaps 17 actgcttccgcaacttggaggagaactgctgtgtgcgccccctctacattgacttccgac 76 Score 51; DB 1; Length 1505; Pred. No. 1.1e-05; 0; Mismatches 145; Indels SOFTWARE: PATENTIN FELEASE #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/447,570
FILING DATE: 21-FEB-1992
CLASSIFICATION: 536
CLASSIFICATION: 536
FILING DATE: US 810,560
FILING DATE: 20-DEC-1991 Sequence 12, Application US/08447570
Patent No. 5714589
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: OPPERMANN, HERMANN
APPLICANT: RUBERASAMPATH, THANGAVEL
APPLICANT: RUBERA, DAVID C.
APPLICANT: RUBER, DAVID C.
APPLICANT: PANG, ROY H.L.
TITLE OF INVENTION: OSTEOGENIC DEVICES
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: TESTA, HURWITZ & THIBEAULT
STREET: 53 STATE STREET FILING DATE: 20-DEC-1991
PROOR APPLICATION DATA:
APPLICATION NUMBER: US 827,052
FILING DATE: 28-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 660,162
FILING DATE: 22-FEB-1991
PROOR APPLICATION DATA:
APPLICATION NUMBER: US 621,988
FILING DATE: 04-DEC-1990 MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS 15.0%; 50.5%; Query Match
Best Local Similarity 50.55
Matches 157; Conservative MASSACHUSETTS: U.S.A. COMPUTER READABLE FORM: MEDIUM TYPE: Floppy FILING DATE: 04-DEC-PRIOR APPLICATION DATA: 1421 GAAACATGGTG 1431 308 acatggtggtg 318 BOSTON COUNTRY: U ZIP: 02109 US-08-447-570-12 CITY: 1 STATE: q qq QΩ g δλ δλ δy ŏ

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1301 CGCTGGTCCACTTCATCAACCCGGAAACGGTGCCCCAAGCCCTGCTGTGCGCCCACGCAGC 1360
                                                                                                                        188 gactgtacaacactctgaaccctgaagcatctgcctcgccttgctgcgtgccccaggacc 247
                                                                                              248 tggagccctgaccatcctgtactatgttgggaggaccccaaagtggagcagctctcca 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/449,700
FILING DATE: 21-FEB-1992
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: OPPERMANN, HERMANN
APPLICANT: OZKAYNAK, ENGIN
APPLICANT: RUBERASAMPATH, THANGAVEL
APPLICANT: RUBERR, DAVID C.
APPLICANT: RUBERR, DAVID C.
TITLE OF INVENTION: OSTEOGENIC DEVICES
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
STREET: 53 STATE STREET
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FILNG DATE: 28-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION UNBER: US 660,162
FILNG DATE: 22-FEB-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 621,988
FILNG DATE: 04-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 621,849
FILNG DATE: 04-DEC-1990
PRIOR APPLICATION NUMBER: US 621,849
FILNG DATE: 21-NOV-1990
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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APPLICATION NUMBER: US 810,560
FILING DATE: 20-DEC-1991
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                 ; Sequence 12, Application US/08449700
; Patent No. 5863758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         UMBER: US 599,543
18-OCT-1990
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PRIOR APPLICATION DATA:
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PRIOR APPLICATION DATA:
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CITY: BOSTON
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                                                                                                                                                                                                                                                                                                    RESULT 74
US-08-449-700-12
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/product= "OPIC"
/note= "OPIC - FUSION"
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FILING DATE: 17-OCT-1989
PRIOR APPLICATION NUMBER: US 315,342
FILING DATE: 23-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 232,630
FILING DATE: 15-AUG-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 179,460
FILING DATE: 08-APR-1988
ATTORNEY/AGENT INFORMATION:
NAME: PITCHER, EDMUND R.
REGISTRATION NUMBER: CDD-0010
                FILING DATE: 04-DEC-1990

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 616,374

FILING DATE: 21-NOV-1990

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 600,024

FILING DATE: 18-OCT-1990

PRIOR APPLICATION DATA:
RELIGIOR DATE: 18-OCT-1990

FILING DATE: 18-OCT-1990
                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 579,865
FILING DATE: 07-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 569,920
FILING DATE: 20-AUG-1990
APPLICATION NUMBER: US 621,849 FILING DATE: 04-DEC-1990
                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 483,913
FILING DATE: 22-FEB-1990
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: CR
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/248-7000
TELEFAX: 617/248-7100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 12:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 1505 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear MOLECULE TYPE: CDNA HYPOTHETICAL: YES
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OTHER INFORMATION:
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OTHER INFORMATION:
US-08-447-570-12
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NAME/KEY:
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APPLICATION NUMBER: US 483,913

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1181 ACCTGGGCTGCCAGGACCTGGATCATCGCGCCTGAAGGCTACGCCCCTACTACTGTGAGG 1240
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                                                                                                                   ANTIBODIES TO OSTEOGENIC PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /function- "OSTEOGENIC PROTEIN"
/product- "OPIC"
/note- "OPIC - FUSION"
                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/449,699A
FILING DATE: 24-MAY-1995
CLASSIFICATION: 424
                                                                                                                            NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: TESTA, HURWITZ & THIBEAULT
STREET: 125 HIGH STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: STK-001CP6CN TELECOMMUNICATION INFORMATION: TELEPHONE: 617/248-7000
                 APPLICANT: OZKAYNAK, ENGIN
APPLICANT: KUBERASAMPATH, THANGAVEL
APPLICANT: RUGGER, DAVID C.
APPLICANT: DAWG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/147,023
FILING DATE: 01-NOV-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                    COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27,829
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1505 base pairs
                                                                                                PANG, ROY H.L.
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EDNESS: single
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OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                         APPLICANT: PANG, RC TITLE OF INVENTION:
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HYPOTHETICAL: YES
                                                                                                                                                                                                                        CITY: BOSTON
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/product= "OPIC"
/note= "OPIC - FUSION"
                                                                                                                                                                                                                                                                                                                                                                 CRP-001CP6
                                                                              FILING DATE: 17-OCT-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 315,342
FILING DATE: 23-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 232,630
FILING DATE: 15-AUG-1988
RESULT 75
US-08-449-699A-12
Sequence 12, Application US/08449699A
Sequence 5958441
GENERAL INFORMATION:
APPLICANT: OPPERMANN, HERMANN
                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 179,460
FILING DATE: 08-APR-1988
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                           NAME: PITCHER, EDMUND R.
REGISTRATION NUMBER: 27,829
REFERENCE/POCKET UNMBER: CRP-(SCHUNICATION INFORMATION:
TELEPHONE: 617/248-7000
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENTH: 1505 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match 15.0 Best Local Similarity 50.5 Matches 157; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: singl
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LOCATION: 1...
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/product= "OPI"
/evidence= EXPERIMENTAL
/standard\_name= "OPI" FILING DATE: 12-AUG 100 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 179,460
FILING DATE: 08-APR-1988
ATTORNEY/AGENT INFORMATION:
NAME: PITCHER, EDMUND R.
REGISTRATION NUMBER: 27,829
REFREENCE/DOCKET NUMBER: CRP-001CP6
TELECOMMUNICATION INFORMATION:
TELEPRAN: 617/248-7000
INFORMATION FOR SEQ ID NO: 1:
SEGUIENCE CHARACTERISTICS:
LENGTH: 1822 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: SINGle NAME/KEY: CDS

LOCATION: 49..1341

LIDENTIFICATION METHOD: experimental
OTHER INFORMATION: /function="OSTEC"
OTHER INFORMATION: /product="OP1"
OTHER INFORMATION: /evidence= EXPERI
OTHER INFORMATION: /standard\_name="US-07-841-646-1" RUEGER, DAVID C KUBERASAMPATH, THANGAVEL OPPERMANN, HERMANN APPLICATION NUMBER: US 232,630 FILING DATE: 15-AUG-1988 Sequence I, Application US/07901703; Patent No. 5344654; GENERAL INFORMATION: APPLICANT: RUGGER, DAVID C APPLICANT: KUBERASAMPATH, THANGI ORGANISM: HOMO SAPIENS TISSUE TYPE: HIPPOCAMPUS Matches 157; Conservative PRIOR APPLICATION DATA: 1310 GAAACATGGTG 1320 MOLECULE TYPE: CDNA HYPOTHETICAL: NO 308 acatggtggtg 318 Best Local Similarity ANTI-SENSE: NO ORIGINAL SOURCE: APPLICANT: US-07-901-703-1 Query Match δŏ à q δλ ò δ

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SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/147,023
                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: TESTA, HURWITZ & THIBEAULT STREET: 53 STATE STREET
                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-FEB-1992
                                                                                                                                                                                                                          APPLICANT: OPPERNANN, HERMANN
APPLICANT: OZKAYNAK, ENGIN
APPLICANT: KUBERASAMPATH, THANGAVEL
APPLICANT: RUEGER, DAID C.
APPLICANT: PANG, ROY H.L.
TITLE OF INVENTION: OSTEOGENIC DEVIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 810,560
FILING DATE: 20-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 827,052
FILING DATE: 28-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 660,162
FILING DATE: 2-FEB-1991
FILING DATE: 0-FEB-1991
FILING DATE: 0-FEB-1991
FILING DATE: 0-FEB-1991
FILING DATE: 0-PEC-1990
FILING DATE: 0-PEC-1990
FILING DATE: 0-PEC-1990
FILING APPLICATION NUMBER: US 616,374
FILING APPLICATION NUMBER: US 600,024
FILING DATE: 18-CCT-1990
PRIOR APPLICATION NUMBER: US 599,543
FILING DATE: 18-CCT-1990
PRIOR APPLICATION NUMBER: US 599,543
FILING DATE: 18-CCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 599,543
FILING DATE: 18-CCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 599,543
FILING DATE: 18-CCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 579,865
FILING DATE: 07-SEP-1990
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APPLICATION NUMBER: US 569,920
FILING DATE: 20-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 483,913
FILING DATE: 22-FEB-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 315,342
FILING DATE: 23-FEB-1989
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 422,613
FILING DATE: 17-OCT-1989
                                                                                                                                                             ; Sequence 1, Application US/08147023
; Patent No. 5468845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MASSACHUSETTS
                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
                                                   1310 GAAACATGGTG 1320
           308 acatggtggtg 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: U.S.A. ZIP: 02109
                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 21 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   BOSTON
                                                                                                                     RESULT 78
US-08-147-023-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 15.0%; Score 51; DB 1; Length 1822; Best Local Similarity 50.5%; Pred. No. 1.2e-05; Matches 157; Conservative 0; Mismatches 145; Indels
APPLICANT: OZAKAYNAK, ENGIN
TITLE OF INVENTION: PROSTHETIC DEVICES HAVING ENHANCED
TITLE OF INVENTION: OSTEOGENIC PROPERTIES
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                    CURENT APPLICATION DATA:
CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/901,703
FILING DATE: 19920616
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: PITCHER ESQ. EDMUD R
REGISTRATION NUMBER: 27,829
REFERENCE/DOCKET NUMBER: STR-057
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
SEQUENCE CHARACTERISTICS:
LENGTH: 1822 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TYPE: ULDOCAY: Ilnear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /function= "OSTEOGENIC PROTEIN"
/product= "OPI"
/evidence= EXPERTAL
/standard_name= "OPI"
                                                                                                            E: TESTA, HURWITZ & THIBEAULT
EXCHANGE PLACE, 53 STATE STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             experimental
                                                                                                                                                                                                                   ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE TYPE: HIPPOCAMPUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: CDS
COCATION: 49.1341
LOCATION: 49.1341
LIDENTIFICATION METHOD: 6
OTHER INFORMATION: /func
OTHER INFORMATION: /evic
COTHER INFORMATION: /evic
SOTHER INFORMATION: /stan
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: CDNA
                                                                                                                                                    BOSTON
                                                                                                                                                                                               COUNTRY: USA
ZIP: 02109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ANTI-SENSE: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HYPOTHETICAL:
                                                                                                         ADDRESSEE:
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77 aggatetggggetggaagtgggteeatgaacetaagggetaetatgecaaettetgeteag 136
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  APPLICANT: OZKAYNAK, ENGIN
APPLICANT: KUBERASAMPATH, THANGAVEL
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
TITLE OF INVENTION: RECOMBINANT OSTEOGENIC PROTEIN PRODUCTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15.0%; Score 51; DB 1; Length 1822; 50.5%; Pred. No. 1.2e-05; ive 0; Mismatches 145; Indels
                                                                                         NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: PATENT ADMINISTRATOR/CREATIVE BIOMOLECULES,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /function= "OSTEOGENIC PROTEIN"
/product= "OPI"
/evidence= EXPERINENTAL
/standard_name= "OPI"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/027,070
FILING DATE: 04-MAR-1993
PRIOR APPLICATION NUMBER: US 07/841,646
FILING DATE: 21-FEB-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/206,864
                                                                                                                                                                                                                                                                                                                                                   IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: PITCHER, EDWUND R
REGISTRATION NUMBER: 27,829
REFERENCE/DOCKET NUMBER: CR
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/7000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 617/248-7100
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1822 base pairs
                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE TYPE: HIPPOCAMPUS
                                                                                                                                                                                       STREET: 45 SOUTH STREET CITY: HOPKINTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 50.5
Matches 157; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HOMO SAPIENS
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IDENTIFICATION METHOD:
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OTHER INFORMATION:
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COTHER INFORMATION:
US-08-206-864-1
                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE
                                                                                                                                                                                                                                                                                01748
                                                                                                                                                                                                                                       STATE: MA
                                                                                                                                                                   ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1070 ACCTGGGCTGGCAGGACTGGTCGCGCCTGAAGGCTACGCGCCTACTACTACTGTGAGG 1129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1190 CGCTGGTCCACTTCATCAACCCGGAAACGGTGCCCAAGCCCTGCTGTGCGCCCACGCAGC 1249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1250 TCAATGCCATCTCCGTCCTCTACTTCGATGACAGCTCCAACGTCATCCTGAAGAAATACA 1309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  77 aggatotggggctggaagtgggtccatgaacctaagggctactatgccaacttctgctcag 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          188 gactgtacaacactctgaacctgaagcatctgcctcgccttgctgcgtgccccaggacc 247
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17 actgcttccgcaacttggaggagaactgctgtgtgcgccccctctacattgacttccgac 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           137 gcccttgcccat-----acctccgcagtgcagacacaacccacagcacggtgctgg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: .u.s

LOCATION: 49..1341

LIDENTFICATION METHOD: experimental

OTHER INFORMATION: /function= "OSTEOGENIC PROTEIN"

OTHER INFORMATION: /product= "OP1"

OTHER INFORMATION: /evidence= EXPERIMENTAL

OTHER INFORMATION: /standard_name= "OP1"
                                                                                                                                                                                         CRP-001CP6
                                                                 APPLICATION NUMBER: US 179,460 FILING DATE: 08-APR-1988 ATTORNEY/AGENT INFORMATION:
APPLICATION NUMBER: US 232,630 FILING DATE: 15-AUG-1988
                                                                                                                                  REGISTRATION NUMBER: 27,829
REGISTRATION NUMBER: 27,829
REFERENCE/DOCKET NUMBER: CRP-
TELECOMMUNICATION INFORMATION:
TELEPAN: 617/248-7000
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 1822 base pairs
TYPE: nucleic acid
STRANDENNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-206-864-1; Sequence 1, Application US/08206864
; Sequence 1, Application US/08206864
; Patent No. 5610021
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: RUEGER, DAVID C
APPLICANT: JONES, WILLIAM K
APPLICANT: TUCKER, ROMALD F
APPLICANT: OPPERMANN, HERMANN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: HOMO SAPIENS
TISSUE TYPE: HIPPOCAMPUS
                   FILING DATE: 15-AUG-1
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1310 GAAACATGGTG 1320
                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear MOLECULE TYPE: cDNA HYPOTHETICAL: NO
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MOLECULE TYPE:
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ZIP: 01748
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US-08-480-528A-3
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                          1190 CGCTGGTCCACTTCATCAACCGGAAACGGTGCCCAAGCCCTGCTGCGCGCCACGCAGC 1249
                                                                                                            1010 ACAGCAGCAGCAGCAGAGGCAGGCCTGTAAGAAGCACGAGCTGTATGTCAGCTTCCGAG 1069
188 gactgtacaacactctgaaccctgaagcatctgcctcgccttgctgcgtgccccaggacc 247
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                                                                                248 tggagccctgaccatcctgtactatgttgggaggaccccaaagtggagcagctctcca
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Pred. No. 1.2e-05;
0; Mismatches 145; Indels
                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: SMRT, JOHN
APPLICANT: OPPERMANN, HERMAN
APPLICANT: OPPERMANN, HERMAN
APPLICANT: CARAYNAK, ENGIN
APPLICANT: KUBERSAMPATH, THANGAVEL
APPLICANT: RUBERSAMPATH, THANGAVEL
APPLICANT: PANG, ROY H.L.
APPLICANT: COHEN, CHARLES M.
TITLE OF INVENTION: MORPHOGENIC PROTEIN SCREENING METHOD
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES 45 SOUTH STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/278,729A
FILING DATE: 20-JUL-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: PITCHER ESQ., EDMUND R.
REGISTATION NUMBER: 27,829
REFERENCE/DOCKET NUMBER: CRP-058CPFW
TELECOMMUNICATION INFORMATION:
TELEPHONE: (508) 435-9001
TELEPHONE: (508) 435-901
INFORMATION FOR SEQ. ID NO: 16:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CRP-058CPFW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: /product= "HOP-1"
US-08-278-729A-16
                                                                                                                                                                                                                                                                                                                    Sequence 16, Application US/08278729A
Patent No. 5650276
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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50.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 01748
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                            1310 GAAACATGGTG 1320
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 157; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HOPKINTON
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  USA
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                                                                                                                                                                                                                                                                                               US-08-278-729A-16
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1190 CGCTGGTCCACTTCATCAACCCGGAAACGGTGCCCAAGCCCTGCTGTGCGCCCCACGCAGC 1249
                                       1070 ACCTGGGCTGGCAGGACTGGATCATCGCGCCTGAAGGCTACGCCGCCTACTACTGTGAGG 1129
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77 aggatctgggctggaagtgggtccatgaacctaagggctactatgccaacttctgctcag 136
                                                                                 137 gocottgcccat-----acctccgcagtgcagacacaacccacaggcaggtgctgg 187
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/product= "hOP1-PP"
/note= "hOP1 cDNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: OPPERMANN, HERMANN
APPLICANT: OZRAYNAK, ENGIN
APPLICANT: KUBERRASAMARH, THANGAVEL
APPLICANT: RUBEGER, DAVID C.
APPLICANT: PANG, ROY H.L.
APPLICANT: POHG, ROY H.L.
APPLICANT: COHEN, CHARLES M.
TITLE OF INVENTION: OP3-INDUCED MORPHOGENESIS
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: FENTON ESQ., GILLIAN M.
REGISTRATION NUMBER: 36,508
REFERENCE/DOCKET NUMBER: CRP-07
TELECOMUNICATION INFORMATION:
TELEPHONE: (617) 248-7560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 3, Application US/08480528A Patent No. 5652118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (617) 248-7100 INFORMATION FOR SEQ ID NO: 3 SEQUENCE CHARACTERISTICS:
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EDNESS: single
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LOCATION: 49..1341
OTHER INFORMATION: /
OTHER INFORMATION: /
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CITY: HOPK
STATE: MA
      NAME/KEY:
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                                                                                                                                                                          Query Match
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                                                                                    17 actgetteegeaacttggaggagaactgetgtgtgegeeecetetacattgaetteegae 76
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  Length 1822;
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Score 51; DB 1; Length 182
Pred. No. 1.2e-05;
0; Mismatches 145; Indels
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: US/08/479,666
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: OZKAYNAK, HERMANN
APPLICANT: OZKAYNAK, ENGIN
APPLICANT: KUBERSAAMPATH, THANGAVEL
APPLICANT: RUBERSAAMPATH, THANGAVEL
APPLICANT: RUBER, DAVID C.
APPLICANT: CHEN, ROY H.L.
APPLICANT: CHEN, CHARLES M.
TITLE OF INVENTION: OP3-INDUCED MORPHOGENESIS
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY, AGENT INFORMATION:
NAME: FEBRON ESQ., GILLIAN M.
REGISTRATION NUMBER: 36,508
REFERENCE/DOCKET NUMBER: CRP-076DV
TELECOMMUNICATION INFORMATION:
TELEPHONE: (508) 435-6951
TELEPHONE: (508) 435-6951
TELEPHONE: (508) 435-6951
TELEPHONE: (508) 435-6951
TELEPHONE: (508) ESC 010
SEQUENCE CHARACTERISTICS:
LENGTH: 1822 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
STRANDEDNESS: single
TYPE: MOLECULE TYPE: CDNA
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 3, Application US/08479666 Patent No. 5652337 GENERAL INFORMATION:
15.0%;
ilarity 50.5%;
Conservative
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COMPUTER READABLE FORM:
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                      Similarity
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                                            Matches 157;
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Query Match
Best Local
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1250 TCAATGCCATCTCCGTCCTTTCGATGACAGCTCCAACGTCATCCTGAAGAAATACA 1309
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APPLICANT: KUBERASAMPATH, THANGAVEL
APPLICANT: KUBERASAMPATH, THANGAVEL
APPLICANT: RUBGER, DAVID C.
APPLICANT: OPPERMANN, HERMAN
APPLICANT: COHEN, CHARLES M.
APPLICANT: PANG, ROY H.L.
TITLE OF INVENTION: RECENERATION.
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES
STREET: 45 SOUTH STREET
CITY: HOPKINTON
                                                                                                                                                                                                                           6
                                                                                                                                                                           Length 1822;
                                                                                                                                                                                                                           145; Indels
COCATION: 49..1341

COTHER INFORMATION: /function= "OSTEOGENIC PROTEIN"
OTHER INFORMATION: /product= "hop1-pp"
US-08-479-666-3
US-08-479-666-3
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                                                                                                                                                                        Score 51; DB 1; Dred. No. 1.2e-05; 0; Mismatches 145
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMEDUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-155-343A-16; Sequence 16, Application US/08155343A; Patent No. 5656593
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NAME: FENTON ESQ., GILLIAN M.
REGISTRATION NUMBER: 36,508
REFERENCE/DOCKET NUMBER: CRP-06
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7560
TELEFAX: (617) 248-7100
                                                                                                                                                                           15.0%;
50.5%;
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Matches 157; Conservative
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TITLE OF INVENTION: TREATMENT TO PREVENT LOSS OF AND/OR
TITLE OF INVENTION: INCREASE BONE MASS IN METABOLIC BONE DISEASES
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1070 ACCTGGGCTGGCAGGACTGGATCACGGCCCTGAAGGCTACGCCGCCTACTGTGAGG
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50.5%; Pred. No. 1.2e-05;
Live 0; Mismatches 145; Indels
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ADDRESSER: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES STREET: 45 SOUTH STREET
CITY: HOPKINTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: INTERPOYMENT OF COMPUTED OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PATENTIN Release #1.0, Version #1.30 APPLICATION NATA: US/08/406,672 FILING DATE: 20-MAR-1995
                                                                                                                                                                                    LOCATION: 49..1341
COTHER INFORMATION: /product= "HOP-1"
US-08-155-343A-16
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APPLICANT: COHEN, CHARLES M.
APPLICANT: OPPERMANN, HERMANN
APPLICANT: OZKAYNAK, ENGIN
APPLICANT: RUGGER, DAVID C.
APPLICANT: PANG, ROY H.L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 16, Application US/08406672 Patent No. 56744844
                                  LENGTH: 1822 base pairs
TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                Best Local Similarity 50.5
Matches 157; Conservative
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                               TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: CDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
                                                                                                                                                                   NAME/KEY: CDS
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US-08-406-672-16
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                                                                                                                                                                                                                                                                                            Query Match
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1010 ACAGCAGCAGCACCAGAGGCAGGCCTGTAAGAAGCACGAGCTGTATGTCAGCTTCCGAG 1069
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APPLICANT: PANG, ROY H.L.
APPLICANT: COHEN, CHARLES M.
AITLE OF INVENTION: MORPHOGENIC PROTEIN SCREENING METHOD NUMBER OF SEQUENCES: 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES
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Pred. No. 1.2e-05;
0; Mismatches 145; Indels
                                                                                                                                                                                                   REFERENCE/DOCKET UNMER:
TELECOMUNICATION INFORMATION:
TELEPHONE: (617) 248-7560
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 1822 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; LOCATION: 49..1341
; OTHER INFORMATION: /product= "HOP-1"
US-08-406-672-16
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APPLICANT: OZKAYNAK, ENGIN
APPLICANT: KUBERASAMPATH, THANGAVEL
                APPLICATION NUMBER: US 752,857
FILING DATE: 30-AUG-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 667,274
FILING DATE: 11-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: FENYON ESG., GILLIAN M.
REGISTRATION NUMBER: 36,508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 16, Application US/08643563A Patent No. 5707810
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Best Local Similarity 50.5
Matches 157; Conservative
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APPLICANT: SMART, JOHN
APPLICANT: OPPERMANN, I
APPLICANT: OZKAYNAK, EN
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PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: CDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                        linear
                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 85
US-08-643-563A-16
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COMPOUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPOUTER: IBM PC compatible
COMPOUTER: IBM PC compatible
COMPOUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CUBRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/447,570
FILING DATE: 21-FEB-1992
CLASSIFICATION NUMBER: US 810,560
FILING DATE: 20-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 827,052
FILING DATE: 28-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 827,052
FILING DATE: 28-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60,162
APPLICATION NUMBER: US 60,162
TITLE OF INVENTION: OSTEOGENIC DEVICES NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS: TESTA, HURWITZ & THIBEAULT STREET: 53 STATE STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CRP-001CP6
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PRICE APPLICATION DATA:

APPLICATION NUMBER: US 621,988
FILING DATE: 04-DEC-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 621,849
FILING DATE: 04-DEC-1990

PRIOR APPLICATION NUMBER: US 616,374
FILING DATE: 21-NOV-1990

PRIOR APPLICATION NUMBER: US 600,024
FILING DATE: 18-OCT-1990

PRIOR APPLICATION NUMBER: US 599,543
FILING DATE: 18-OCT-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 599,543
FILING DATE: 18-OCT-1990

PRIOR DATE: 18-OCT-1990
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PRIOR APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 08-APR-1988
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 07-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 569,920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 23-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 232,630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US 315,342
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US 422,613
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REFERENCE/DOCKET NUMBER: CRI
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/248-7000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 20-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 483
FILING DATE: 22-FEB-1990
PRIOR APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 17-OCT-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 617/248-7100
INFORMATION FOR SEQ ID NO: 1:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 1822 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: U
                                                                                                                                                     STATE: MASSACHUSETTS
                                                                                                                                                                            COUNTRY: U.S.A.
                                                                                                                           BOSTON
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 51; DB 1; Length 1822;
Pred. No. 1.2e-05;
0; Mismatches 145; Indels
                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                           CLASSLITATION:

ATTORNEY AGENT INFORMATION:

NAME: TWOMEY ESQ., MICHAEL J.

REGISTRATION UNBER: 38.349

REFERENCE/DOCKET NUMBER: CRP-058CN2

TELECOMMUNICATION INFORMATION:

SEQUENCE CHARACTERISTICS:

LENGTH: 1822 base pairs

TYPE: nucleic acid

STRANDEDNESS:

SINGLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; NAME/KEY: CDS
; LOCATION: 49..1341
; OTHER INFORMATION: /product= "HOP-1"
US-08-643-563A-16
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OZKAYNAK, ENGIN
KUBERASAMPATH, THANGAVEL
RUBGER, DAVID C.
PANG, ROY H.L.
                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/643,563A FILING DATE: 06-MAY-1996 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-447-570-1; Sequence 1, Application US/08447570; Patent No. 5714589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 15.0%;
Best Local Similarity 50.5%;
Matches 157; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1310 GAAACATGGTG 1320
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APPLICANT: OPPERMAN
APPLICANT: OZKAYNAR
APPLICANT: KUBERAS;
APPLICANT: RUGGER,
APPLICANT: PANG, R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
     HOPKINTON
                                           COUNTRY: US
ZIP: 01748
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ADDRESSEE:
     SOFTWARE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1250 TCAATGCCATCTCCGTCCTCTACTTCGATGACAGCTCCAACGTCATCCTGAAGAAATACA 1309
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      248 tggagcccctgaccatcctgtactatgttgggaggacccccaaagtggagcagctctcca 307
                                                                                                                                                                                                                                                                                                                                                                                                                actgcttccgcaacttggaggagaactgctgtgtgcgccccctctacattgacttccgac 76
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: KUBERAAMPATH, THANGAVEL
APPLICANT: RUEGER, DAVID C.
APPLICANT: OPPERMANN, HERMAN
APPLICANT: COHEN, CHARLES M.
APPLICANT: PANG, ROY H.L.
TITLE OF INVENTION: MORPHOGENIC-INDUCED PERIODONTAL TISSUE
NUMBER OF SEQUENCES: 33
                                                                                                                                                                                                                                                                                                                                               Length 1822;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES
STREET: 45 SOUTH STREET
                                                                                                                                                                                                                                                                                                                                            Score 51; DB 1; Length 182
Pred. No. 1.2e-05;
0; Mismatches 145; Indels
                                                                                                                                                                                                                          "OSTEOGENIC PROTEIN'
                                                                                                                                                                                                                        /function= "OSTEOGENIC
/product= "OP1"
/evidence= EXPERIMENTAL
/standard_name= "OP1"
                                                                                                                                                                                                          experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Z1F: v1,v2
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OBERBATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 16, Application US/08643763A Patent No. 5733878 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                            15.0%;
                                                                                                                                    TISSUE TYPE: HIPPOCAMPUS FEATURE:
                                                                                                                     HOMO SAPIENS
                                                                                                                                                                    NAME/KEY: CDS
LOCATION: 49..1341
IDENTIFICATION METHOD:
OTHER INFORMATION: /ft
                                                                                                                                                                                                                                                                                                                                                                              Conservative
TYPE: nucleic acid
STRANDEDNESS: single
                               TOPOLOGY: linear MOLECULE TYPE: CDNA HYPOTHETICAL: NO ANTI-SENSE: NO ONGINAL SOURCE: ORGANISM: HOMO SAPI)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ) OTHER INFORMATION:
) OTHER INFORMATION:
) OTHER INFORMATION:
US-08-447-570-1
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                                                                                                                                                                                                                                                                                                                                                           Similarity
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                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Simil
Matches 157; (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-643-763A-16
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1010 ACAGCAGCAGCGACCAGAGGCAGGCCTGTAAGAAGCACGAGCTGTATGTCAGCTTCCGAG 1069
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APPLICANT: OZRAYNAK, ENGIN
APPLICANT: SMART, JOHN E.
TITLE OF INVENTION: MORPHGEN TREATMENT OF GASTROINTESTINAL
TITLE OF INVENTION: ULCERS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 1822;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 51; DB 1; Length 182
Pred. No. 1.2e-05;
0; Mismatches 145; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES
PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; LOCATION: 49..1341
; OTHER INFORMATION: /product= "HOP-1"
US-08-643-763A-16
                                                                                                       CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: FERTON ESG., GILLIAN M.
REGISTRATION NUMBER: 36,508
REGISTRATION NUMBER: CFP-067CN
                                      JMBER: US/08/643,763A
06-MAY-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COHEN, CHARLES M.
CHARETTE, MARC F.
KUBERASAMPATH, THANGAVEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 16, Application US/08462623 Patent No. 5739107
                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7560
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: KUBERASAMPATH, THAI
APPLICANT: RUEGER, DAVID C.
APPLICANT: OPPERMANN, HERMANN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15.0%;
50.5%;
                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 1822 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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Best Local Similarity 50.5'
Matches 157; Conservative
                              CURRENT APPLICATION DATA
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CORRESPONDENCE ADDRESS
                                                   APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1310 GAAACATGGTG 1320
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APPLICANT: COHEN,
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                                                                                 FILING DATE:
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Gaps

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1310 GAAACATGGTG 1320
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                                                                                                                                                                                                                                                                                 01748
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                                                                                                                                                                                                                                            STATE:
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Best Local Similarity 50.5%; Pred. No. 1.2e-05;
Matches 157; Conservative 0; Mismatches 145; Indels
                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                    CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/445,882
FILING DATE: 22-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: FENTON ESG., GILLIAN M.
REGISTRATION NUMBER: 36,508
REFERENCE/DOCKET NUMBER: CRP-074CN
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: (508) 435-901
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product= "HOP-1"
                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/462,623 FILING DATE:
                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Sequence 16, Application US/08451953A
Patent No. 5741641
Patent No. 5741641
Patent No. 5741641
Patent SMRPAL INFORMATION:
APPLICANT: SMART, JOHN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 1822 base pairs TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear
: .45 SOUTH STREET HOPKINTON
                                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; LOCATION: 49.1341
; OTHER INFORMATION:
US-08-462-623-16
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                                                       COUNTRY: US
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APPLICANT: OZKAYNAK, ENGIN
APPLICANT: KUBERASAMPATH, THANGAVEL
APPLICANT: RUGGER, DAVID C.
APPLICANT: PANG, ROY H.L.
APPLICANT: POHEN, CHARLES M.
TITLE OF INVENTION: MORPHOGENIC PROTEIN SCREENING METHOD
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: APATEMT ADMINISTRATOR, CREATIVE BIOMOLECULES
STREET: 45 SOUTH STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 51; DB 1; Length 182
Pred. No. 1.2e-05;
0; Mismatches 145; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/451,953A FILING DATE: 26-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 26-MAY 1995
CLASSIFICATION: 435
ATTORNEY AGENT INFORMATION:
NAME: PITCHER ESQ., EDMUND R.
REGISTRATION NUMBER: 27,829
REFERENCE/DOCKET NUMBER: 27,829
TELECOMMUNICATION INFORMATION:
TELEFAN: (508) 435-9001
TELEFAX: (508) 435-6951
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
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CTHER INFORMATION: /product= "HOP-1"
US-08-451-953A-16
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                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
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Best Local Similarity 50.5%;
Matches 157; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: single
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
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; 1190 CGCTGGTCCACTTCATCAACCCGAAACGGTGCCCAAGCCCTGCTGTGCGCCCACGCAGC 1249 1250 TCAATGCCATCTCCGTCCTCTACTTCGATGACAGCTCCAACGTCATCCTGAAGAAATACA 1309 1010 ACAGCAGCAGCGACCAGAGGCAGGCCTGTAAGAAGCACGAGCTGTATGTCAGCTTCCGAG 1069 248 tggagcccctgaccatcctgtactatgttgggaggacccccaaagtggagcagctctcca 307 Gaps 17 actgcttccgcaacttggaggagaactgctgtgtgcgcccctctacattgacttccgac 76 137 gocottgoccat----acotocgoagtgoagacacacacacacaggtgotgg 188 gactgtacaacactctgaaccctgaagcatctgcctcgccttgctgcgtgccccaggacc Length 1822; Sequence 16, Application US/08445468A
Patent No. 5849686
GENERAL INFORMATION:
APPLICANT: RUBERASAMPATH, THANGAVEL
APPLICANT: OPPERMANN, HERMAN
APPLICANT: PANG, ROY H.L.
APPLICANT: POMEN, MORPHOGEN-INDUCED LIVER REGENERATION
TITLE OF INVENTION: MORPHOGEN-INDUCED LIVER REGENERATION E: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES 45 SOUTH STREET Pred. No. 1.2e-05; 0; Mismatches 145; Indels COMPUTER TEADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFWWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 22-MAY-1995
CLASSIFICATION: 514 Score 51; DB 2; Pred. No. 1.2e-0 CRP-072FW2 ATTORNEY/AGENT INFORMATION:
NAME: FENTON ESQ., GILLIAN M.
REGISTRATION UNDRER: 36,508
REFERENCE/DOCKET UNDRER: CRP-(TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7560
INFORMATION FOR SEQ. ID NO: 16:
SEQUENCE CHARACTERISTICS: 15.0%; 50.5%; LENGTH: 1822 base pairs TYPE: nucleic acid STRANDEDNESS: single Matches 157; Conservative NUMBER OF SEQUENCES: 1310 GAAACATGGTG 1320 308 acatggtggtg 318 TOPOLOGY: linear MOLECULE TYPE: CDNA Query Match Best Local Similarity STREET: 45 CTTY: HOPKINTON FILING DATE: 23 CLASSIFICATION: USA COUNTRY: US ZIP: 01748 RESULT 91 US-08-445-458A-16 ADDRESSEE:

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1190 CGCTGGTCCACTTCATCAACCCGGAAACGGTGCCCAAGCCCTGCTGTGCGCCCACGCAGC 1249
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                                                                                                                                                                                                                                                                                                           15.0%; Score 51; DB 2; Length 1822; 50.5%; Pred. No. 1.2e-05; ive 0; Mismatches 145; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: TELD DICKE, Peter
APPLICANT: HELDIN, Carl-Henrik
APPLICANT: MIYAZONO, Kohei
APPLICANT: SAMPATH, Kuber T.
TITLE OF INVENTION: Morphogenic Protein-Specific Cell
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
                                                                                                                                                                              /function= "OSTEOGENIC PROTEIN"
/product= "hOP1-PP"
/note= "hOP1 cDNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Testa, Hurwitz & Thibeault
STREET: 125 High St.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/481,337A FILING DATE: 02-UUN-1995 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 9, Application US/08481337A; Patent No. 5863738; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
    LENGTH: 1822 base pairs
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                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 50.53
Matches 157; Conservative
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CURRENT APPLICATION DATA:
                                                 single
                                                                                                             FEATURE:
NAMBEKEY: CDS
COCATION: 49.1341
COTHER INFORMATION:
COTHER INFORMATION:
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COTHER OF THE INFORMATION:
US-08-901-200A-3
                             nucleic acid
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                                                                                        MOLECULE TYPE: CDNA
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                                                                      linear
                                        STRANDEDNESS:
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                                                                    TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-481-337A-9
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CITY: BC
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                                                                                                                                                                                                                                                                                                                Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                           1190 CGCTGGTCCACTTCATCAACCGGAAACGGTGCCCAAGCCCTGCTGCGCGCCACGCAGC 1249
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                                                                                                                                                                                                                                                                                                         77 aggatctggggctggaagtgggtccatgaacctaagggctactatgccaacttctgctcag 136
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                                                                                                                                                                                                                   17 actgettecgeaacttggaggagaactgetgtgtgegeeeeetetacattgaetteegae 76
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                                                                                                                                                                              6
                                                                                                                                   Score 51; DB 2; Length 1822;
Pred. No. 1.2e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREES: HOPKINTON
STATE: MA
                                                                                                                        15.0%; Score J., 50.5%; Pred. No. 1.2e-05; +ive 0; Mismatches 145; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 3, Application US/08901200A
Fatent No. 5854071
GENERAL INFORMATION:
APPLICANT: OPPERMANN, HERMANN
APPLICANT: CAKAYNAK, ENGIN
APPLICANT: RUBERASAMPALY, THANGAVEL
APPLICANT: RUBERASAMPALY, THANGAVEL
APPLICANT: RUBERES, DAVID C.
APPLICANT: COHEN, CHARLES M.
APPLICANT: COHEN, CHARLES M.
APPLICANT: APPLICANT: 10 COHEN, CHARLES M.
APPLICANT: 10 COHEN, CHARLES M.
ANDMER OF SEQUENCES: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:

FILLING DATE: US/08/901,200A PILLING DATE: 28-JUL-1997
                                      ; OTHER INFORMATION: /product= "HOP-1"
US-08-445-468A-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-JUL-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CRP-076DV2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 530
ATORNEY/AGENT INFORMATION:
NAME: MEYERS, THOMAS. C.
REGISTRATION NUMBER: 36,989
REFERENCE/DOCKET NUMBER: CRP-OFECOMUNICATION INFORMATION:
TELEPHONE: (508) 435-6951
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                   Best Local Similarity 50.5
Matches 157; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS
NAME/KEY: CDS
LOCATION: 49..1341
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ZIP: 01748
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-901-200A-3
                                                                                                                                 Query Match
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/449,700
FILING DATE: 21-FEB-1992
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 810,560
FILING DATE: 20-DEC-1991
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER: 27,829
REPERENCE/DOCKFY NUMBER: CRP-001CP6
TELECOMMUNICATION:
TELEPHONE: 617/248-7000
                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 827,052
FILING DATE: 28-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION DATA:
RELING APPLICATION DATA:
FILING APPLICATION DATA:
APPLICATION NUMBER: US 60,162
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 621,988
FILING DATE: 04-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 621,849
FILING DATE: 04-DEC-1990
PRIOR APPLICATION NUMBER: US 616,374
FILING DATE: 21-NOV-1990
PRIOR APPLICATION NUMBER: US 616,374
FILING DATE: 21-NOV-1990
PRIOR APPLICATION NUMBER: US 616,374
FILING DATE: 118-OCT-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: O7-SEP-1990
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 569,920
FILING DATE: 20-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 483,913
FILING DATE: 22-FEB-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 422,613
FILING DATE: 17-OCT-1989
PRIOR APPLICATION NUMBER: US 315,342
FILING DATE: 23-FEB-1989
PRIOR APPLICATION NUMBER: US 232,630
FILING DATE: 15-AUG-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 232,630
FILING DATE: 15-AUG-1988
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 232,630
FILING DATE: 08-APR-1988
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 599,543
FILING DATE: 18-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 579,865
FILING DATE: 07-SEP-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: 617/248-7000
TELEFAX: 617/248-7100
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: HOMO SAPIENS
TISSUE TYPE: HIPPOCAMPUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: PITCHER, EDMUND R. REGISTRATION NUMBER: 27,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS
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STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                  /function= "OSTEOGENIC PROTEIN"

/product= "OPE"

/evidence= EXPERIMENTAL

/standard_name= "OPI"
REGISTRATION NUMBER: 36,989
REFERENCE/DOCKET NUMBER: CRP-097CP2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
FELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CARRACTERISTICS:
LENGTH: 1822 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: OPPERMANN, HERMANN
APPLICANT: OZKAYNAK, ENGIN
APPLICANT: KUBERASAMPATH, THANGAVEL
APPLICANT: RUBGER, DAVID C.
APPLICANT: RANG, ROY H.L.
TITLE OF INVENTION: OSTEOGENIC DEVICES
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: TESTA, HURWITZ & THIBEAULT STREET: 53 STATE STREET
                                                                                                                                                                                                                                                                                                                                                                              experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1, Application US/08449700 Patent No. 5863758 GENERAL INFORMATION:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                              LOCATION: 49.1341

DENTIFICATION METHOD: e

OTHER INFORMATION: /func

OTHER INFORMATION: /func

OTHER INFORMATION: /evid

COTHER INFORMATION: /evid

US-08-481-337A-9
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STATE: MASSACHUSETTS
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                        NAME/KEY: CDS
LOCATION: 49..1341
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    248 tggagcccctgaccatcctgtactatgttgggaggaccccaaagtggagcagctctcca 307
                                                                                                                                                                                                                                                                                  17 actgetteegeaacttggaggagaactgetgtgtgegeeecetetaeattgaetteegae 76
                                                                                                                                                                                                                                            6
                                                                                                                                                                                                 Length 1822;
                                                                                                                                                                                             15.0%; Score 51; DB 2; Length 182
50.5%; Pred. No. 1.2e-05;
Live 0; Mismatches 145; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: OZRAYNAK, HERMANN
APPLICANT: OZRAYNAK, ENGIN
APPLICANT: KUBERASAMPATH, THANGAVEL
APPLICANT: RUBGER, DAVID C.
APPLICANT: PANG, ROY H.L.
TITLE OF INVENTION: ANTHBODIES TO OSTEOGENIC PROTEINS
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
                                        /function= "OSTBOGENIC PROTEIN"
/product= "OP1"
/evidence= EXPERIMENTAL
/standard_name= "OP1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
ELICATION NUMBER: US/08/449,699A
FILING DATE: 24-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: PITCHER, EDMUND R.
REGISTRATION NUMBER: 27,829
REFERENCE/DOCKET NUMBER: STK-001CP6CN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: TESTA, HURWITZ & THIBEAULT
STREET: 125 HIGH STREET
                        experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/147,023
FILING DATE: 01 NOV-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1, Application US/08449699A; Patent No. 5958441; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Floppy disk
                                                                                                                                                                                             Query Match 15.0%
Best Local Similarity 50.5%
Matches 157; Conservative
LOCATION: 49..1341
IDENTIFICATION METHOD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MASSACHUSETTS: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                      CTHER INFORMATION:
COTHER INFORMATION:
OTHER INFORMATION:
COTHER INFORMATION:
US-08-449-700-1
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STATE: MASSACHI
COUNTRY: U.S.A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 15.0%; Score 51; DB 2; Length 182 Best Local Similarity 50.5%; Pred. No. 1.2e-05; Matches 157; Conservative 0; Mismatches 145; Indels
                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: /function= "OSTEOGENIC PROTEIN"
OTHER INFORMATION: /product= "OP1"
OTHER INFORMATION: /evidence= EXPERIMENTAL
US-08-449-699A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: ICHIJO, HIDENORI
APPLICANT: ICHIJO, HIDEKI
APPLICANT: SAMPATH, KUBER T.
TITLE OF INVENTION: NOVEL SIGNALLING RECEPTOR FOR TITLE OF INVENTION: MORPHOGENIC PROTEINS
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Testa, Hurwitz & Thibeault
STREET: 125 High St.
                                                                                                                                                                                                                                                                                                                                                                                         experimental
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/248-7000
TELEFAX: 617/248-7100
                                                             INFORMATION FOR SEQ ID NO: 1:
                                                                             SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
LENGTH: 1822 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                 TISSUE TYPE: HIPPOCAMPUS
                                                                                                                                                                                                                                                                               HOMO SAPIENS
                                                                                                                                                                                                                                                                                                                                                              LOCATION: 49..1341
IDENTIFICATION METHOD:
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                                                                                                                                                                                                                                                                                                                                             NAME/KEY: CDS
                                                                                                                                                                                                                                     ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: HOM
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ZIP: 02110
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STATE:
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                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES STREET: 45 SOUTH STREET
                  TITLE OF INVENTION: MORPHOGEN TREATMENT FOR LIMITING TITLE OF INVENTION: PROLIFERATION OF EPITHELIAL CELLS. NUMBER OF SEQUENCES: 33
                                                                                                                                                                                                                                                                                                                                                SOFTWARE PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,397A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: PITCHER ESO, EDMUND R.
REGISTRATION NUMBER: 27,829
REFERENCE/POCKET UNBER: CRP-074FW2
TELECOMMUNICATION:
TELEPHONE: 617/248-7000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; NAME/KEY: CDS
; LOCATION: 49..1341
.: OTHER INFORMATION: /product= "HOP-1"
US-08-461-397A-16
                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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US-08-912-088-16
; Sequence 16, Application US/08912088
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 617/248-7100
INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 1822 base pairs
           SMART, JOHN E.
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Best Local Similarity 50.5
Matches 157; Conservative
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                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
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                                                                                                                                                               CITY: HOPKINTON STATE: MA
                                                                                                                                                                                                                   USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /function= "Osteogenic Protein"
/product= "OP1"
/standard_name= "OP1"
                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/696,268B
                                                                                                                                                                                                ATTORNEY AGENT INFORMATION:
NAME: MEYERS, Thomas C.
REGISTRATION NUMBER: 36,989
REFERENCE/DOCKET NUMBER: CRP-117
TELECOMMUNICATION INFORMATION:
TELEFAX: (617) 248-7000
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1822 base pairs
TYPE: nucleic acid
STRANDENNESS: single
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CHARETTE, MARC F.
KUBERASAMPATH, THANGAVEL
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Patent No. 5972884
GENERAL INFORMATION:
APPLICANT: COHEN, CHARLES M.
APPLICANT: CHARRETE, MARC F.
APPLICANT: KUBERASAMPATH, THANGAVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RUEGER, DAVID C.
OPPERMANN, HERMANN
PANG, ROY H.L.
OZKAYNAK, ENGIN
                         Floppy disk
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Best Local Similarity 50.59
Matches 157; Conservative
COMPUTER READABLE FORM:
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OTHER INFORMATION: OTHER INFORMATION: OTHER INFORMATION: /
                                                                                                                                                                                  CLASSIFICATION: 435
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                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY:
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APPLICANT:
APPLICANT:
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1250 TCAATGCCATCTCCGTCCTCTACTTCGATGACAGCTCCAACGTCATCCTGAAGAAATACA 1309
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                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: KUBERASAMPATH, THANGAVEL
APPLICANT: COHEN, CHARLES M.
APPLICANT: COHEN, DAVID C.
APPLICANT: OPPERANN, HERMAN
APPLICANT: PANG, ROY H.L.
TITLE OF INVENTION: MORPHOGENIC-ENRICHED DIETARY COMPOSITION
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 1822;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES STREET: 45 SOUTH STREET
CITY: HOPKINTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 51; DB 3; Length 182
Pred. No. 1.2e-05;
0; Mismatches 145; Indels
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OTHER INFORMATION: /product= "HOP-1"
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CRP-071FW
                                                                                                                                                                                                                           RESULT 99
VS-08-278-730A-16
Sequence 16, Application US/08278730A
; Patent No. 6022853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: FENTON ESQ., GILLIAN M.
REGISTRATION NUMBER: 36,508
REFERENCE/DOCKET NUMBER: CRP-07
TELECOMMUNICATION INFORMATION:
TELEPAX: (617) 248-7560
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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Best Local Similarity 50.5%;
Matches 157; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1822 base pairs
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                            1310 GAAACATGGTG 1320
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                                                                308 acatggtggtg 318
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                                                                          APPLICANT: OPPERANN, HERMAN
APPLICANT: OZKAYNAK, ENGIN
APPLICANT: OZKAYNAK, ENGIN
APPLICANT: RUBERSAMAPATH, THANGAVEL
APPLICANT: RUBGER, DAVID C.
APPLICANT: RUBGER, DAVID C.
APPLICANT: PANG, ROY H.L.
APPLICANT: OCHEW, CHARLES M.
TITLE OF INVENTION: MORPHOGENIC PROTEIN SCREENING METHOD NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES STRRET: HOPKINTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15.0%; Score 51; DB 2; Length 1822; 50.5%; Pred. No. 1.2e-05;
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OTHER INFORMATION: /product= "HOP-1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: CR
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (508) 435-9001
TELEPAX: (508) 435-6951
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 01748
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 1822 base pairs
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Matches 157; Conservative
                                                         APPLICANT: SMART, JOHN
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STRANDEDNESS: single
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OPERATING SYSTEM:
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APPLICANT: SAMPATH, KUBER T.
APPLICANT: SAMPATH, KUBER T.
APPLICANT: RUEGER, DAVID C.
TITLE OF INVENTION: MANUFACTURE OF AUTOGENOUS REPLACEMENT
TITLE OF INVENTION: BODY PARTS
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OD: experimental
/function="OSTEOGENIC PROTEIN"
/product= "OP1"
/evidence= EXPERIMENTAL
/standard_name= "OP1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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Patent No. 6027743
GENERAL INFORMATION:
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ATTORNEY/AGENT INFORMATION:
NAME: KELLEY, ROBIN D.
REGISTRATION NUMBER: 34,637
REFERENCE/DOCKET NUMBER: CRP-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/248-7000
TELEFAX: 617/248-7100
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1822 base pairs
TYPE: NUCLEIC acid
STRANDENESS: SINGLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
~~unimeR: IBM PC compatible
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TISSUE TYPE: HIPPOCAMPUS
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CITY: BOSTON
STATE: MASSACHUSETTS
COUNTRY: U.S.A.
"TP: 02109
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IDENTIFICATION METHOD:
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COTHER INFORMATION:
OTHER INFORMATION:
COTHER INFORMATION:
US-08-458-811-1
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OPERATING SYSTEM:
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MOLECULE TYPE: CD
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1070 ACCTGGGCTGGCAGGACTGGATCATCGCGCCTGAAGGCTACGCCGCCTACTACTACTGTGAGG 1129
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                           Gaps
                                                    17 actgcttccgcaacttggaggagaactgctgtgtgcgccccctctacattgacttccgac 76
                        145; Indels
   Pred. No. 1.2e-05;
0; Mismatches 145
50.5%;
                      Conservative
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 Best Local Similarity
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                    Matches 157;
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Search completed: October 30, 2001, 11:50:43 Job time: 4305 sec

Query Match

15.0%; Score 51; DB 3; Length 1822;

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                    GenCore version 4.5
Copyright (c) 1993 · 2000 Compugen Ltd.
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Maximum Match 1008
Listing first 100 summaries
                                                                                            OM nucleic - nucleic search, using sw model
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gb\_est45:\*
gb\_est46:\*
gb\_est47:\*

gb\_est41:'
gb\_est43:'
gb\_est43:'
gb\_est44:'

em\_estro18:\*

em\_gss\_huml:\* em\_gss\_hum2:\* em\_gss\_hum3:\*

gb\_est110:\*
gb\_est111:\*
gb\_htc:\*
em\_gss\_fun:\*

em\_gss\_hum4:\*
em\_gss\_hum5:\*
em\_gss\_hum7:\*
em\_gss\_hum7:\*
em\_gss\_hum8:\*
em\_gss\_hum8:\*
em\_gss\_hum9:\*
em\_gss\_lun1:\*
em\_gss\_luv1:\*

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| 1187 | 91 cest48| ...
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| 120 | 93 cest56| .
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em\_gss\_inv3:\*
em\_gss\_other:\*
em\_gss\_other:\*
em\_gss\_pln1:\*
em\_gss\_rod1:\*
em\_gss\_rod2:\*
em\_gss\_rod3:\*
em\_gss\_rod4:\*
em\_gss\_rod4:\*
em\_gss\_rod4:\*
em\_gss\_rod4:\*
em\_gss\_rod5:\*
em\_gss\_rod5:\*
em\_gss\_rod5:\*
em\_gss\_rod5:\*
em\_gss\_rod6:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

em\_gss\_rod8: gb\_gss35:\* gb\_gss36:\* gb\_gss37:\*

gb\_gss33:\* gb\_gss34:\* em\_gss\_inv4:\*

gb\_gss29:\* gb\_gss30:\* gb\_gss31:\* gb\_gss32:\* em\_gss\_rod6 em\_gss\_rod7

C 69 145.4 47.5 409 114 A 14 A 14 A 14 A 14 A 14 A 14 A 17 A 18 A 17 A 18 C 71 138 40.7 561 118 A 17 C 72 137.2 40.5 587 156 C	136.4 40.2 456 159 136.2 40.2 571 17 135.2 39.9 878 107	134.6 39.7 392 134.2 39.6 542	79 133.4 39.4 583 110	130.4 38.5	129.2 38.1 915 127.4 37.6 301	125.2 36.9 560	86 123.6 36.5 748 168	123 36.3 533 1	89 122.4 36.1 398 187	122 36.0 259 118	92 115.8 34.2 867 145	114.2 33.7	95 112 33.0 175 164	96 112 33.0 255 171	9/ 111 32./ 428 13 98 110.4 32.6 248 118	110 32.4 266	100 109.8 32.4 3/9 169			L 4:1118:34		LOCUS AL532438 964 bp DEFINITION AL532438 LT NFLOD1 NBC4	prime, mRNA sequence	ACCESSION AL532438 VERSION AL532438 1 GT-12795931	S EST.	SOURCE human.		Mammalia; Eutheria;				Genoscope – Centre Natio BP 191 91006 EVRY cedex		FEATURES Location/Qualit Source 1964		/db_xrer="taxon /clone="CS0DM01	/clone_lib="LTI	/sex="mare" /tissue_type="n	/lab_host="DH10		enriched, doubl	ctor.	by Life Technol
Description	AL532438 AL532438 AW412139 uq46g03.y	BG175423 602337778 BF542567 UI-R-G3-S BE101707 601764767	AV670561 114647 MA	AA312041 V201907.1 BG244370 602356090	AW823286 ur71c12.y AA657145 vr26d03.r	AW958056 EST370126 AT951831 WX38h08 W	BF726995 by15c03.y	AI131171 qc15c11.x AI089904 qa16a08 x	AW073988 xb06a06.x	BF543086 UI-R-AFI- BF645704 7-274510 V	BE464068 hx84h02.x	AI148173 qb56d01.x	AI760533 Wh88b09.x	AI927187 WO88c02.x	A1991139 WU30903.X A1743724 WG53b06.X	BG180040 602329596	AI323791 mm47e08.x	AW919738 EST351042	A139939 EST251662 BF287476 EST452067	AI323392 mj35f01.x RG518882 602578182	AI323037 mj35f01.y	AW627667 hh89h10.x AI433146 ti32a11.x	AA000733 mg35b06.r	AI434956 ti46t04.x BF042894 HP250019B	BF044612 BP250020A	W45844 mc77e02.rl	A1157673 ue48g10.r	AI824845 wb02f01.x	AW600944 RC1-BN001	BG058796 naf10f12.	A1421250 tf14d02.x	AW600952 RC1-BN001 BE575698 dc62d10.x	BG058804 naf10909.	AL530080 AL530080 AI304490 qo54e06.x	AI360877 qy01c06.x	A12/2940 4130901.X A1273619 q156c01.x	AA049522 mj35f01.r	AU016729 AU016729	AI634937 tz74f09.x W98872 mf89e01 r1	BF682484 602117568	AI604914 me44c04.x AW600938 RC1-RNO01	AA021815 mh85d06.r	BG540633 602570520
t Que:	1 339 100.0 291 85.8	286.2 84.4 503 15 279 82 3 1820 14	257.4 75.9 477 11 234.8 69.3 560 13	224.6 66.3 966 17	9 224.2 66.1 509 12 0 207.6 61.2 530 10	1 204.6 60.4 505 12 2 204.6 60.4 598 10	3 204.6 60.4 600 16	4 203 59.9 727 16 5 201.8 59.5 480 16	6 201.4 59.4 572 11	/ 200.4 59.1 471 15 8 198.2 58.5 474 13	9 198.2 58.5 568 13	0 198.2 58.5 785 16 1 197.8 58.3 646 11	2 196.8 58.1 546 24	3 195.8 57.8 578 10 4 103 6 57 1 589 10	5 193.6 57.1 778 24	6 193.4 57.1 431 17	8 193.4 57.1 681 18	9 191.8 56.6 510 12 0 101 8 56 6 520 22	1 191.8 56.6 529 14	2 190.2 56.1 573 18 3 190.2 56.1 721 15	188.2 55.5 477 18	5 188 55.5 466 11 6 184.4 54.4 505 20	7 183.8 54.2 431 1	8 183 54.0 56/ 20 9 180.6 53.3 515 14	0 180.2 53.2 514 14	1 1/8.8 52.7 4/8 19 2 178.6 52.7 460 23	3 176 51.9 339 16	4 176 51.9 441 10 5 176 51 0 517 16	6 175.6 51.8 336 11	7 175.6 51.8 403 173 8 173 8 173 8	9 173.6 51.2 540 20	0 1/1.2 50.5 325 11 1 171 50.4 445 13	2 171 50.4 559 17	3 1/0.8 50.4 /98 10 4 168.6 49.7 449 18	5 166.4 49.1 328	7 160.4 47.3 499 18	8 158.4 46.7 477 1 9 155.4 45.8 583 15	0 152.8 45.1 576 10	1 152.4 45.0 2 151.6 44.7	3 151.4 44.7 996 168	4 146.2 43.1 403 5 145.2 42.8 267	6 144 42.5 558 1 AA	/ 143.6 42.4
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 ACC24716
 ACC2

ALIGNMENTS

AL532438 964 bp mRNA EST 13-FEB-2001
DEFINITION AL532438 1-1-RFL001\_NBC4 Homo sapiens CDNA clone CSODMO147D15 5
ACCESSION AL532438 LTI\_RFL001\_NBC4 Homo sapiens CDNA clone CSODMO147D15 5
ACCESSION AL532438.1 G1:12795931
EST.
SUURCE Duman
LD532438.1 G1:12795931
EST.
ENTH-REFERENCE LOOPER CONTRACT OF AUTHORIS ENTH-REPORT OF AUTHORS ENTH-REFERENCE LIAMB. Gruber. C. Jessee, J. and Polayes, D. TITLE RU1-Length CDNA libraries and normalization
JOORNAL Unpublished (2001)
CONTRACT CONTRACT CONTRACT SERVED CONTRACT

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Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-blo.llnl.gov/bbrp/image/image.html
Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax: (1) 301 610 8371 Email: filangelifetech.com URL: http://fulllength.invitrogen.com" 248 c 269 g 200 t 2 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AW412139 645 bp mRNA EST 08-FEB-2000 uq46g03.yl NCI_GCAP_Mam5 Mus musculus cDNA clone IMAGE:2812468 5' similar to gb:M32745 mouse transforming growth factor beta-3 mRNA, Complete (MOUSE); mRNA sequence.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 645)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NCI-CGAP institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                                                                                                                                           tacattgacttccgacaggatctgggctggaagtgggtccatgaacctaagggctactat 120
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                                                                                                                                           Length 964;
                                                                     2 others
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100.0%; Score 339; DB 106;
Best Local Similarity 100.0%; Pred. No. 8.1e-86;
Matches 339; Conservative 0; Mismatches 0; I.

    .645
    /organism="Mus musculus"

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High quality sequence stop: 446.
Location/Qualifiers
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TITLE
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Rodentia; Sciurognathi; Muridae; Mus. 1 (bases 1 to 812)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

L Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: Gapbar-rémail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

High quality sequence stop: 735.

High quality sequences
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602337778F1 NCI_CGAP_Mam1 Mus musculus CDNA clone IMAGE:4460706 5',
                                                                                                        /note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: Sal1; Site_2: Not1; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigators
                                                                                                                                                                             providing samples: Lothar Hennighausen/Robin Humphreys,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          240
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Pred. No. 3.2e-72;
0; Mismatches 30;
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/clone_lib="NCI_CGAP_Mam5"
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/lab_host="DH108"
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BG175423
BG175423.1 GI:12682126
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ilarity 91.2%;
Conservative (
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BF101203 1820 bp mRNA EST 19-OCT-2000 601754782F1 NCI_CGAP_Mam1 Mus musculus cDNA clone IMAGE:3983588 5',
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/lab_host="DH10B (Life Technologies)"
LLNL (info@image.llnl.gov). IMAGE ID= 1768868
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                   Seg primer: M13 Forward
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Best Local Similarity 91.5%;
Matches 303; Conservative C
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Fax: 319 335 8250
Fax: 319 335 9565
Email: msoares@blue.weeg.uiowa.edu
Email: msoares@blue.weeg.uiowa.edu
EDNA Library Preparation: M.B. Soares Lab Clone distribution:
clones will be available through Research Genetics (www.resgen.com)
This clone is also available through the I.M.A.G.E. Consortium at
                                                                                                                                                                                                                                                                                                                     ö
                              /clone_lib="NCI_CGAP_Mam1"
/clone_lib="NCI_CGAP_Mam1"
/tissue_type="tumor, blopsy sample"
/dev_stage="3 months, virgin"
/lab_host="hlost="nummary, vector: pCMV-SPORT6; Site_l: Sall;
/note="Organ: mammary; Vector: pCMV-SPORT6; Site_l: Sall;
Site_l: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"
210 c 245 g 160 t
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bonaldo,M.F., Lennón,G. and Soares,M.B. Normalization and subtraction: two approaches to facilitate gene
                                                                                                                                                                                                                                                                                                                                                                                                                               240
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UI-R-C3-sm-a-12-0-UI.rl UI-R-C3 Rattus norvegicus cDNA clone
UI-R-C3-sm-a-12-0-UI 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      239 GTGCTTGGACTATACAACACCCTGAACCCAGAGGCGTCTGCCTCGCCATGCTGCGTCCCC
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Program for Rat Gene Discovery and Mapping
University of Iowa
                                                                                                                                                                                                                                                                              Score 291; DB 174;
Pred. No. 3.4e-72;
0; Mismatches 30;
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/strain="FVB/N"
/db_xref="taxon:10090"
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91.2%;
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g δ g δ qq δ g ŏ Dp δy 셤

/nap\_nost="DBLD" (LITE" TECHNOLOGIES)"
/note="Vector: pTT7D=Pac (Pharmacia) with a modified polylinker; Site\_1: Not I; Site\_2: Eco RI; The UI-R-C3 library is a subtracted library of a series, ultimately derived from a mixture of individually tagged normalized libraries from rat placenta, adult lung, brain, liver, kidney, heart, spleen, ovary, muscle, and B, 12 and 18-day embryos, after a series of subtractions to reduce the representation of CDNAs from which ESTS had already been generated. The following serially subtracted libraries were generated in this process: UI-R-C3, UI-R-C2P, UI-R-C4, UI-R-C0, UI-R-C1, UI-R-C1, UI-R-C1, UI-R-C1, UI-R-C1, UI-R-C3, UI-R-C3, UI-R-C3, UI-R-C3, UI-R-C3, UI-R-C3, UI-R-C3, UI-R-C3, UI-R-C3, UI-R-C3) was constructed as follows: PCRamplified cloridin of a clone within themixture. The subtracted library of origin of a clone within themixture. The subtracted library of origin of a clone within themixture as follows: PCRamplified cloridin of a clone within themixture in a hybridization with the UI-R-C3 library in the form of single-stranded circles and been derived was used as a driver in a hybridization with the UI-R-C2P library in the form of single-stranded circles and clone and subtracted into DH10B bacteriae (LifeTechnologies) to generate the UI-R-C3 library. This procedure has been previously described (Bonaldo, Lennon and Soares, Genome Research 6:791-206, 1996, 240 248 300 121 CTTCCGGCAGGATCTAGGCTGGAAATGGGTCCACGAACCTAAGGGTTACTATGCCAACTT 180 0; Gaps 68 cttccgacaggatctgggctggaagtgggtccatgaacctaagggctactatgccaactt 9 caccaattactgcttccgcaacttggaggagaactgctgtgtgggcccctctacattga ctgctcaggcccttgcccatacctccgcagtgcagacacaaccacagcacggtgctggg DB 150; Length 503; Score 286.2; DB 150; Lengt Pred. No. 7.1e-71; 0; Mismatches 28; Indels

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MARC 1PIG Sus scrofa cDNA 5', mRNA sequence
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                                                                                                          E I (bases 1 to 1820)

NIH-MGC http://mgc.nci.nih.gov/.

NIH-MGC http://mgc.nci.nih.gov/.

NIH-MGC http://mgc.nci.nih.gov/.

L Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-rémail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.

CONA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLAM9184 row: d column: 21

High quality sequence stop: 601.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: Sall; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigator providing silbert Smith, NIH"

533 c 590 g 184 t
                                                                   Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="taxon:10090"
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/tissue_type="tumor, biopsy sample"
/dev_stage="3 months, virgin"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1. .1820
/organism="Mus musculus"
/strain="FVB/N"
                        BF101203.1 GI:10883729
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sednence
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09-JUL-2000

EST

mRNA

477 bp

AW670561

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Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
                                                                                                                                                             Casas, E.,
                                                                                                                       1 (bases 1 to 477)
Fahrenkrug,S.C., Freking,B.A., Rohrer,G.A., Smith,T.P.L., Casas,E. Stone,R.T., Heaton,M.P., Grosse,W.M., Bennett,G.A., Laegreid,W.W. and Keele,J.W.
                                                                                                                                                                                                                       Design and use of two pooled tissue normalized cDNA libraries for EST discovery in swine Unpublished (2000)
                                                                                             Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI; Library made from pooled tissue from day 11, 13, 15, 20, and 30 embryos." 90 t
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Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae;
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                                                                                                                                                                                                                                                                                    Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Sus scrofa"
/db_xref="taxon:9823"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BACKWARD: GTTTTCCCAGTCACGACG
Plate: 43 row: B column: 5
Seg primer: ATTTAGGTGACACTATAG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="pooled"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FORWARD: AGGAAACAGCTATGACCAT
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PCR PRimers
GI:7527075
                                                                                                                                                                                                                                                                                                                                                       Tel: 402 762 4366
Fax: 402 762 4390
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                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 560)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Organ: mammary gland; Vector: pT7T3D-Pac (Pharmacia ) with a modified polylinker; Site_1: Not I; Site_2: Eco FI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' Prim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (1996)
Contact: Marra M/Mouse EST Project
Washlugton University School of MedicineP
Washlugton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
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factor beta-3 mRNA, complete (MOUSE);, mRNA sequence.
AA915041
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/organism="Mus musculus"
/strain="C57Bis,Ga"
/strain="C57Bis,Ga"
/clone="InAGE:1314492"
/clone="InhaGE:1314492"
/clone_lib="Soares_mammary_gland_NbMMG"
/tissue_type="mammary gland"
/dev_stagg="4" weeks"
/lab_host="DH10B"
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Pred. No. 2.9e-56;
0; Mismatches 27
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Best Local Similarity 90.4%;
Matches 273; Conservative
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Fax: 314 286 1810
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/clone_lib="NCI_CGAP_Mam1"
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/de_stage="3 months, virgin"
/lab_host="host="nummary, vector: pcWv-SPORT6; Site_l: Sall;
/note="Organ: mammary; Vector: pcWv-SPORT6; Site_l: Sall;
Site_2: NotI; cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
providing amples: Gilbert Smith, NIH"

273 c 251 g 214 t
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10325 row: c column: 23
High quality Sequence stop: 656.
Location/Qualifiers
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (Jases 1 to 966)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
72 ccgacaggatctgggctggaagtgggtccatgaacctaagggctact-atgccaacttct 130
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/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                            mRNA sequence.
BG244370
BG244370.1 GI:12754185
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/clone="IndexCollings"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tumor Gene Index
Unpublished (1997)
Other_ESTS: ur7lc1.x1
Ontact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Chu-Xia Deng Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be image.llnl.gov/image/html/iresources.shtml
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                           ur7lc12.yl NCI_cGAP_Mam3 Mus musculus cDNA clone IMAGE:3155734 5' similar to gb:M32745 mouse transforming growth factor beta-3 mRNA, complete (MOUSE);, mRNA sequence.
502 CTATACAACACCCTGAACCCAGAGGCGTCTGCCTCTGCCATGCTGCGTCCCCCAGGACCT 443
                                                                                                  tacattgacttccgacaggatctgggctggaagtgggtccatgaacctaagggctactat 120
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Pred. No. 2.9e+53;
0; Mismatches 30; Indels 1; Gaps
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                                                             249 ggagccctgaccatcctgtactatgttgggaggacccccaaagtggagcagctctccaa
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/organism="Mus musculus"
/strain="129 - C57/B6 - FVBN"
/db_xref="taxon:10090"
                                                                                                                                                                                          309 catggtggtgaagtcttgtaaatgtagctga 339
                                                                                                                                                                                                                                      Seq primer: -40RP from Gibco
High quality sequence stop: 418.
Location/Qualifiers
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Best Local Similarity 89.0%;
Matches 252; Conservative 0
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3']; double-stranded cDNA was ligated to Eco RI adaptors RATTCGGATCCTTG], digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library constructed by Bob Barstead. The C2C12 cell line (available from ATCC, catalog # CRL-1772) differentiates rapidly, forming contractile myotubes and producing characteristic muscle proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 (bases 1 to 530)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Hartin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             vr26d03.rl Barstead mouse myotubes MPLRB5 Mus musculus cDNA clone MAGE:1121765 5. similar to qp:030341 TRANSPORMING GROWTH FACTOR BETA 3 PRECURSOR (HUMAN); qp:M3745 mouse transforming growth factor beta-3 mRNA, complete (MOUSE);, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information. MGI:611101
                                                288 TATATTGACTTCCGGCAGGATCTAGGCTGGAAATGGGTCCACGAACCTAAGGGTTACTAT 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The WashU-HHMI Mouse EST Project
Unpublished (1996)
Contact: Marra MyMouse EST Project
WashU-HHMI Mouse EST Project
WashIngton University School of MedicineP
H444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                       241 caggacctggagccctgaccatcctgtactatgttgggagga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Seq primer: -28m13 rev2 ET from Amersham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Mus musculus"
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Location/Qualifiers
1. .530
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/clone="IMAGE:1121765"
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukarmalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 505)
Hegde,P., Qi,R., Abernathy,K., Dharap,S., Gaspard,R., Gay,C., Holt
v.L.E., Saeed,A.I., Sharov,V., Lee,N.H., Yeatman,T.J. and
                                                                                                                                                                                                                                                                                                                                                                                   AW958056 505 bp mRNA EST 01-JUN-2000
EST370126 MAGE resequences, MAGE Homo sapiens cDNA, mRNA sequence.
AW958056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Assessment of gene expression patterns in a model of colon tumor metastasis using a 19,200 element cDNA microarray unpublished (2000)

Contact: John Quackenbush
The Institute for Genomic Research
772 Medical Center Dr., Rockville, MD 20850, USA
773 Fax: 301 838 3528
Fax: 301 838 0208
                                                                                                                                                                                                                          82 ctgggctggaagtgggtccatgaacctaagggctactatgccaacttctgctcaggccct 141
                                                                                                              tgcccatacctccgcagtgcagacacacacacagcacggtgctgggactgtacaacact 201
                                                                                                                                                                       ctgaaccctgaagcatctgcctcgccttgctgcgtgccccaggacctggagcccctgacc 261
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//db_xref="taxon:9606"
/clone_lib="magE resequences, MagE"
/note="Yector: pBluescriptsKm"
137 c 106 g 144 t 3 <
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  DB 10;
Score 207.6; DB 1 Pred. No. 1.5e-48;
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                             Mismatches
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Best Local Similarity 75.2%;
Matches 255; Conservative 0
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Plate: 115
 61.2%;
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              Similarity
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                             Matches 233;
 Query Match
                 Best Local
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A1951831 598 bp mRNA EST 06-SEP-1999 wx38b08.x1 NCI_CGAP_P141 Home spiens cDNA clone INAGE:2245911 3' similar to 9b:X02812_cd31 TRANSFORMING GROWTH FACTOR BETA I PRECURSOR (HUMAN); contains PTR7.t3 MER22 repetitive element ;, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     þe
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173 c 222 g 107 t 1 others
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www.bio.llnl.gov/bbrp/image/image.html
Seq primer: -40UP from Gibco
High quality sequence stop: 425.
Location/Qualifiers
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D.
Bmall: GapbS-remail.nih.gov
Tissue Procurement: Chris Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., cDNA Library Preparation: Life Technologies,
Inc. CDNA Library Arrayed by: Christa Prange, The I.M.A.G.E.
Consortium DNA Sequencing by: Washington University Genome
Sequencing Center
                                                                                                                                                                300
                                                                               gccaacttctgctcaggcccttgcccatacctccgcagtgcagacacaacccacagcacg 180
                                                                                                                                                                                   tacattgacttccgacaggatctgggctggaagtgggtccatgaacctaagggctactat 120
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                                      129 GCCAACTTCTGCCTCGGGCCCTGCCCTACATTTGGAGCCTGGACACGCAGGAGGAGG
                                                                                                                                                                caggacctggagccctgaccatcctgtactatgttgggaggacccccaaagtggagcag
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 598)
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/organism="Homo sapiens"
/organism="Homo sapiens"
/clone="IMAGE:2545911"
/clone="IMAGE:2545911"
/clone="Lib="NGI_GGAP_Pit1"
/lasue_type="four pooled pituitary adenomas"
/lab_host="DH108"
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Best Local Similarity 75.2%; Pred. No. 1.1e-47;
Matches 255; Conservative 0; Mismatches 84
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Unpublished (1997)
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ORIGIN
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AUTHORS
121
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KEYWORDS
SOURCE
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Matches 255; Conserv
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TITLE
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/clone_lib="Human Lens cDNA (Un-normalized, unamplified):
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Wistow,G.J., Bernstein,S., Behal,A. and Smith,D.
NEIBANK: EST analysis and bioinformatics for ocular genomics invest. Ophthalmol. Vis. Sci. 41 (2000) In press
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BF726895 600 bp mRNA EST 05-JAN-2001
by15c03.yl Human Lens cDNA (Un-normalized, unamplified): BY Homo
sapiens cDNA clone by15c03 5', mRNA sequence.
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416 TACATTGACTTCCGCAAGGACCTCGGCTGGAAGTGGATCCACGAGCCCAAGGGCTACCAT 357
                                                                                                                                                                                                                                                                                                                                              121 gccaacttctgctcaggcccttgcccatacctccgcagtgcagacacaaacccacagcacg
                                                                                         181 gigotgggacigiacaacacicigaaccetgaagcaictgccicgccitgctgcgigcc
                                                                                                                                                                                                                    caggacctggagccctgaccatcctgtactatgttgggaggacccccaaagtggagcag
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        176 CTGTCCAACATGATCGTGCGCTCCTGCAAGTGCAGCTGA 138
                                                                                                                                                                                                                                                                                                                                                                                                                                        301 ctctccaacatggtggtgaagtcttgtaaatgtagctga 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              National Eye Institute
6/331, NIH, Bethesda, MD 20892-2740, USA
Tel: 301 402 3452
Fax: 301 496 0078
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Plate: 15 row: c column: 03
Seq primer: M13RP1 reverse primer (ABI).
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/db_xref="taxon:9606"
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/lab_host="EMDH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="Lens"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 727)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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This clone is available royalty-free through LLNL; contact the
This clone is available royalty-free through LLNL; contact the
TMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 782 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 390.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                          gtgctgggactgtacaacactctgaacctgaagcatctgcctcgccttgctgcgtgcc 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          241 caggacctggagccctgaccatcctgtactatgttgggaggaccccaaagtggagcag 300
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   Pred. No. 1.1e-47;
0; Mismatches 84
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/db_xref="taxon:9606"
/clone="IMAGE:1709684"
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al Similarity 75.2%;
255; Conservative
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CDNA Library Arrayed by: Greg Lennon, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image-image-html
Insert Length: 895 Std Brror: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
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NCI/MINDS-GAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute / National Institute of Neurological Josorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BTGAP), Tumor Gene Index
Unpublished (1998)
same fetus as the fetal lung library, Soares fetal lung NbHL19W."
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Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld
                                                                                                                                                                                                                                                    363 GCCAACTTTTGCCTCGGGCCCTGCCCCTACATTTGGAGCCTGGACAGCAGGAGTACAGCAAG
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Pred. No. 3.2e-47,
0; Mismatches 89
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AI089904.1 GI:3428963
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/organism="Homo sapiens"

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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 572)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
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Clone distribution: NCI-CGAP clone distribution information can
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/clone_lib="NCI_CGAP_Brn23"
/tissue_type="glioblastoma (pooled)"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                82;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and M.Fatima Bonaldo."
0 c 179 g 87 t
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Contact: Robert Strausberg, Ph.D.
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75.4%;
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GI:9970015
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al Similarity 74.3%;
252; Conservative
                      Fax: 319 335 9565
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BE645704/c
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                           /note-"Organ: genitourinary tract, Vector: pCMV-SPORT6; Site_1: Sall; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life
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Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BF543086 471 bp mRNA EST 11-DEC-2000 UI-R-AFI-aaq-f-07-0-UI.rl UI-R-AFI Rattus norvegicus cDNA clone UI-R-AFI-aaq-f-07-0-UI 5', mRNA sequence.
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Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
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                                                                                      /db_xref="taxon:9606"
/clone="IMAGE:2575474"
/clone=lib="NCI_CGAP_GUI"
/tissue_type="2 pooled high-grade transitional cell tumors"
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                                                                                                                                                                                                                                                                                                                 86; Indels
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: -40Up from Gibco
High quality sequence stop: 396.
Location/Qualifiers
                                                                                                                                                                                                                                                                                        DB 111;
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Pred. No. 8.8e-47;
                                                                                                                                                                                                                                                                                                               0; Mismatches
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                                                                              /organism="Homo sapiens"
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97044477
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                                                                                                                                                              /lab_host="DH10B"
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                                                                                                                                                                                                                      Technologies.
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/strain="sprague_bawley"
/strain="sprague_bawley"
/db_xref="taxon:10116"
/clone_lib="UI-R-AFI-aaq-f-07-0-UI"
/clone_lib="dult"
/dev_stage="adult"

Email: msoares@blue.weeg.uiowa.edu

CDNA Library Preparation: M.B. Soares Lab Clone distribution:
CDNA Library Preparation: M.B. Soares Lab Clone distribution:
Clones will be available through Research Genetics (www.resgen.com)
This clone is also available through the I.M.A.G.E. Consortium at
LLNL (info@lmage.llnl.gov). IMAGE ID- 1790668
Seq primer: M13 Forward.
Location/Qualifiers
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Pred. No. 1.6e-46;
0; Mismatches 87
                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Rattus norvegicus"
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179 CTGTCCAACATGATCGTGCGTTCCTGCAAGTGCAGCTGA 141
            mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         with a modified polylinker; Plasmid DNA from the normalized library NCI_CGAP_Pr22 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified CDNAs from a pool of 5,000 clones made from the same library (cloneIDs 985608-986759, 1101195-1101959, and 1217928-1220615).

Subtraction by Bento Soares and M. Fatima Bonaldo. " 138 c 176 g 85 t
                                                           Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL, send email to:
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1 (bases 1 to 474)
NCI-CGAP http://www.ncbi.nlm.nfh.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Organ: prostate; Vector: pT7T3D-Pac (Pharmacia)
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74.9%; Pred. No. 6.9e-46;
iive 0; Mismatches 83; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                  /clone="IMAGE:3288259"
/clone_lib="NCI_CGAP_Pr28"
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                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Seq primer: -40UP from Gibco.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /dev_stage="adult"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                             /sex="male"
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BE464068/c
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    REFERENCE
                       AUTHORS
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/note="Organ: Kidney; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: ECO RI; Plasmid DNA from the normalized library NCI_CGAP_Kid3 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 132376-1323911, 1456007-1456775, and 1500552-1502855). Subtraction by Bento Soares and M.
                                                                                                                                                                                                                                                                                                                              Email: cgapbs-remail.ni.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL, send email to:
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                                                                                                     Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                           1 (bases 1 to 568)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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Pred. No. 7.1e-46;
0; Mismatches 88; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone="IMAGE:3194547"
/clone_lib="NCI_CGAP_Kid11"
/lab_host="DH10B"
                                                                                                                                                                                                                                                           Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/db_xref="taxon:9606"
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High quality sequence stop: 395.
Location/Qualifiers
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BE464068.1 GI:9509843
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74.0%;
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Matches 250;
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DEFINITION
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                                                                                                                                                                                                                                   RESULT 21
AW512491/c
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181
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SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequencing Center
information can be
                                                            A1148173 785 bp mRNA EST 26-OCT-1998 qb56d01.x1 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:1704097 3' similar to gb:X02812_cds1 TRANSFORMING GROWTH FACTOR BETA 1 PRECURSOR (HUMAN);contains PTR5.b3 TAR1 repetitive element;, mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                    Email: cgapbs-r@mail.nih.gov
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
                                                                                                                                                                                                                        Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 785)
NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BRGAP), Tumor Gene Index
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Library Preparation: M. Bento Soares, Ph.D., M. Fatima
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 785;
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CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing by: Washington University Genome Sequencing by: North North Cape Clone distribution informed the Limbution of the Clone distribution information that the Clone Sequence of the Clone Marcham High quality sequence stop: 356.

Cocation/Qualifiers

Cocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      88; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone="IMAGE:1704097"
/clone_lib="NCI_CGAP_Brn23"
/tissue_type="q1ioblastoma (pooled)"
/lab_host="PH108"
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Pred. No. 7.6e-46;
0; Mismatches 88
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217 c 267 a 164 +
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/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                       Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                     A1148173.1 GI:3675855
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74.0%;
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                                                                                                                                    sequence.
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ORIGIN
                                          AI148173/C
                                                                                                                                                                                                                        ORGANISM
                                                                                                                                                                                                                                                                                               AUTHORS
TITLE
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KEYWORDS
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n can be
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Organ: lymph node; Vector: pCMV-SPORT6; Site_1: Sall; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dr. Average insert size 1.25 kb. Life Technologies catalog #: 11547-015.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 646)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
9t9ctgggactgtacaacactctgaacctgaagcatctgcctcgccttgctgcgtgcc 240
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                                                                                       317 GTCCTGGCCCTGTACAACCAGCATAACCCGGGGGGCGCTCGGCGGCGCGTGCTTCCG
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Email: cgapbs-r@mail.nih.gov
Life Technologies catalog#: 11547-015
DNA Sequencing by: Washington University Genome
Clone distribution: NCI-CGAP clone distribution
found through the I.M.A.G.E. Consortium/LLNL at:
image.llnl.gov/image/html/iresources.shtml
Seq primer: -400P from Gibco.
High quality sequence stop: 396.
                                                                                                                                                                                  58.3%; Score 197.8; DB 117
74.0%; Pred. No. 9.5e-46;
tive 0; Mismatches 88;
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/clone_lib="NCI_CGAP_Lyml2"
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                                                                                                                                                                                                                                                                                                                                                                                                                                           sequence.
AW512491
AW512491.1 GI:7150569
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Unpublished (1997)
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Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Email: cgapbs-r@mail.nih.gov

Email: cgapbs-r@mail.nih.gov

M.D., Louis M. Staudt, M.D., Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

Www.bio.llnl.gov/bbrp/image/image.html

Insert Length: 714 Std Error: 0.00

Seg primer: -40UP from Gibco

High quality sequence stop: 465.
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MABRDO9.X1 NCI_CGAP_CCLLI HOMO Sapiens CDNA clone IMAGES.2887801 3/
similar to gb.:X02812_cd51 TRANSFORMING GROWTH FACTOR BETA 1
PRECURSOR (HUMAN); contains element TAR1 repetitive element ; mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

    (bases 1 to 546)

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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                    242 aggacctggagccctgaccatcctgtactatgttgggaggaccccaaagtggagcagc 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      caattactgcttccgcaacttggaggagaactgctgtgtgggcccctctacattgactt 71
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AI760533.1 GI:5176200
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Matches
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AI760533/c
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VERSION
KEYWORDS
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182
                                  315
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TITLE
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DB 24; Length 546;
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/clone="INACETATION"
/clone="INACETATION"
/clone="InyCarollogue"
/clone="InyCarollogue"
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/note="Organ: Kidney: Site\_1: Not I: Site\_2: Eco RI:
Plasmid DNA from the normalized library NCI\_CGAP\_Kid3 was
prepared, and ss circles were made in vitro. Following HAP
purification, this DNA was used as tracer in a subtractive
hypridization reaction. The driver was PCR-amplified CDNAs
from a pool of 5,000 clones made from the same library
(cloneIDs 132276-1333911, 1456007-1456775, and
1500552-1500585). Subtraction by Bento Soares and M.
Fatina Bonaldo. Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NOI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-blo.llnl.gov/Dbrp/image/image.html
Insert Length: 1358 Std Error: 0.00 A1927187 578 bp mRNA EST 08-MAR-2000 wo88c02.x1 NCI\_CGAP\_Kid11 Homo sapiens cDNA clone lMAGE:2462402 3' similar to 9b:XO2812\_cGal TRANSFORMING GROWTH FACTOR BETA 1 PRECURSOR (HUMAN); contains element MER22 repetitive element ; mRNA Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 578)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), 286 251 252 gococtgaccatcotgtactatgttgggaggaccoccaaagtggagcagctctccaacat 311 132 ctcaggcccttgcccatacctccgcagtgcagacacaacccacaggacgtgctgggact 345 cercegecereceeracartregaeceregaeacaceagracageaacerecer 192 gtacaacactctgaaccctgaagcatctgcctcgccttgctgcgtgccccaggacctgga 105 t /organism="Homo sapiens" /db\_xref="taxon:9606" Seq primer: -40UP from Gibco High quality sequence stop: 394. 312 ggtggtgaagtcttgtaaatgtagctga 339 165 GATCGTGCCTCCTGCAAGTGCAGCTGA 138 Location/Qualifiers 175 g Fatima Bonaldo AI927187 AI927187.1 GI:5663151 166 c Tumor Gene Index Unpublished (1997) 1. .578 sednence. 127 human. AI927187/c LOCUS source DEFINITION ORGANISM BASE COUNT REFERENCE AUTHORS TITLE ACCESSION JOURNAL KEYWORDS SOURCE FEATURES VERSION COMMENT 셤 q à g à ò g ò à

g ò 셤 ò qq ò g ò q à g

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/lab_host="DH10B"
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Best Local 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A1991139 589 bp mRNA EST 27-OCT-1999 WANA WASBQ3.x1 Soares_Dieckgraefe_colon_NHCD Homo sapiens cDNA clone IMAGE:252356 3' similar to gb:x02812_cds1 TRANSFORMING GROWTH FACTOR BETA 1 PRECURSOR (HUMAN);contains element TAR1 TAR1 repetitive element; mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

    (bases 1 to 589)

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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tumor Gene Index
Unpublished (1997)
Contact: Roberts Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: -40UP from Gibco
High quality sequence stop: 459.
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                                              DB 103; Length 578;
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/clone_lib="Soares_Dieckgraefe_colon_NHCD"
                                                                           91; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /lab_host="DH10B (phage-resistant)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                  175 CrgrccaAcarGarcGrGcGcrccrGcAAGrGCAGCrGA 137
                                                             Pred. No. 3.4e-45;
                                                                          0; Mismatches
                                              Score 195.8;
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                                            57.8%;
73.2%;
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                                                                          Conservative
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                                                          Similarity
                                                       Best Local Simi
Matches 248;
                                            Query Match
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A1991139/C
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SOURCE
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ORIGIN
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ij
went through one round of normalization. Tissue samples provided by Dr. Brian Dieckgraefe (Washington University, dieck@im.wustl.edu); colonic mucosa represents a range of disease involvement from moderate to severe Crohn's disease; samples include both perforating (fistulas) and non-perforating samples. Library constructed by Bento Soares and M. Fatima Bonaldo. " 5 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AI743724 778 bp mRNA EST 19-DEC-1999
9853b06.x1 Soares_NSF_RE_PB_9W_OT_PA_P_S1 Homo sapiens cDNA clone
IMAGE.2368787 3' similar to gb:x07812_cds1 TRANSFORMING GROWTH
FACTOR BETA 1 PRECURSOR (HUMAN); contains element MSR1 repetitive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Euteleostomi;
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NCI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: Gapus-remail.nih.gov
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 863 Std Error: 0.00
Seq primer: -400P from Gibco
High quality sequence stop: 449.
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Pred. No. 1.5e-44;
0; Mismatches 84; Indels
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                                                                       Following Marp Durification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 5 libraries. The pools consisted of the following libraries and cloneIDs: Soares NbHSF pool 1: 309384-310919, 323208-325895 Soares NbHP pool 1: 145032-147335, 147720-148103, 148872-149255, 15002 - 150407, 151176-152327 Soares NbHPR 9W pool 1: 758280-760583, 772104-774407 Soares NbHPA pool 1: 758280-760583, 772104-774407 Soares NbHPA pool 1: 723720-726407, 739080-740999 Subtraction by Bento Soares and M. Fatima Bonaldo. " 4 others
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/note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site=1: Not I; Site=2: Eco RI; Equal amounts of plasmid DNA from five normalized libraries were mixed, and ss circles were made in vitro.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi, Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 431)
NIH-MGC http://mgc.nci.nih.gov/.
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75.0%; Pred. No. 1.5e-44;
iive 0; Mismatches 84; Indels
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
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/db_xref="taxon:0506"
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/clone="Inb="klH_MGC_91"
/tissue_type="adenocarcinoma, cell line"
/tissue_type="adenocarcinoma"
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H3055G07-3 NIA Mouse 15K cDNA Clone Set Mus musculus cDNA clone
H3055G07 3', mRNA sequence.
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Pred. No. 1.6e-44;
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                                                                                       High quality sequence stop: ...
Location/Qualifiers
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transforming growth factor-beta2 (MOUSE);, mRNA sequence.
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//note="Vector: pSPORT1; Site_1: SalI; Site_2: NotI; This close "Avector: pSPORT1; Site_1: SalI; Site_2: NotI; This close is among a rearrayed set of 15.247 clones from 11 embryo close is among a rearrayed set of 15.247 clones from 11 embryo close is said to the state of t
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Genet 7: 1967-1978."
137 c 145 g 174 t 1 others
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                                                                                                                                                                                                                                                                                                /clone_lib="NIA Mouse 15K cDNA Clone Set"
/sex="Clones arrayed from a variety of cDNA libraries"
/dev_stage="Clones arrayed from a variety of cDNA
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visit http://lgsun.grc.nia.nih.gov/cDNA/15k.html for details.
Plate: H3055 row: G column: 07
Seg primer: -21M13 Forward
High quality sequence stop: 608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 gctttggacaccaattactgcttccgcaacttggaggagaactgctgtgtgcgcccctc 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23-DEC-1998
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73.2%; Pred. No. 1.7e-44;
ive 0; Mismatches 91
                                                                                                                                                                                          /organism="Mus musculus"
                                                                                                                                                                                                                                              /db_xref="taxon:10090"
/clone="H3055G07"
                                                                                                                                         Location/Qualifiers
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                                                                                                                                                                                                                   /strain="C57BL/6J
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Matches 248; Conservative
                                                                                                           POLYA=Yes.
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AI323791/C
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DEFINITION
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 681)
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This clone was previously sequenced on the 5' end only, this new data is from the 3' end High quality sequence stop: 366.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
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/organism="Mus musculus"
/do_reref="texton:10090"
/clone="IMAGE:524678"
/clone_lib="Stratagene_mouse_melanoma (#937312)"
                                                                                                                                                                                                                                                                                             Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of Medicinep
44444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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Pred. No. 1.7e-44;
0; Mismatches 91;
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AI323791.1 GI:4058220
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73.28;
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Matches 248; Conservative
                                                                       Mus musculus
                                                                                                                                                                                                                                                           Waterston, R.
                          EST.
house mouse.
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Ouery Match 56.6
Best Local Similarity 72.9
Matches 247; Conservative
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VERSION
KEYWORDS
SOURCE
ORGANISM
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                                                                                                                                                                                    AW919738 510 bp mRNA EST 25-MAY-2000 SET 25-MAY-2000 SET 25-MAY-2000 are serious at the serious contact and serious contact away men and serious contact away men awa
                                                                                                                                                                                                                                                                                                                                                                     Norway rat.
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Lee,N.H., Glodek,A., Chandra,I., Mason,T.M., Quackenbush,J.,
Kerlavage,A.R. and Adams,M.D.
Rat Genome Project: Generation of a Rat EST (REST) Catalog & Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Rattus norvegicus"
/db_xref="texon:10116"
/clone="RGIG52"
/clone=lib="Rat gene index, normalized rat, norvegicus,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 gccaacttctgctcaggcccttgcccatacctccgcagtgcagacacaacccacagcacg 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (1998)
Contact: Lee, NH
The Institute for Genomic Research
9712, Medical Center Drive, Rockville, MD 20850, USA
Tel: (301)-838-3529
Fax: (301)-838-0208
Email: nhlee@tigr.org
This clone is available through the ATCC, contact the A tel#703-365-2700 for further information
Seq primer: M13 Reverse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue_type="mix - brain, ovary, placenta,
liver, embryo, heart, muscle, spleen"
/lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 56.6%; Score 191.8; DB 122; Lengt Best Local Similarity 72.9%; Pred. No. 4.6e-44; Matches 247; Conservative 0; Mismatches 92; Indels
301 ctctccaacatggtggtgaagtcttgtaaatgtagctga 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
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AI599959 529 bp mRNA EST 21-APR-1999
EST251662 Normalized rat embryo, Bento Soares Rattus sp. cDNA clone
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Rattus sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Rat
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//dev_stage="embryo 8, 12, 18 dpc"
//note="Vector: pr773Pac; Site_l: EcoRI; Site_2: NotI"
142 c 194 g 105 t
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Lee, N. H., Glodek, A., Chandra, I., Mason, T. M., Quackenbush, J.,
Kerlavage, A. R. and Adams, M. D.
Rat Genome Project: Generation of a Rat EST (REST) Catalog &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 gctttggacaccaattactgcttccgcaacttggaggagaactgctgtgtgcgcccctc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Gene Index
Unpublished (1998)
Contact: Lee, NH
The Institute for Genomic Research
9712, Medical Center Drive, Rockville, MD 20850, USA
Tel: (301)-838-3229
Fax: (301)-838-0208
Email: nhlee@tigr.org
Seq primer: M13-21.
301 ctctccaacatggtggtgaagtcttgtaaatgtagctga 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1. 529
/organism="Rattus sp."
/db_xref="taxon:10118"
/clone="REMEK51"
                                                                                                                                                                  REMEK51 3' end, mRNA sequence.
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                                                                                                                                                                                                              AI599959.1 GI:4609007
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DEFINITION mj35f01.x1 Soares mouse embryo NbME13.5 14.5 Mus musculus cDNA clone IMAGE.478105 3' similar to gb:X02812_cds1 TRANSFORMING GROWTH FACTOR BETA 1 PRECURSOR (HUMAN); gb:M32745 mouse transforming growth factor beta-3 mRNA, complete (MOUSE);, mRNA sequence.  ACCESSION A1323392.1 GI:4057821  KEKYMORDS SGT.  ONGANISM Mus musculus Butaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Butaryota: Metazoa; Chordata; Craniata; Muridae; Musinae; Mus.  REFERENCE 1 (bases 1 to 573)		IMAGE Consortium (info@image.llnl.gov) for further information.  MGI:288849 This clone was previously sequenced on the 5' end only, this new data is from the 3' end High quality sequence stop: 454.  High quality sequence stop: 454.  Location/Qualifiers  1578L/6J"  Source /organism="Mus musculus" /Strain="C57BL/6J" /Glone="IMAGE:478105" /clone="IMAGE:478105" /clone=Lib="Soares mouse embryo NbME13.5 14.5"	/tissue_type="embryo" /tissue_type="embryo" /dev_stage="13.5-14.5dpc total fetus" /lab_host="balloB" /note="Vector: pT7130-pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5, TGTTACCAATCTGAAGTGGGAGGGGCGGGGAAATTTTTTTT	Definition, and was constructed by Bento Soares and M.Fatima Bonaldo.  Matches 246; Conservative 0; Mismatches 93; Indels 0; Gaps	Oy 1 getttggacaccaattactgcttccgcaacttggaggagaactgctgtgtgcgcccctc 60
529 bp mRNA EST 28-NOV-20 t Gene Index, normalized rat, Rattus norvegicus glcus cDNA clone RGIGG52 3' sequence, mRNA sequ GI:11218546 glcus etazoa; Chordata; Craniata; Vertebrata; Eutelec theria; Rodentia; Sciurognathi; Muridae; Murin	AUTHORS Malek, R. L., Cho, J., Lee, Y., Karamycheva, S., Parvizi, B., Pertea, G., Sultana, R., Tsai, J., White, J., Quackenbush, J. and Lee, N. H.  TITLE Generation of ESTS from Normalized Rat Embryo, Bento Soares JOURNAL Unpublished (2000)  COMMENT Other_ESTS: EST351042  CONTact: Lee, NH The Institute for Genomic Research 9712, Medical Center Drive, Rockville, MD 20850, USA Tel: (301)-838-3529  Fax: (301)-838-0208  Email: nhlee@tigr.org This clone is available through the ATCC, contact the ATCC tel#703-365-2700 for further information.  FERATURES Location/Qualifiers Source 1.529	/Organism="Rattus norvegicus" //db.xref="texxon:10116" //clone="RatGG52" //clone="Rat Gene Index, normalized rat, Rattus norvegicus cDNA" //tissue="type="mixed tissue" //tab_host="DH5-alpha" //note="Vector: pT3T7Pac; Site_1: EcoR1; Site_2: Not1; Combination of ROV, RBR, RKI, RLI, RPL, RLU, REM, RWU, RSP , RHE, RPC, RPN" ORIGIN ORIGIN	Query Match         56.6%;         Score 191.8;         DB 146;         Length 529;           Best Local Similarity 72.9%;         Pred. No. 4.6e-44;         Matches 247;         Conservative 0;         Mismatches 92;         Indels 0;         Gaps 0;           Qy         1 gctttggaacaccaattactgcttccgaacttggaggagaactgctgtgtgggaactgctgtgtggccccccc 60         1	QY 121 gccaacttctgctcaggcccttgcccatacctccgcagtgcagacaccacagcacg 180	Db 237 [1111   1

121 gccaacttctg 416 GCCAACTTCTG 181 gtgctggactt 181 gtgctggactt 476 GTCCTGCCTT 241 caggacctggact 1							
Oy 121 9 Db 416 6 Oy 181 9 Db 476 6 Oy 241 0 Db 536 C Oy 301 0 Db 596 T	RESULT 34 LOIS 3037 LOCUS DEFINITION ACCESSION VERYWORDS SOURCE ORGANISM REFERENCE AUTHORS	TITLE JOURNAL COMMENT FEATURES SOUTCE					
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359 GCCAACTTCTGTCTGGGACCCTGCCCTATATTTGGAGCCTGGACACACAGTACAGCAAG 300  181 gtgctgggactgtacaacactctgaaccctgaagcatctgcctcgccttgctggtgccc 240  1	BG518882 BG5	CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:	DASE COUNT 164 a 232 c 187 g 138 t  Ouery Match  Duery Match  Duery Match  Est Local Similarity 72.6%; Pred. No. 1.4e-43;  Matches 246; Conservative 0; Mismatches 93; Indels 0; Gaps 0;  Oy 1 gctttggacaccaattactgcttccgcaacttggaggagactgctgtgtgccccctc 60  I				
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7 477 bp mRNA EST 23-DEC-1998
yl Soares mouse embryo NbME13.5 14.5 Mus musculus cDNA
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BETTA 1 PRECURSOR (HUMAN); gb:X32745 mouse transforming
factor beta-3 mRNA, complete (MOUSE);, mRNA sequence. ., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., nberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., 9, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and on, R. ca; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; 1; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 2s 1 to 477) id is a RESEQUENCE of a previously sequenced mouse clone id has been verified (found to hit its original self in the nouseest@watson.wustl.edu one is available royalty-free through LLNL ; contact the onsortium (info@image.llnl.gov) for further information. tgtacaacactctgaaccctgaagcatctgcctcgccttgctgcgtgccc 240 geteaggecettgeceatacetecgeagtgeagacacaaccacagcacg 180 shed (1996)
: Marra M/Mouse EST Project
:MI Mouse EST Project
ton University School of MedicineP
rest Park Parkway, Box 8501, St. Louis, MO 63108 /clone\_lib="Soares mouse embryo NbME13.5 14.5" /sex="unknown" /tissue\_type="embryo" /dev\_stage="13.5-14.5dpc total fetus" /lab\_host="DH10B" /organism="Mus musculus" /strain="C57BL/6J" /db\_xref="taxon:10090" /clone="IMAGE:478105" NU-HHMI Mouse EST Project ner: -40RP from Gibco llity sequence stop: 415. Location/Qualifiers .1 GI:4057466 orientation) 1. .477

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 466)
S NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: Chris Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D. CDNA Library Preparation: Life
Technologies, Inc. CDNA Library Arrayed by: Christa Prange, The
T.M.A.G.E. Consortium DNA Sequencing by: Washington University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
Image.lln.gov/lmage/thml/iresources.shtml
Seq primer: -40UP from Gloco
High quality sequence stop: 378.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AW627667 466 bp mRNA EST 31-MAR-2000 hh89h10.xl NCI_CGAP_GU1 Homo sapiens CDNA clone IMAGE:2970019 3' similar to 9b:X02812_cds1 TRANSFORMING GROWTH FACTOR BETA 1 PRECURSOR (HUMAN);contains element TAR1 repetitive element;, mRNA
cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo. " 91 t
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/db_xref="taxon:9606"
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AUTHORS
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Antiquia cancer institute, cancer denome anatomy Figject (carry), reflect Robert Strausberg, Ph.D.

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-rémail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Mashington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

Nwww.bio.lnl.gov/bbrp/image/image.html
Insert Length: 2004 Std Error: 0.00

Seq primer: -400P from Gibco
High quality sequence stop: 376.
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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1323211.X1 NCI_CGAP_GAS4 Homo sapiens DANA clone IMAGE:2132156 3'
similar to gb:X02812_cds1 TRANSFORMING GROWTH FACTOR BETA 1
PRECURSOR (HUMAN);contains element TAR1 repetitive element; mRN
                                                                                                               /note="Organ: genitourinary tract; Vector: pCWV-SPORT6; Site_1: Sall; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies."
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'Lissue_type="2 pooled high-grade transitional
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Pred. No. 5.4e-43;
0; Mismatches 85; Indels 0
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                                                                                      /lab_host="DH10B"
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AI433146.1 GI:4287132
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                                                                                                                                                                                                                                                                                                                                                                                          Matches 239; Conservative
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (Dases 1 to 431)

Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Stepto,M., Tan,F., Underwood,K., Moors,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                 /note="Organ: stomach; Vector: pCMV-SPORT6; Site_1: Sall; Salte_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Average Insert size 1.69 kb. Life Technologies catalog #: 11549-011"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         70 ttocgacaggatctgggctggaagtgggtccatgaacctaagggctactatgccaacttc 129
                                                                                                                                                                                                                                                                                                                                                                                                                                         tgctcaggcccttgcccatacctccgcagtgcagacacaacccacagcacggtgctggga 189
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (1996)
Contact: Marra M.Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
                                                                                                                                                                                                                      95 t
                                  /organism="Homo sapiens"
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The WashU-HHMI Mouse EST Project
 Location/Qualifiers
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

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/tissue_type="embryo"
/dev_stage="13.5-14.5dpc total fetus"
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/dab_host="lub"
/dab_host="unition"
/dab_host=
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Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
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/strain="C57BL/6J"
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/clone="IMAGE:425747"
/clone="Lib="soares mouse embryo NbME13.5 14.5"
/sex="unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ó
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                                                                                                                                                                             Potative full length read vector to vector length is 661 Seq primer: Erprimer High quality sequence stop: 321. Location/Qualifiers
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ORGANISM

VERSION KEYWORDS SOURCE

REFERENCE AUTHORS JOURNAL

COMMENT

TITLE

FEATURES

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Fax: 217 333 5998

Fax: 217 244 5617

Email: h-lewineuluc.edu

Funding for cattle EST sequencing was provided by the USDA National

Research Initiative, Animal Genome Resource Grant AG 99-3205-8534

To H. A. Lewin and J. E. Womack. Base Calling/Quality Scores: PHRED

from Mashington University Genome Center. Vector Trimmi g:

Cross_match from Washington University Genome Center PHRAP suite.

This sequence is vector free and at least 200 bp in length.
                                                                                                                                                                                       Lewin, H.A., Soares, M.B., Rebeiz, M., Pardinas, J., Liu, L. and Larson
                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                             Contact: Lewin, H. A.
W. M. Keck Center for Comparative and Functional Genomics
University of Illinois at Urbana-Champaign
340 Edward R. Madigan Laboratory, 1201 W. Gregory Dr., Urbana, IL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Organ: placenta; Vector: pT7T3Pac; Site_1: BcoRI; Site_2: NotI; The cDNA library was contributed by the Soares laboratory and it was constructed and normalized as described by Bonaldo, M.F., Lennon, G. and Soares, M.B. (1996), Genome Research 6(9): 791-806. "
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score rocc.
Pred. No. 7e-41;
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FORWARD: TAATACGACTCACTATAGGG
BACKWARD: ATTAACCTCACTAAAG
INSERT LENGTH: 515 Std Error: 0.00
Plate: BP25019B10 row: B column: 3
Seq primer: AGCGGATAACAATTCACACAGGA
High quality sequence stop: 515.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Bos taurus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
1. .515
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       BF042894.1 GI:10759949
                                                                                                                                            Bovidae; Bovinae; Bos.
                                                                                                                                                                    (bases 1 to 515)
                                                                                                                                                                                                                                                             Unpublished (2000)
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                                                                                                                                                                                                                                          Contact: Robert Strausberg, Ph.D.

Email: cgapbs-rémail.nih.gov
Life Technologies catalog #: 11547-015

DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 873 Std Error: 0.00
Seq primer: -400P from Gibco
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Organ: lymph node; Vector: pCMV-SPORT6; Site_1: Sal1; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dr. Average insert size 1.25 kb. Life Technologies catalog #: 11547-015"

163 c 209 g 107 t 1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2133535"
/clone_lib="NOI_CGAP_Lyml2"
/tissue_type="lymphoma, follicular mixed small and large cell"
                                                                                         Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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Pred. No. 1.5e-41;
0; Mismatches 91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    High quality sequence stop: 380.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /lab_host="DH10B"
AI434956.1 GI:4299804
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Best Local Similarity 72.3%;
Matches 237; Conservative
                                                                                    Eukaryota; Metazoa;
Mammalia; Eutheria;
1 (bases 1 to 567)
                                                                                                                                                                                                       Tumor Gene Index
Unpublished (1997)
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Lewin, H.A., Soares, M.B., Rebeiz, M., Pardinas, J., Liu, L. and Larson
                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Organ: placenta; Vector: pT7T3Pac; Site_1: EcoRI; Site_2: NotI; The cDNA library was contributed by the Soares laboratory and it was constructed and normalized as described by Bonaldo, M.F., Lennon, G. and Soares, A.B. (1996), Genome Research 6(9): 791-806. "

1 113 c 110 g 163 t 2 others
                                                                                                                                                          normalized bovine placenta Bos taurus cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        W. M. Keck Center for Comparative and Functional Genomics
University of Illinois at Urbana-Champaign
340 Edward R. Madigan Laboratory, 1201 W. Gregory Dr., Urbana,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 tacattgacttccgacaggatctgggctggaagtgggtccatgaacctaagggctactat 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         475 GCTCTGGATGCAGCCTATTGCTTTAGAAATGTGCAGGATAATTGTTGCCTACGCCCNNTT 416
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0; Mismatches 100; Indels
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                     174 CTTTCTAATATGATTGTCAAGTCTTGCAAATGCAGCTAA 136
301 ctctccaacatggtggtgaagtcttgtaaatgtagctga 339
                                                                                                                                                        BP250020A20D5 Soares normalized bovine clone BP250020A20D5 5', mRNA sequence.
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BACKWARD: ATTAACCTCACTAAAG
Insert Length: 514 Std Error: 0.00
Plate: BP250020A20 row: D column: 5
Seq primer: AGCGGATAACAATTTCACACAGGA
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/clone="BP250020A20D5"
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Fax: 217 244 5617
Email: h-lewin@uiuc.edu
                                                                                                                                                                                                                      BF044612.1 GI:10761667
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70.5%;
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T 3'], on equal amounts of mRNA from 2 13.5dpc and 2 14.5dpc embryos [total RNA provided by Minoru Ko, Wayne State Univ., from 2 ]; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      W45844 478 bp mRNA EST 23-MAY-1996 mC7402.r1 Soares mouse embryo NDME13.5 14.5 MUS musculus CDNA mouse IMDRAGE.354554 5 similar to 9b:X02812_cds1 TRANSFORMING GROWTH FACTOR BETA 1 PRECURSOR (HUMAN); 9b:M32745 mouse transforming
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 478)
Marray.M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
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                                                                                                                240
                                                                                                                                                                                                                                                                   241 caggacctggagccctgaccatcctgtactatgttgggaggaccccaaagtggagcag 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                growth factor beta-3 mRNA, complete (MOUSE);, mRNA sequence
                         181 gigetgggaetgiacaacaetetgaaecetgaageateigeetegeetigetgegigeee
gecaacttetgeteaggeeettgeecataceteegcagtgeagacacaaeccacagcacg
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WashU-HHMI Mouse EST Project
Washington University School of Medicinep
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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/dev_stage="13.5-14.5dpc total fetus"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                     301 ctctccaacatggtggtgaagtcttgtaaatgtagctga 339
                                                                                                                                                                                                                                                                                                                                                                                       1. .478 /organism="Mus musculus"
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The WashU-HHMI Mouse EST Project
Unpublished (1996)
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/clone="IMAGE:354554"
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460 bp mRNA EST 17-DEC-1999 wb63404.XI NCLCAPE_GCG Homo sapiens cDNA clone IMAGE.2310343 3' similar to gb:X02812_cds1 TRANSFORMING GROWTH FACTOR BETA 1 PRECURSOR (HUMAN); contains PTR5.t3 PTR5 MSR1 repetitive element ;,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequencing Center
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 460)
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Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
R. Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCI-CGAP http://www.ncbi.nlm.nih.gov/nciogap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
     was constructed by Bento Soares and
                                                                                                                                                                                                                                                                                                                                                  319
                                                                                                                                                                                                                                                                                                                                                                                      240
                                                                                                                                                                                            tacattgacttccgacaggatctgggctggaagtgggtccatgaacctaagggctactat 120
                                                                                                                                                                                                                                                                                                                  gocaacttotgotcaggocottgoccatacotcogcagtgoagacacaacccacagcacg 180
                                                                                                                                                                                                                                                                                                                                                                                                                  320 Grecirgecerciacaaceaacaaccagececircegecercacergecegece 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                    241 caggacctggagccctgaccatcctgtactatgttgggaggaccccaaagtggagcag 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           439
                                                                                                                                                                                                                                                                                                                                260 GCCAACTTCTGTCTGGGACCCTGCCCTATATTTGGAGCCTGGACACACAGTACAGCAAG
                                                                                                                                                                                                                                                                                                                                                                                    1 gotttggacaccaattactgcttccgcaacttggaggagaactgctgtgtgcgcccctc
                                                                                                                                                                                                                                                                             200 TACATTGACTTTAGGAAGGACCTGGGTTGGAAGTGGATCCACGAGGCCCAAGGGCTACCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 190; Length 478;
                                       1 others
                                                                                                                                           Indels
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DNA Sequencing by: Washington University Genome
Clone distribution: NCI-CGAP clone distribution
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbpp/image/image.html
Insert Length: 519 Std Error: 0.00
                                                                                                     Score 178.8; DB 190;
Pred. No. 2.2e-40;
0; Mismatches 93;
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                                   90
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/db_xref="taxon:9606"
/clone="IMAGE:2310343"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Seq primer: -400P from Gibco
High quality sequence stop: 206.
Location/Qualifiers
normalization, and M.Fatima Bonaldo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mRNA sequence.
A1654506
A1654506.1 GI:4738485
                                                                                                     Ouery Match 52.7%;
Best Local Similarity 72.3%;
Matches 245; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tumor Gene Index
Unpublished (1997)
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Best Local S
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DEFINITION
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                                 BASE COUNT
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/note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Plasmid DNA from the normalized library NCI_CGAP_GC4 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made 1from the same library (cloneIDs 1257096-1258631, 1469064-1470983, and 1475592-1476743). Subtraction by Bento Soares and M. Fatima Bonaldo. "
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 339)
Marray M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ue48g10.r2 Soares_mammary_gland_NMLMG Mus musculus cDNA clone IMAGE:1494402 5' similar to gb:M32745 mouse transforming growth factor_beta-3 mRNA, complete (MOUSE);, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     153 ccgcagtgcagacacaacccacagacacggtgctgggactgtacaacactctgaaccctga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        273 tgttgggaggaccccaaagtggagcagctcccaacatggtggtgaagtcttgtaaatg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HMI Mouse EST project
WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                Length 460;
                                                                                                                                                                                                                                                                                                                                                                                                                           Score 178.6; DB 23; Length
Pred. No. 2.5e-40;
0; Mismatches 81; Indels
                      /tissue_type="pooled germ cell tumors"
/lab_host="DH10B"
/clone_lib="NCI_CGAP_GC6"
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                                                                                                                                                                                                                                                                                                                                                                                                                              52.7%;
73.6%;
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CDNA was
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                                                                                                                                                                                                                                                                                                                                                         /note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker: 1st strand cDNA was prepared from mammary polylinker: 1st strand cDNA was prepared from mammary gland tissue from a lactating female, and was then primed with a Not I - 0.1190(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 wb02f01.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2304505 37 similar to gb:X02812_cds1 TRANSFORMING GROWTH FACTOR BETA 1 PRECURSOR (HUMAN); contains element TAR1 MER22 repetitive element mRNA sequence.
A1824845
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 441)
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 tacattgacttccgacaggatctgggctggaagtgggtccatgaacctaagggctactat 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 gccaacttctgctcaggcccttgcccatacctccgcagtgcagacacaacccacagcacg 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                109 GCCCTGGACACCAATTACTGCTTCCGCAACCTGGAGAACTGCTGTGTACGCCCCCTT 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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Email: cgapbs-I@mail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Mic
R. Emmert-Buck, M.D., Ph.D.
GDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           51.9%; Score 176; DB 16; Length 339; ilarity 90.0%; Pred. No. 1.3e-39; Conservative 0; Mismatches 21; Indels
                                                                                                                                                                                                                               /clone="IMAGE:1494402"
/clone_lib="Soares mammary_gland_NMLMG"
/sex="female (lactating)"
/tissue_type="mammary gland"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       288 GTGCTTGGACTATACAACACCCTGAACCCAGAGGCGTCTGC 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EST
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                                                                       Seq primer: -28ml3 rev2 ET from Amersham
High quality sequence stop: 267.
Location/Qualifiers
                                                                                                                                                    1. .339 //
/organism="Mus musculus"
                                                                                                                                                                                                          /db_xref-"taxon:10090"
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Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
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Matches 199; Conserv
                                                  MGI:932006
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AI824845/C
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KEYWORDS
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/clone="Introduction" (2006)
/clone="Introduction" (2006)
/clone="Introduction" (2007 GCG"
/tissue_type="pooled germ cell tumors"
/lab_host="DelloB" (2006)
/lab_host="DelloB"
   , Center
on can be
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota, Metazoa; Chordata; Catarrhini; Hominidae; Homo.

I (basea Lo 517)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ó
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DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can l found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 497 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 347.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          224 cgccttgctgcgtgccccaggacctggagcccctgaccatcctgtactatgttgggagga 283
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Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence we farived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl-&t2=QV3-BT0571-030
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The FAPESP/LICR Human Cancer Genome Project
Unpublished (1999)
Contact: Simpson A.J.G.
Laboratorsy of Cancer Genetics
Ludwig Institute for Cancer Research
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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/note="Organ: breast_normal; Vector: pucl8; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions.
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RCl&t2=RCl-BN0014-
210100-012-e01&13-2000-01-21&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 20
High quality sequence stop: 336.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I (bases 1 to 403) NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       254 ccctgaccatcctgtactatgttgggaggacccccaaagtggagcagctctccaacatgg 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              74 gacaggatctggggctggaagtgggtccatgaacctaagggctactatgccaacttctgct 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             134 caggcccttgcccatacctccgcagtgcagacacacaccacaggcacggtgctgggactgt 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7 ACTATIGCTITGAAAATGIGCAGGATAATIGCTGCCTACGTCCACTITACATITCA 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14 attactgcttccgcaacttggaggagaactgctgtgtgcgccccctctacattgacttcc 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           194 acaacactctgaaccctgaagcatctgcctcgccttgctgcgtgccccaggacctggagc
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0; Mismatches
                                                                                                                                                                                                                                                                                          1. .336
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="BM0014"
/dev_stage="Adult"
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COMMENT

source

FEATURES

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Eukaryotta, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia; Eutheria, Rodentia, Sciurognathi; Muridae, Murinae; Mus. 1 (bases 1 to 317).

Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Materston, R. and Wilson, P.
                                                                                                                                                                                                                                                                                                                                                                             Email: mouseestewatson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
This read is a RESEQUENCE of a previously sequenced mouse clone
This read has been verified (found to hit its original self in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95 gggtccatgaacctaagggctactatgccaacttctgctcaggcccttgcccatacctcc 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Marra M/WashU-NCI Mouse EST Project 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
T=1: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          35 aggagaactgctgtgtgcgcccctctacattgacttccgacaggatctgggctggaagt
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone_lib="Soares mouse embryo NbME13.5 14.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 20; Length 317;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue_type="embryo"
/dev_stage="13.5-14.5dpc total fetus"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 173.8; DB 2 Pred. No. 5.4e-39;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /strain="C57BL/6J"
/db_xref="taxon:10090"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    High quality sequence stop: 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Seq primer: -40RP from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 M.Fatima Bonaldo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /sex="unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         51.3%;
73.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 correct orientation)
MGI:242174
                                                                                                                                                                                                                                                  Unpublished (1999)
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                                                                                          REFERENCE
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                                                                                                                            DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: info@image.llnl.gov
Trace considered overall poor quality
Seq primer: -40UP from Gibco
High quality sequence stop: 1.

Location/Qualifilers
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                                                                                                                                                                                                                                                                                                                                                                        /clone="Index:1440814"
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/tasue_type="lymphocyte"
/tab_host="bH10B (phage-resistant)"
/note="Organ: blood; Vector: pT7T3D-Pac; Site_1: NotI;
Site_2: EcoRi; lst strand cDNA was primed with a Not I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gccaacttctgctcaggcccttgcccatacctccgcagtgcagacacaacccacagcacg 180
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                                                                cDNA Library Preparation: M. Bento Soares, Ph.D. and M.Fatima
Bonaldo, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     214 GCCAACTTCTGCATCGGGCCCTGCCCCTACATTTGGAGCCTGGACACGCAGTACAGCAAG 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94 CAGGTGCTGGACCCGCTGCCCATTGTGTACTACGTGGCCCGCAAGGTGGAGGAG 35
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                                                                                                            CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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Pred. No. 1.7e-39;
0; Mismatches 99; Indels 0;
                                                Ph.D.
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: M. Bento Soares,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     301 ctctccaacatggtggtgaagtcttgtaaatgta 334
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Best Local Similarity 70.4%;
Matches 235; Conservative (
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BASE COUNT

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VERSION KEYWORDS

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information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
                                                                                                                                                                                      AI421250 540 bp mRNA EST 28-MAR-1999 tf14d02.xl NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:2096163 3' similar to 9b:X02812_cds1 TRANSFORMING GROWTH FACTOR BETA 1 PRECURSOR (HUMAN);contains element TAR1 repetitive element;, mRNA
                                                                                                                                                                                                                                                                                                                                                       Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 540)
NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/PRGAP). Tumor Gene Index
(Unpublished (1998)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
275 ttgggaggaccccaaagtggagcagctctccaacatggtggtgagtcttgtaaatgta
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bonaldo, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Seq
Clone distribution: NCI-CGAP clone distribution inf
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 874 Error: 0.00
Seq primer: -400P from Gibco
High quality sequence stop: 373.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo saplens"
/db_xref="taxon:9606"
/clone="InAsc:2096163"
/clone_lb="NCI_CGAP_Brn23"
/tissue_type="glioblastoma (pooled)"
/lab_host="BH108"
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Pred. No. 6.8e-39;
0; Mismatches 89;
                                                                                                                                                                                                                                                                                          AI421250.1 GI:4267181
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ilarity 72.6%;
Conservative
                                                                                                                                                                                                                                                                                                                                            Homo sapiens
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Fax: +55-11-2704922
Fax: +55-11-2707001
Fax: +55-11-2707001
Fax: +55-11-2707001
Final: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC1&t2=RC1-BN0014-
210100-012-2f1&t3=2000-01-21&t4=1)
Seq primer: puc 18 forward: 10
High quality sequence start: 10
High quality sequence stop: 325.
Location/Qualifiers
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/dev_stage="Adult"
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/note="organ: breast_normal; Vector: pucl8; Site_l: Smal;
/note="organ: breast_normal; Vector: pucl8; Site_l: Smal;
/note="organ: hain:library was made by cloning products
/organ: mini-library was mi
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BN0014 Homo sapiens CDNA, mRNA sequence.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                         286
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Pred. No. 3e-38;
0; Mismatches 88; Indels
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The FAPESP/LICR Human Cancer Genome Project
Unpublished (1999)
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76 c 63 g 88
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//tissuc_type="embryo (stage 10)"
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/note="Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI;
/notice="Vector: pCMV-SPORT6; Site_1: NotI; Site_2: No
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: Martha Rebbert, Steven L. Klein, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: Xenopus clones from this library are available
through the I.M.A.G.E. Consortium/LLNL at: info@image.llnl.gov
Seq primer: -40UP from Gibco
High quality sequence stop: 417.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BES75698 445 bp mRNA EST 15-AUG-2000 dc62d10.x1 NICHD XGC Emb1 Xenopus laevis cDNA clone IMAGE:3401683 3' similar to gb:Y00083 TRANSFORMING GROWTH FACTOR BETA 2 PRECURSOR (HUMAN); gb:X57413 Mouse mRNA for transforming growth factor-beta 2 BES75698
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1 (bases 1 to 445)

NCI-GAP http://www.ncbi.nlm.nih.gov/ncicgap.
NTI-GAP nttp://www.ncbi.nlm.nih.gov/ncicgap.
Tumor Gene Institute, Cancer Genome Anatomy Project (CGAP), Unpublished (1997)
                                                                                                                                                                                                                                                                                                                  tggaagtgggtccatgaacctaagggctactatgccaacttctgctcaggcccttgccca 147
                                                                                                                                             70 TGGAAATGGATACACGAACCCAAAGGGTACAATGCCAACTTCTGTGCTGGAGCATGCCCG 129
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Pred. No. 3.6e-38;
); Mismatches 105;
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Matches 234; Conservative
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cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3'); double-stranded cDNA was ligated to Eco RI adaptors (Pharmacla), digested with Nor I and cloned into the Not I and Eco RI sites of the modified pT773 vector. Library is normalized, constructed in the laboratory of M. Bento
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 naf10909.x1 Soares_NPBMC Homo sapiens cDNA clone IMAGE:4140856 3' similar to SW:TGF1_BOVIN P18341 TRANSFORMING GROWTH FACTOR BETA 1 PRECURSOR; contains element TAR1 repetitive element; , mRNA
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                    240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: M. Bento Soares, Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D. and M.Fatima
Bonaldo, Ph.D.
                                                                                                       tacattgacttccgacaggatctgggctggaagtgggtccatgaacctaagggctactat 120
                                                373 GCTCTCGATGCTGCCTATTGCTTTAGGAACGTTCAGGACAATTGCTGTCTACGTCCCTTA 314
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                                                                                                                                       gocaacttctgctcaggcccttgcccatacctccgcagtgcagacacaacccacaggacg
                                                                                                                                                                                                                                                                                                                                  181 gigcigggacigiacaacacicigaacccigaagcaicigccicgccitgcigcgigccc
                                                                                                                                                                                                                                                                                                                                                                                                                                                  caggacctggagccctgaccatcctgtactatgttgggaggacccccaaagtggagcag
getttggacaccaattactgettecgcaacttggaggaggaactgetgtgtgegeeeete
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Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         301 ctctccaacatggtggtgaagtcttgtaaatgtagctga 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/db_xref="taxon:9606"
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Seg primer: -40UP from Gibco
High quality sequence stop: 125.
Location/Qualiflers
1. .559
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BG058804.1 GI:12525628
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Mammalia; Eutheria;
1 (bases 1 to 559)
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Unpublished (1997)
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50.48;
72.88;
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                                                                                     Best Local Similarity 72.8
Matches 246; Conservative
 228
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AI304490
AI304490.1
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   142
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                                                                     Query Match
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AI304490/c
LOCUS
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 BASE COUNT
ORIGIN
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//note="Organ: brain: Vector: pcwvsport 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pcwvsport 6 vector. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies. Contact : Feng Liang Life Technologies. Contact : Feng Liang Life Trennelogies, a division of Invitrogen 9800 Medical Center Prive Rockville, Maryland 20850, USA Fax : (1) 301 610 http://fulllength.invitrogen.com"
                                                                                                                      1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 798)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full:length cDNA libraries and normalization
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AL530080 798 bp mRNA EST 13-FEB-2001 AL530080 LTLNFL001 NBC4 Homo sapiens cDNA clone CS0DD009YM06 3 prime, mRNA sequence.
AL530080
                                                                                                                                                                                                                                                                                              180
                                                                                                                                                                                                                      gigotigggacigiacaacacicigaacccigaagcaicigccicgcciigcigcgigccc 240
                                                                                                                                                                        caggacctggagcccctgaccatcctgtactatgttgggaggacccccaaagtggagcag 300
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                                                                                                                       Gaps
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Genoscope - Centre National de Sequencage
BP 191 91006 EVRX cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
                                                                                                                                                                                                                                                                                            gecaacttetgeteaggecettgeceatacetecgeagtgeagacaeaacecaeageaeg
                                                                                                                                                                                                                                                                                                                304 GTCCTGGCCCTGTACAACCAGCATAACCCGGGCGCCTCGGCGCCCCCGTGCTGCGTTCCG
                                                                                                                      3;
                                                                                    Length 559;
                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /tissue_type="neuroblastoma cells"
                                                                                    50.4%; Score 171; DB 173; 71.1%; Pred. No. 3.8e-38;
                                                                                                                    95;
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Soares (University of Iowa)."
148 c 206 g 108 t
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/db_xref="taxon:9606"
/clone="cSODD009YM06"
/clone_lib="LTI_NFL001_NBC4"
/sex="male"
                                                                                                      Pred. No. 3.8e
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
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                                                                                                    Best Local Similarity /1.1
Matches 241; Conservative
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              97 a
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TITLE
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                                                                                                                                                                                                                                                                                            121
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Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NI-GAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                  ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AI304490 449 bp mRNA EST 01-FEB-1999 9054606.X1 NCI_CGAP_CO8 Home sapiens cDNA clone IMAGE:19121354 3' similar to gb:X02812_cG1 TRANSFORMING GROWTH FACTOR BETA 1 PRECURSOR (HUMAN); contains PTR5.13 TAR1 repetitive element ;, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryotani Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I (bases 1 to 44) NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                          240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            222 GTCCTGGCCCTGTACAACCAGCATAACCCGG--GCCTCGGCGGCGCGCGTGC-GCGTGCC 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   300
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                                                                                                                                                  3;
                                                                                                 106; Length 798,
                                                                                                                      Pred. No. 4.6e-38;
1; Mismatches 88; Indels
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/clone="IMAGE:1912354"
/clone=lib="MCI_CGAP_CO8"
/tissue_type="adenocarcinoma"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              www-bio.llni.gov/bbrp/image/image.html
Insert Length: 933 Std Error: 0.00
     ų
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               105 CTGTCCAACATGGTCGTGCGCTCCTGCAAGGGCCGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Insert Length: 933 Std Error: 0.00
Seq primer: -400P from Glbco
High quality sequence stop: 385.
Location/Qualifiers
                                                                                                 Score 170.8;
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274
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Local Simi

113 389 173

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Query Match Best Loca Matches

BASE COUNT

ORIGIN

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A1272940 292 bp mRNA EST 18-NOV-1998 q156901.x1 Soares_WhMPu_S1 Homo sapiens cDnA clone IMAGE1.875368 3' similar to 9b.x02812_cds1 TRANSFORMING GROWTH FACTOR BETA 1 PRECURSOR (HUMAN);contains element MER22 repetitive element;; mRNA
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 292)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Email: capabs-remail.nih.gov
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gagococtgaccatoctgtactatgttgggaggacccccaaagtggagcagctctccaac 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             70 ttccgacaggatctgggctggaagtgggtccatgaacctaagggctactatgccaacttc 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       130 tgctcaggcccttgcccatacctccgcagtgcagacacaacccacagcacggtgctggga 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10 accaattactgcttccgcaacttggaggagaactgctgtgtgcgcccctctacattgac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   190 ctgtacaacactctgaaccctgaagcatctgcctcgccttgctgcgtgccccaggacctg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 19; Length 328;
                             /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="InAGE:2010730"
/clone_lib="NCI_CGAP_Brn23"
/tissue_type="qlioblastoma (pooled)"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                49.1%; Score 166.4; DB 19;
69.2%; Pred. No. 6.9e-37;
iive 0; Mismatches 101;
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AI272940.1 GI:3895208
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A1272940/c
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/note="Organ: colon; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from colon adenocarcinoma, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is normalized. Library was constructed by Bento Scares and M. Fatima Bonaldo. "
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DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              qy01c06.xl NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:2010730 3/
similar to gb:X02812_cds1 TRANSFORMING GROWTH FACTOR BETA 1
PRECURSOR (HUMAN);, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Hominidae; Homo.
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1 (bases 1 to 328)
NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BTGAP), Tumor Gene Index
Unpublished (1998)
                                                                                                                                                                                                                                                                                                                                                                                                            53 gcccctctacattgacttccgacaggatctggggctggaagtgggtccatgaacctaagg 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gctactatgccaacttctgctcaggcccttgcccatacctccgcagtgcagacacaaccc 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gogtgccccaggacctggagcccctgaccatcctgtactatgttgggaggaccccaaag 292
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                                                                                                                                                                                                                                                                                                                                          .;
0
                                                                                                                                                                                                                                                                                         49.7%; Score 168.6; DB 18; Length 449; 74.2%; Pred. No. 1.7e-37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bento Soares, Ph.D.,
                                                                                                                                                                                                                                                                                                                                        74; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tggagcagctctccaacatggtggtgaagtcttgtaaatgtagctga 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             209 TGGAGCAGCTGTCCAACATGGTGCGCGCTCCTGCAAGTGCAGCTGA 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                          Pred. No. 1.7e-37;
0; Mismatches 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Trace considered overall poor quality
Insert Length: 628 Std Error: 0.00
Seg primer: -400P from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 High quality sequence stop: 1.
Location/Qualiflers
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VERSION KEYWORDS SOURCE

AUTHORS TITLE

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JOURNAL

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RESULT 55 AI360877/c LOCUS

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226; Conservative
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                                                                                                                                                                                      /lab_host="DH10B"
//note="Organ: mixed (see below); Vector: pT7T3D-Pac
//note="Organ: mixed (see below); Vector: pT7T3D-Pac
//note="Organ: mixed (see below); Vector: pT7T3D-Pac
//note="Organ: with a modified polylinker; Site_I: Not I;
Site_I: Eco RI; Equal amounts of plasmid DNA from three
normalized libraries (melanocyte 2NbHM, pregnant uterus
NbHPU, and fetal heart NbHH19W) were mixed, and ss circles
were made in vitro. Following HAP purification, this DNA
was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from pools of
5,000 clones made from the same 3 libraries. The pools
consisted of I.M.A.G.E. clones 260232-265223,
340488-34479, and 484488-489479."
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 499)
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Emall: cgapbs-remail.nih.gov
This clone is available royalty-free through LLNL; contact the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              46 tgtgtgcgcccctctacattgacttccgacaggatctgggctggaagtgggtccatgaa 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  106 cctaagggctactatgccaacttctgctcaggcccttgcccatacctccgcagtgcagac 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CCCAAGGGTACCATGCCAACTTTTGCCTCGGGCCCTGCCCTACATTTGGAGCCTGGAC 173
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                                                                                                                                                    /tissue_type="Pooled human melanocyte, fetal heart, pregnant uterus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. 1.1e-36;
0; Mismatches 79;
                                                                                                            /clone="IMAGE:1876368"
/clone_lib="Soares_NhHMPu_S1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     48.8%; Score 165.6; 72.9%; Pred. No. 1.16
                                                                         /organism="Homo sapiens"
Seq primer: -40UP from Gibco
High quality sequence stop: 1.
                                                                                             /db_xref="taxon:9606
                                     Location/Qualiflers
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AI273619/c
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/note="Organ: mixed (see below); Vector: pT7T3D-Pac /note="Organ: mixed (see below); Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (melanocyte 2NbHM, pregnant uterus NbHPU, and fetal heart NbHH19W) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDMAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 260232-265223, 340488-489479, and 484488-489479. 1 others
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 477)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
                                                                                                                                                                                                                                                                                                                                               /tissue_type="Pooled human melanocyte, fetal heart, and pregnant uterus" /lab_host="DH108"
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 760 Std Error: 0.00
Seg primer: -400P from Gibco
High quality sequence stop: 366.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AA049522 477 bp mRNA EST 09-SEP-1996 mj35f01.rl Scares mouse embryo NDWEl3.5 14.5 Mus musculus cDNA clone IMAGE:478105 5' similar to gb:X02812_cds1 TRANSFORMING GR FACTOR BETA 1 PRECURSOR (HUMAN); gb:M32745 mouse transforming growth factor beta-3 mRNA, complete (MOUSE); mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     201 tetgaaccetgaagcatetgeetegeettgetgegtgeeceaggaeetggageeetgae 260
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              141 ttgcccatacctccgcagtgcagacacaacccacaggacggtgctgggactgtacaacac 200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 499;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. 3.8e-35;
0; Mismatches 92
                                                                                                                                                                                                       /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1876320"
/clone_lib="Soares_NhHMPu_S1"
                                                                                                                                           Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                             ñ
                                                                                                                                                                                                  This clone is available royalty-free through LLNL; contact the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gocaacttotgotcaggocottgocoatacotcogoagtgoagacacaaaccoacagcacg 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               142 GCCCTGGATACCAACTATTGCTT-CACTCCACAGAGAAGAACTGCTGTGTGCG-GCACTG 199
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Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
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                                                                                                                                                                                                                           MGI:288849
Seq primer: -28M13 rev2 from Amersham
High quality sequence stop: 450.
Location/Qualifiers
1. 477
/ Organism="Mus musculus"
/ strain="C5/PBL/6J"
/ db_xref="taxon:10090"
/ clone="IMAGE:478105"
/ clone="lib="Soares mouse embryo NDME13.5 14.5"
/ sex="unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .;
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                                                                                                                                       Louis, MO 63108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              91; Indels
                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="embryo"
/dev_stage="13.5-14.5dpc total fetus"
/lab_host="DH10B"
                                             Waterston, R.
The WashU-HMI Mouse EST Project
Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HMI Mouse EST Project
WashIngton University School of Medicinep
4444 Forest Park Parkway, Box 8501, St. Loui
Fax: 314 286 1800
Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 158.4; DB 1;
Pred. No. 1.4e-34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
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71.68;
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Best Local Similarity 71.6
Matches 235; Conservative
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Doj.H.
Systematic analyses of genes expressed in fertilized mouse eggs(The Systematic analyses of genes expressed in fertilized mouse eggs(The ERATO/Doi Project at Wayne State University)
Unpublished (1998)
Contact: Hirofumi Doi
Doi Bloasymmetry Project, ERATO
Japan Science and Technology Corporation (JST)
WBG Marive East 12F, 2-6 Nakase, Mihama-ku, Chiba 261-71, Japan
Email: hd@bloa.jst.go.jp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3;
                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. I (basea 1 to 58)
Ko,M.S.H, Kitchen,J.R., Wang,X., Wang,X., Threat,T.A., Sun,T., DePalma,G.E., Liang,Y., Kargul,G.J., Sharara,R., Paonessa,P.D. and
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AU016729 Mouse two-cell stage embryo cDNA Mus musculus cDNA clone
AU0128008 3', mRNA sequence.
AU016729 GI:3371733
C86879 583 bp mRNA EST 11-MAR-1998
C86879 Mouse fertilized one-cell-embryo cDNA Mus musculus cDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 156; Length 583;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          // Organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="J0356C9"
/clone="J0356C9"
/dev_stage="fertilized one-cell-embr/dev_stage="fertilized one-cell-embryo"
124 c 134 g 166 t 17 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      151 TTTCCAATATGATTGTCAAGTCTTGTAAATGCAGCTAA 114
                                    clone J0235C05 3', mRNA sequence. C86879
                                                                                      C86879.1 GI:2918836
                                                                                                                                                               Mus musculus
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240; Conserv
                                                                                                                                            house mouse.
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                            Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Murinae; Murinae;
Mus.a. 1 (Dases 1 to 576)
Ko,M.S.H, Kitchen,J.R., Wang,X., Threat,T.A., Sun,T., DePalma,G.E.,
Lidng,Y., Kargul,G.J., Sharara,R. and Doi,H.
Systematic analyses of genes expressed in 2-cell stage mouse
embryos (The ERATO/Doi Project at Wayne State University) (Ko
Jupublished (1998)
Contact: Hirofumi Doi
Doi Bloasymmetry Project, ERATO
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 408)
                                                                                                                                                                                                                         Japan Science and Technology Corporation (JST)
WBG Marive East 12F, 2-6 Nakase, Mihama-ku, Chiba 261-71, Japan
Email: hd@bioa.jst.go.jp.
Location/Qualifiers
1. 576
/organism="Mus musculus"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60 ctacattgacttccgaca-ggatctgggctggaagtgggtccatgaacctaagggctact 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                214 CCCAGGATCTGGAACCACTGACCATTCTCTATTACATTGGAAATACGCCCAAGATCGAAC 155
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     119 atgccaacttctgctcaggccttgcccatacctccgcagtgcagacacaaacccacaga
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 107; Length 576;
                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:10090"
/clone="J0728H08"
/clone_lib="Mouse two-cell stage embryo cDNA"
                                                                                                                                                                                                                                                                                                                                                                                                          11 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     88; Indels
                                                                                                                                                                                                                                                                                                                                                                                          /dev_stage="two-cell stage embryo"
123 c 134 g 164 t 11
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73.0%; Pred. No. 5.6e-33;
tive 0; Mismatches 88
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                  house mouse.
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Matches 249; Conserv
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W98872 431 bp mRNA EST 16-JUL-1996 mf89e01.rl Soares mouse embryo NDME13.5 14.5 Mus musculus CDNA clone IMAGE:421464 5' similar to gb:X02812_cds1 TRANSFORMING GROWTH FRACTOR BETA 1 PRECURSOR (HUMAN);, mRNA sequence.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 431)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                          Sequencing Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Organ: pancreas; Vector: pCMV-SPORT6; Site_1: Sall; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.72 kb. Life Technologies catalog #:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                           Life Technologies catalog #: 11548-013

Life Technologies catalog #: 11548-013

DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:

www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 614 Std Error: 0.00

Seq primer: -400P from Gibco.

Location/Qualifiers
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     142 tgcccatacctccgcagtgcagacacaacccacagcacggtgctgggactgtacaacact 201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .8e-33;
                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2294345"
/clone_lib="NCI_CGAP_Pan1"
/tissue_type="adenocarcinoma"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      78 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 152.4; I
Pred. No. 6.8e-
0; Mismatches
                                                                                                             Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         154 g
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Best Local Similarity 74.4%;
Matches 192; Conservative C
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a 118 c
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                                                      Tumor Gene Index
Unpublished (1997)
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239
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                                       ACCESSION
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                                                                                                         This close is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         218 GCCAACTTCTGTCTGGGACCCTGCCCTATATTTGGACCTGGACACACAGAGAACAGAAG 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          240
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44.7%; Score 151.6; DB 191; Length 431;
Best Local Similarity 71.4%; Pred. No. 1.2e-32;
Matches 227; Conservative 0; Mismatches 89; Indels 2;
The WashU-HHMI Mouse EST Project
Unpublished (1996)
Contact: Marra MyMouse EST Project
WashU-HHMI Mouse EST Project
WashIngton University School of MedicineP
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                                 /strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:421464"
/clone_lib="Sgares mouse embryo NbMEl3.5 14.5"
                                                                                                                                                                                                                                                                             /tissue_type="embryo"
/dev_stage="13.5-14.5dpc total fetus"
/lab_host="DH108"
                                                                                                                                  MGI:256016
Trace considered overall poor quality
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 85 t
                                                                                                                                                                                                       /organism-"Mus musculus"
                                                                                                                                                        Seg primer: ETPTIMEA
High quality sequence stop: 1.
Location/Qualifiers
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                                                                                                                                                                                                                                                                   /sex="unknown'
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ORIGIN
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COMMENT
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note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from mammary gland tissue from a lactating female, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo. " 243 c 317 g 197 t
                                                                                                                                                                                                                                                                                                                                                                 Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: M. Bento Soares, Ph.D.
Tissue Procurement: M. Bento Soares, Ph.D.
CDNA Library Preparation: Bento Soares and M. Fatima Bonaldo
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM8476 row: h column: 18
High quality sequence start: 37
High quality sequence stop: 636.
                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. I to 996)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
602117568T1 Soares_mammary_gland_NMLMG Mus musculus cDNA clone IMAGE:3468737 3', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 44.7%; Score 151.4; DB 168; Lengt
Best Local Similarity 71.6%; Pred. No. 1.6e-32;
Matches 240; Conservative 0; Mismatches 91; Indels
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AW600938
AW600938.1 GI:7305677
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72.1%;
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Matches 189; Conservative
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ORIGIN
                             197
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Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T.,
Underwood,K., Steptce,M., Theksing,B., Allen,M., Bowers,Y., Person
,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter
,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R.,
The Washu-NcI Mouse EST Project 1999

Contact: Marra M/WashU-NCI Mouse EST Project 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                 A1604914 403 bp mRNA EST 21-APR-1999 me44c04.x1 Soares mouse embryo NbME13.5 14.5 Mus musculus cDNA clone IMAGE:390342 3' similar to 95:X02812_cds1 TRANSPORMING GROWTH FACTOR BETA 1 PRECURSOR (HUMAN); 9b:M32745 mouse transforming growth factor beta-3 mRNA, complete (MOUSE);, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    I 3'], on equal amounts of mRNA from 2 13.5dpc and 2
14.5dpc embryos [total RNA provided by Minoru Ko, Wayne
State Univ., from 2 ]; double-stranded cDNA was ligated to
Eco RI adaptors (Pharmacia), digested with Not I and
cloned into the Not I and Eco RI sites of the modified
pryT3 vector. Library went through one round of
normalization, and was constructed by Bento Soares and
M.Fatima Bonaldo.
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                                                                                                                                                                                                                                                                                                                                     Sciurognathi; Muridae; Murinae; Mus
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. This clone was previously sequenced on the 5' end only, this new data is from the 3' end.
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0
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43.1%; Score 146.2; DB 22; Length
Best Local Similarity 72.2%; Pred. No. 3.9e-31;
Matches 190; Conservative 0; Mismatches 73; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue_type="embryo"
/dev_stage="13.5-14.5dpc total fetus"
/lab_host="DH10B"
135 GTCCAACATGATTGTGCGCTCCTGCAAGTGCAGCT 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:390342"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /sex="unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .403
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                                                                              AI604914/c
                                                                                                                      DEFINITION
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SOURCE
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                                                                                                                                                                                                                                                                                                                                                                         AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURES
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/db\_xref="taxon:9606"
/clone\_lib="BN0014"
/dev\_stage="Adult"
/dev\_stage="Adult"
/note="Organ: breast\_normal; Vector: pucl8; Site\_1: SmaI; Site\_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and CDNA amplification were performed under Email: asimpsoneludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RCl&t2=RCl-BN0014-310100-012-03\_l&f3=2000-01-21&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 257. Unpublished (1999)
Contact: Simpson A.J.G.
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Euteleostomi; 122 TGCCCATCGTCTACTACGTGGGTCGCAAGCTCGAAGCTGGAGTTGTCCAACATGATTG 163 138 cccttgcccatacctccgcagtgcagacacaacccacagcacggtgctgggactgtacaa 197 AGCATGCCCGTATTTATGGAGTTCAGACACTCAGCACAGAGGTCCTGAGCTTATATA 147 78 ggatctgggctggaagtgggtccatgaacctaagggctactatgccaacttctgctcagg 137 23-MAR-2000 Gaps 257 tgaccatcctgtactatgttgggaggacccccaaagtggagcagctctccaacatggtgg 266 GGATCTAGGGTGAAAATGGATACACGAACCCAAAGGGTACAATGCCAACTTCTGTGCTGG AW600938 267 bp mRNA EST 23-MAR-20 RC1-BN0014-210100-012-c03\_1 BN0014 Homo sapiens CDNA, mRNA Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Butele Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. DB 118; Length 267; . 0 73; Indels 1 (bases 1 to 267) HCGP http://www.ludwig.org.br/ORESTES. The FAPESP/LICR Human Cancer Genome Project Score 145.2; DB 1. Pred. No. 6.9e-31; 0; Mismatches conditions. 1. .267 /organism="Homo sapiens" Location/Qualifiers low stringency cond 52 c 62 g

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Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   T 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization, and was constructed by Bento Soares and M.Fatima Bonaldo."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 58)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /dev_stage="adult"
/lab_host="DH108"
/note="Organ: placenta; Vector: pT7T3D-Pac (Pharmacia)
with a modified polylinker; Site_1: Not I; Site_2: Eco RI;
lst strand cDNA was primed with a Not I - oligo(dT) primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The WashU-HMI Mouse EST Project
Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
WashIngton University School of MedicineP
4444 Forest Parkway, Box 8501, St. Louis, MO 63108
Fax: 314 286 1810
Fax: 314 286 1810
Fmail: mouseest@watson.wustl.edu
This clone is available royalty-free through LINE; contact the
                                                                               317
                                        87
                                                                                                    146 TACCATAAATCCAGAAGCATCTGCTACTCCTTGCTGCGTGTCCCAAGATTTAGAACCTCT
                                                                               gaccatcctgtactatgttgggaggaccccaaaagtggagcagctctccaacatggtggt
198 cactctgaaccctgaagcatctgcctcgccttgctgcgtgccccaggacctggagccct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="taxon:10090"
/clone="IMAGE:457739"
/clone=lib="Soares mouse placenta 4NbMP13.5 14.5"
/sex="unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Seg primer: -28M13 rev2 from Amersham
High quality sequence stop: 454.
Location/Qualifiers
1..558
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/strain="C57BL/6J"
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Length 558;

42.5%; Score 144; DB 1;

Query Match

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/clone_lib="NIH_MGC_77"
/lab_host="DH10B (T1 phage-resistant)"
/lab_host="DH10B (T1 phage-resist
                                            5
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NIH-WGC http://mgc.nci.nih.gov/.
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Tissue Procurement: CLONTECH Laboratories, Inc.
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNE)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
                                                                                                                                                                                            222 GCCCTGGATACCAACTATTGCTTCAGCTCCACAGAAACTGCTGTGTGCGGCAGTNG 281
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/db_xref="taxon:9606"
/clone="IMAGE:4694836"
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High quality sequence stop: 562.
Location/Qualifiers
    Pred. No.
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BG540633
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71.0%;
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230 C
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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TAG_TISSUE=prostate
TAG_SEQ=AAGTG"
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AI192407.1 GI:3743616
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Best Local Similarity 73.55
Matches 183; Conservative
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AI192407/c
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The sequence contained an oligo-dr track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. cDNA interpretation: M.B. Soares Lab Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/ILNL at:
                                                                                             1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Vector: pr7T3D-Pac (Pharmacia) with a modified bolylinker; Site_1: Not I; Site_2: Eco RI; The NCI_CGAP_Sub3 library is a subtracted library derived from the NCI_CGAP_Sub1 library, which is a subtracted library
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 409)
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AW295761 409 bp mRNA EST 16-JAN-2000 UI-H-BII-afh-a-02-0-UI.sl NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2721675 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                www-bio.llnl.gov/bbrp/image/image.html The following repetitive
elements were found in this cDNA sequence: 102-157,
>GC_rich#Low_complexity
                                                                                                                                                                                                   274 GCTTTGGATGCGCCTATTGCTTTAGAAATGTGCAGGATAATTGCTGCCTACGTCCACTT 333
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                                                                                                                                                                                                                                                                                                                                                                                                                         240 ccaggacctggagccctgaccatcctgtactatgttgggaggacccccaaagtggagca 299
                                                                                                                          1 gctttggacaccaattactgcttccgcaacttggaggagaactgctgtgtgcgcccctc 60
                                                                                             1; Gaps
                                                       DB 155; Length 889;
                                                                                             Indels
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/lab_host="DH10B (Life Technologies)"
                                        /organism="Homo sapiens"
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/clone="IMAGE:2721675"
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68.28;
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Unpublished (1997)
                                                                                      Matches 214; Conservative
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ORIGIN
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derived from BI. BI constitutes a mixture of 21
normalized or subtracted NCI\_CGAP\_IDraries: NCI\_CGAP\_CO4
, NCI\_CGAP\_CA12, NCI\_CGAP\_RIG1, NCI\_CGAP\_CA10,
NCI\_CGAP\_CA16, NCI\_CGAP\_RIG1, NCI\_CGAP\_LA12,
NCI\_CGAP\_BC16, NCI\_CGAP\_RIG1, NCI\_CGAP\_LA12,
NCI\_CGAP\_BC13, NCI\_CGAP\_LA11, NCI\_CGAP\_LA14,
NCI\_CGAP\_BC13, NCI\_CGAP\_LA11, NCI\_CGAP\_LA14,
NCI\_CGAP\_LA19, NCI\_CGAP\_LA16, NCI\_CGAP\_LA14,
NCI\_CGAP\_BC13, NCI\_CGAP\_GC4, NCI\_CGAP\_CA14,
NCI\_CGAP\_LA19, NCI\_CGAP\_GC4, NCI\_CGAP\_LA14,
NCI\_CGAP\_LA19, NCI\_CGAP\_GC4, NCI\_CGAP\_LA16,
NCI\_CGAP\_LA19, NCI\_CGAP\_GC4, NCI\_CGAP\_CA16,
NCI\_CGAP\_LA13 pool 1 LLAM 334-337, 3682-3683,
NCI\_CGAP\_KA13 pool 1 LLAM 334-337, 3682-3683,
NCI\_CGAP\_KA13 pool 1 LLAM 334-337, 3682-3683,
NCI\_CGAP\_KA13 pool 1 LLAM 334-337, 3682-3883,
NCI\_CGAP\_KA13 pool 1 LLAM 334-337, 3682-3883,
NCI\_CGAP\_KA13 pool 1 LLAM 3164-3167,
NCI\_CGAP\_KA13 pool 1 LLAM 3164-3167,
NCI\_CGAP\_KA13, NCI\_CGAP\_CA16743); NCI\_CGAP\_LA1991,
NCI\_CGAP\_CA1993, NCI\_CGAP\_GC4 pool 1 LLAM 3164-3167,
NCI\_CGAP\_CA1993, NCI\_CGAP\_GC4 pool 1 LLAM 3164-3167,
NCI\_CGAP\_CA1993, NCI\_CGAP\_GC4 pool 1 LLAM 3164-3167,
NCI\_CGAP\_CA1993, NCI\_CGAP\_GC4 pool 1 LLAM 2457-2459, 2758-2759, 3062-3068 (IMAGE CloneIDS 140908-1417991,
NCI\_CGAP\_CO10 pool 1 LLAM 2644-145351); NCI\_CGAP\_CO10 pool 1 LLAM 2457-2459, 2758-2759, 3062-3068 (IMAGE CloneIDS 16008-16008), NCI\_CGAP\_CO10 pool 1 LLAM 2457-2459, 2758-2759, 3062-3068 (IMAGE CloneIDS NCI\_CGAP\_CO10 pool 1 LLAM 2457-2459, 2758-2759, 3062-3068 (IMAGE CloneIDS NCI\_CGAP\_CO10 pool 1 LLAM 2457-2459, 2758-2759, 3062-3068 (IMAGE CloneIDS NCI\_CGAP\_CO10 pool 1 LLAM 2457-2459, 2758-2759, 3062-3068 (IMAGE CloneIDS NCI\_CGAP\_CO10 pool 1 LLAM 2457-2459, 2758-2759, 3062-3068 (IMAGE CloneIDS NCI\_CGAP\_CO10 pool 1 LLAM 2457-2459, 2758-2759, 3062-3068 (IMAGE CloneIDS NCI\_CGAP\_CO10 pool 1 LLAM 2457-2459, 2758-2759, 2758-2759, 2758-2759, 2758-2759, 2758-2759, 2758-2759, 2758-2759, 2758-2759, 2758-2759, 2758-2759, 2758-2759, 2758-2759, 2758-2759, 2758-2759, 2758-2759, 2758-2759, 2758-2759, 2758-2759, 2758-2759, 2758-2759, 2758-2759, 2758-2759, 2758-2759, 2758-2759, ö Soares (1996): Normalization and Subtraction: Two Approaches To Facilitate Gene Discovery. Genome Research 6, 791-806. AI192407 348 bp mRNA EST 28-OCT-1998 qc98c09.xl Soares\_pregnant\_uterus\_NbHPU Homo sapiens cDNA clone IMAGE:1722256 3' similar to gb:Y00083 TRANSFORMING GROWTH FACTOR BETA 2 PRECURSOR (HUMAN);, mRNA sequence. 151 ctccgcagtgcagacacacacacagcacggtgctgggactgtacaacactctgaacct 210 91 aagtgggtccatgaacctaagggctactatgccaacttctgctcaggcccttgcccatac 150 349 ATTIGGAGCCTGGACACGCAGTACAGCAAGCTCCTGGCCCTGTACACACGCATAACCCG 42.3%; Score 143.4; DB 114; Length 409; 73.5%; Pred. No. 2.4e-30; ö ee; Indels 0; Mismatches 84

pe

AUTHORS TITLE

JOURNAL

COMMENT

FEATURES

REFERENCE

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/note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: Sall; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigator providing samples: Gibert Smith, NIH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AW600940 261 bp mRNA EST 23-MAR-2000 RC1-BN0014-210100-012-d06 BN0014 Homo sapiens cDNA, mRNA sequence.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 261)

HCGP http://www.ludwig.org.br/ORESTES.

The FARESP/LICR Human Cancer Genome Project
Unpublished (1999)

Contact: Simpson A.J.G.
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NIH-MGC http://mgc.ncl.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                           DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can lfound through the I.M.A.G.E. Consortium/LLNL at:
http://imagollnl.gov
Plate: LLAMI0337 row: h column: 09
High quality sequence stop: 491.
Location/Qualifiers
                                                                             Email: cgapbs-r@mail.nih.gov
Lissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 175; Length 494;
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Pred. No. 7.6e-29;
0; Mismatches 18; Indels
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/clone_lib="NCI_CGAP_Man1"
/tissue_type="tumor, biopsy sample"
/dev_stage="3 months, virgin"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                         1. .494 // /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                               /strain="FVB/N"
/db_xref="taxon:10090"
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Best Local Similarity 89.2
Matches 149; Conservative
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 494)
                                                                   Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs.remail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 672 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 157.
            1 (bases 1 to 348)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gecaacttetgeteaggecettgeceataceteegeagtgeagacaeaacecaeageaeg 180
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0
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                                                                                                                                                                                                                                                                                                                                                                  /clone_lib="Soares_pregnant_uterus_NbHPU"
/sex="female"
                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1722256"
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/lab_host="DH10B"
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// Organism="Homo sapiens"
// Organism="Homo sapiens"
// Ob__xref="taxon:9606"
// Clone_lib="Bw0014"
// Adv_stage="Adult"
// Adv_
Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RCl&t2=RCl-BN0014-210100-012-d06&t3=2000-01-21&t4=1)
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Unpublished (1998)
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Ko.M.S.H. Kitchen,J.R., Wang,X., Wang,X., Threat,T.A., Sun,T., Depalma,G.E., Liang,Y., Kargul,G.J., Sharara,R., Paonessa,P.D. and
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Japan Science and Technology Corporation (JST)
WBG Marive East 12F, 2-6 Nakase, Mihama-ku, Chiba 261-71, Japan
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Pred. No. 7.7e-29;
0; Mismatches 75;
                                                                                     Seq primer: puc 18 forward
High quality sequence start: 15
High quality sequence stop: 261.
Location/Qualifiers
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Location/Qualifiers
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70.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Hirofumi Doi
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Eukaryotta; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

(hassol 1 to 456)
Hillier, L., Lennon, G., Becker, M., Bonaldo, M. F., Chiapelli, B., Chissoe, S., Dietrich, N., DuBuque, T., Te, M., Le, M., Mardis, E., Moore, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Meg, J., Trevaskis, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R. and Marra, M. Generation and analysis of 280,000 human expressed sequence tags
                                                                                                                                                                                                                                                                                                              ä;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N55274 456 bp mRNA EST 28-JAN-1997 4746405.s1 Soazes fetal liver spleen lNFLS Homo sapiens cDNA clone IMAGE:245769 3' similar to gb:J03241 TRANSFORMING GROWTH FACTOR BETA 3 PRECURSOR (HUMAN); mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Washington University School of Medicine
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Fel: 314 286 1810
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
INSERT Length: 1001 Std Error: 0.00
Seq primer: m13 -40 forward
High quality sequence stop: 424.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                   50 tgcgcccctctacattgacttccgacagg-atctgggctggaagtgggtccatgaacct 108
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                                       /strain="C57BL/GJ"
/db_xref="taxon:10090"
/clone="j0244G10"
/clone_lib="Mouse fertilized one-cell-embryo cDNA"
/dev_stage="fertilized one-cell-embryo"
a 128 c 140 g 166 t 6 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           169 acccacagcacggtgctgggactgtacaacatctgaaccctgaagcatctgcctcgcct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      283 CAACACCAAAAGTCCTCAGCCTGTACAACACCATAAATCCCGAA-CTTCCGCTTCCCCT
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                                                                                                                                                                                                                                                             DB 156; Length 587;
                                                                                                                                                                                                                                                                                                              3;
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Pred. No. 1.5e-28;
0; Mismatches 74; Indels
                        musculus"
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1. .587
∕organism≕"Mus
                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 73.5%;
Matches 214; Conservative
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N55274/c
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Gaps

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Indels

BASE COUNT

ORIGIN

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Paralichthys olivaceus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii, Neopterygii, Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;
Pleuronectoidei; Bothidae; Paralichthys.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: aoki@tokyo-u-fish.ac.jp
clone WB11-23:similar to rainbow trout transforming growth factor
                                                                                                                                                                                                                    cccaggacctggagcccctgaccatcctgtactatgttgggaggaccccaaagtggagc 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gtccatgaacctaagggctactatgccaacttctgctcaggcccttgcccatacctccgc 156
                                                                                                                          119 atgccaacttctgctcaggcccttgcccatacctccgcagtgcagacacaacccacagca 178
                                                                                                                                                                                                  179 cggtgctgggactgtacaacactctgaaccctgaagcatctgcctcgccttgctgcgtgc 238
                                                                                                                                                                                                                                                                                                      451 CCCAGGATCTGGAACCACTGACCATCCTCTACTACATTGGCAATACGCCCAAGATCGAAC 392
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                AU050770 878 bp mRNA EST 08-JUN-1999 AU050770 Paralichthys olivaceus library (Aoki T) Paralichthys olivaceus cDNA clone WB11-23, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="Paralichthys olivaceus library (Aoki T)"
213 c 186 g 220 t
                                                                                                                                                             571 AIGCIAACTICIGIGGIGCAIGCCCTIAICIGIGGAGIICAGACACACACACACCA
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                                                      DB 17; Length
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69.6%; Pred. No. 6.1e-28;
.ive 0; Mismatches 89; Indels
                                                                                                                                                                                                                                                                                                                                         1. .878
//Organism="Paralichthys olivaceus"
//db_xref="taxon:8255"
/clone="WB11-23"
                                                                                           53;
                                                   Score 136.2; DB 1
Pred. No. 2.9e-28;
0; Mismatches 53,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Japanese flounder leukocyte cDNA (hopblished (1999)
Contact: Takashi Aoki
Genetics and Biochemistry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tokyo University of Fisheries
Konan, 4-5-7, Minato 108, Japan
Tel: 03-5463-0556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AU050770.1 GI:5019223
                                                      40.2%;
76.0%;
                                                      Query Match 40.2
Best Local Similarity 76.0
Matches 168; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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Matches 23
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ORIGIN
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JOURNAL
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                                                                                AI179582 571 bp mRNA EST 20-JAN-1999
EST223304 Normalized rat spleen, Bento Soares Rattus sp. cDNA clone
                                                                                                                                                                                                                                                                                                                                                                                            5
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (REST) Catalog & Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone="RSP0J23"
/clone_lib="Normalized rat spleen, Bento Soares"
/note="Organ: spleen; Vector: pT/T3Pac; Site_1: EcoRI;
Site_2: NotI"
111 c 121 g 195 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                75 acaggatctgggctggaagtgggt-ccatgaacctaagggc-tactatgccaacttctgc 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                             15 ttactgcttccgcaacttggaggagaactgctgtgtgcgccccctctacattgacttccg 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 (bases 1 to 571)
Lea.N.H., Glodek,A.A. Chandra,I., Mason,T.M., Quackenbush,J.
Kerlavage,A.R. and Adams,M.D.
Rat Genome Project: Generation of a Rat EST (REST) Catalog
                                                                                                                                                                                                                                                                                                                                                                                              5;
                                                                                                                                                                                                                                                                                                                                                        Score 136.4; DB 159; Length 456;
Pred. No. 2.4e-28;
0; Mismatches 6; Indels 2;
              /db_xref="taxon:9606"
/clone="INAGE:245769"
/clone_lib="Soares fetal liver spleen INFLS"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Lee, NH
The Institute for Genomic Research
9712, Medical Center Drive, Rockville, MD 20850, USA
Tel: (301)-838-3529
Fax: (301)-838-0208
Email: nhlee@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Rattus sp."
/db_xref="ATCC (inhost):2033997"
/db_xref="taxon:10118"
/db_xref="GDB:3795015"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RSPCJ23 3' end, mRNA sequence.
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AI179582.1 GI:3730220
                                                                                                                                                                                                                                                                                                                                                      40.2%;
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Unpublished (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Seq primer: M13-21
                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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Matches 162; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rattus sp.
Rattus sp.
                                                                                                                                                                                                                                                                                      138
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AI179582/C

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Tumor Gene Index
Unpublished (1997)
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149 GTGCAGCTGA 140
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                                                                                                                                                                                                                                                                                                                                                                                RESULT 77
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with a modified polylinker: plasmid DNA from the
normalized library NCI_CGAP_PT22 was prepared, and ss
circles were made in vitro. Following HAP purification,
this DNA was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from a pool
of 5,000 clones made from the same library (cloneIDS
985608-986759, 1101192-1101959, and 1217228-1220615).
Subtraction by Bento Soares and M. Fatima Bonaldo. "
11 c 150 g 67 t 1 others
                                                                                                                                                                                                                                                                                                                         A191883 392 bp mRNA EST 28-JUL-1999 tul3blo.X1 NCI_CGAP_PT28 Home spiens cDNA clone IMAGE:2250907 3' similar to 9b:X02812_cd31 TRANSFORMING GROWTH FACTOR BETA 1 PRECURSOR (HUMAN);contains element TAR1 MER22 repetitive element ;,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequencing Center
information can be
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 392)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Robert Strausberg, Ph.D.
Bmall: Gapabs-refenall.nih.gov
Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael
Emmert-Buck, M.D., Ph.D.
                                                                                                                         Gaps
                                                     tctgcctcgccttgctgcgtgccccaggacctggagccctgaccatcctgtactattt
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Pred. No. 7.7e-28;
0; Mismatches 65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="taxon:9606"
/clone="IMAGE:2250907"
/clone_lib="NCI_CGAP_Pr28"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1. .392
/organism="Homo sapiens"
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/lab_host="DH10B"
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AI918883.1 GI:5638738
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73.6%;
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Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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Matches 184
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AI918883/c
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AA533093 54.2 bp mRNA EST 21-AUG-1997 njj9904.s1 NCI_CGAP_AA1 Homo sapiens cDNA clone IMAGE:992982 3' similar to gb:XO2812_cGal TRANSFORMING GROWTH FACTOR BETA 1 PRECURSOR (HUMAN); contains element MER22 repetitive element ; mRNA
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information can be
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Organ: adrenal gland; Vector: Bluescript SK-; Site_1: ECORI; Site_2: XhOI; Cloned unidirectionally. Primer: Oligo dr. Two pooled bulk adrenal adenomas. 5' adaptor sequence: 5' GAATTCGCACGAG 3' 3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3' Average insert
                                                                                                                                                                                                                               90 gaagtgggtccatgaacctaagggctactatgccaacttctgctcaggcccttgccata 149
                                                           388 GAAGTGGATCCACGAGCC-AAGGGCTACCATGCCNACTTCTGCCTCGGGCCCTGCCCCTA 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: cgapbs-r@mail.nih.gov
Tissue Procurement: L. Jeffrey Medeiros, M.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: Stratagene, Inc., David B. Krizman,
                                                                                                              8; Length 542;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA Sequencing by: Washington University Genome Clone distribution: NCI-CGAP clone distribution found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html insert Length: 1687 Std Error: 0.00 Seq primer: -40ml3 fwd. ET from Amersham
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/clone_lib="NCI_GGAP_AA1"
/tissue_type="adrenal adenoma"
/lab_host="SoLR (kanamycin resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ph.D. cDNA Library Arraying: Greg Lennon, Ph.D.
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Location/Qualifiers
1. 542.
/organism="Homo sapiens"
/db_xrref="taxon:9606"
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house mouse.
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/db_xref="taxon:9606"
/clone_llb="BN0014"
/dev_stage="Adult"
/dev_stage="Adult"
/note="Organ: breast_normal; Vector: puc18; Site_l: SmaI;
Site_2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions.

13 t 43 c 62 g 73 t
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This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RCl&t2=RCl-BN0014-210100-012-e04_1&t3=2000-01-21&t4-1)
Seq primer: puc 18 forward
High quality sequence stop: 233.
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Catarrhini; Hominidae; Homo.
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Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                            185 tgggactgtacaacactctgaaccctgaagcatctgctcgccttgctgctgctgcccagg 244
                                                                                                                                                                                                                                                                                                                                                             65 ttgacttccgacaggatctgggctggaagtgggtccatgaacctaagggctactatgcca 124
                                                                                                                                                                                                                                                                                                                                          245 acctggagcccctgaccatcctgtactatgttgggaggaccccaaagtggagcagctct 304
                                                                                                                                                                                                125 acttctgctcaggcccttgcccatacctccgcagtgcagacacaaccacaggcacggtgc 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-MAR-2000
                        Gaps
                                                       tggacaccaattactgcttccgcaacttggaggagaactgctgtgtgcgccccctctaca 64
                                                                                                                                                                                                                                                                                                     292 TGGCCCTGTACAACCAGCATAAACGCCGCGCGCTGCGGCGCGCGTGCTGCGT-CCGCAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AW600947 245 bp mRNA EST 23-MAK-20
RC1-BN0014-210100-012-e04_1 BN0014 Homo sapiens CDNA, mRNA
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                    Indels
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Mammalla; Eutheria; Primates; Catarrhini; Ho
1 (bases 1 to 245)
HCGP http://www.ludwig.org.br/ORESTES.
The FAPESP/LICR Human Cancer Genome Project
Unpublished (1999)
 Pred. No. 1.1e-27;
); Mismatches 88;
                                                                                                                                                                                                                                                                                                                                                                                                                305 ccaacatggtggtgaagtcttgtaaatgtagctga 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                174 CCAACATGATCGTGCGCTCCTGCAAGTGCAGCTGA 140
ilarity 72.2%; Pr
Conservative 0;
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AW600947.1 GI:7305686
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Fax: +55-11-2707001
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 Local Similarity
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mh39e08.rl Soares mouse placenta 4NbMP13.5 14.5 Mus musculus cDNA clone IMAGE144902 5' similar to 95:X02812_cdSt_TRANSFORMING GROWTH FACTOR BETA 1 PRECURSOR (HUANN); 9b:M32745 mouse transforming growth factor beta-3 mRNA, complete (MOUSE); mRNA sequence.
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                                                         ö
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (Dases 1 to 53)

Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. MGI:270238
                                                                                                                                             184 TCAGACACTCAGCAGCAGCAGCGTCCTGAGATAATAATACCTTAAATCCAGAAGCATCT 125
                                                                                                                100 catgaacctaagggctactatgccaacttctgctcaggcccttgcccatacctccgcagt 159
                                                                                                                                                                                                                              160 gcagacacaacccacagcacggtgctgggactgtacaacactctgaaccctgaagcatct 219
                                                                                                                                                                                                                                                                                                                                         220 geetegeettgetgegtgeeceaggacetggageeetgaeeateetgtaetatgttggg 279
                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                         280 aggacccccaaagtggagcagctctccaacatggtggtgaagtcttgtaaatgtagct 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone="IMAGE:444902"
/clone_lib="Soares mouse placenta 4NbMP13.5 14.5"
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Contact: Marra M/Mouse EST Project
WashU-HMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
  Length 245;
                                                         Indels
  Score 134; DB 118;
Pred. No. 1e-27;
); Mismatches 65;
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                                                      0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: mouseest@watson.wustl.edu
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/dev_stage="adult"
/lab_host="DH10B"
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Location/Qualifiers
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/db_xref="taxon:10090"
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AA016742.1 GI:1479043
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39.5%;
72.7%;
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                                                         Matches 173; Conservative
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Fax: 314 286 1810
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AU016439/c
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T 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization, and was constructed by Bento Soares and M.Fatima Bonaldo."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Systematic analyses of genes expressed in fertilized mouse eggs(The ERATO/Doi Project at Wayne State University) Unpublished (1998)
Contact: Hirofumi Doi
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WHG Marive East 12F, 2-6 Nakase, Mihama-ku, Chiba 261-71, Japan Email: hdebioa.jst.go.jp.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                     122 GCCCTGGATACCAACTATGCTTCAGCTCCACAGAGAAGAACTGCTGTGTGCGGCACGTG 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tacattgacttccgacaggatctgggctggaagtgggtccatgaacctaagggctactat 120
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/strain="C57BL/6J"
/db_xref="texon:10090"
/clone="J033c11"
/clone=lib="Mouse fertilized one-cell-embryo cDNA"
/dev_stage="fertilized one-cell-embryo"
123 c 141 g 171 t 9 others
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Pred. No. 2.4e-27;
0; Mismatches 107;
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Pred. No. 1.8e-27
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C86748 Mouse fertilized
Clone J0232C11 3', mRNA
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72.4%;
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ilarity 67.4%;
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C86748.1 GI:2918705
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Mus musculus

Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 465)

Ko, Ma.S.H. Kitchen, J.R., Wang, X., Threat, T.A., Sun, T., DePalma, G.E., Liang, Y., Kargul, G.J., Sharara, R. and Doi, H.

Systematic analyses of genes expressed in 2-cell stage mouse embryos (The ERATO/Doi Project at Wayne State University) (Ko

M.S.H. et al.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AU016439 465 bp mRNA EST 15-OCT-1998
AU016439 Mouse two-cell stage embryo cDNA Mus musculus cDNA clone
307025908 3', mRNA sequence.
AU016439 GI:3371443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Hirofumi Doi
Contact: Hirofumi Doi
Doi Bioasymmetry Project, ERATO
Japan Science and Technology Corporation (JST)
WBG Marive East 127, 2-6 Nakase, Mihama-ku, Chiba 261-71, Japan
Email: hdebioa.jst.go.jp.
Location/Qualifiers
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acattgacttccgacaggatctgggctggaagtgg--gtccatgaacctaagggctacta
                                                                                            tgccaacttctgctcaggccttg-cccatacctccgcagtgcagacacaaacccacaga
                                                                                                                    cagacacaac-ccacagcacggtgctgggactgtacaacactctgaacctgaagcatct
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                                                                                                                                                                                                                                         274 AAGTCCTCAGCCTGTACAACACCATAAATCCCGAAGCTTCCGCTTCCCCTTGCTGTGT
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/clone="J0725B08"
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Matches 212; Conservative
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181 gtgctgggactgtacaacactctgaaccctgaagcatctgcctcgccttgctgcggcgc Seq primer: mob.REGA+ET /sex="unknown 37.6%; 72.1%; W70801.1 GI:1380934 Query Match 37.6 Best Local Similarity 72.1 Matches 220; Conservative Unpublished (1996) house mouse. Mus musculus Waterston, R. MGI:242174 65 241 cagg 244 427 GAAG 430 W70801 source KEYWORDS SOURCE ORGANISM LOCUS 83 BASE COUNT TITLE JOURNAL REFERENCE AUTHORS ACCESSION FEATURES VERSION RESULT W70801 COMMENT g 엄 à ò /clone\_lib="NIH\_MGC\_39"
/clone\_lib="NIH\_MGC\_39"
/tissue\_type="adenocarcinoma"
/lab\_host="DylbB (phage-resistant)"
/note="Organ: pancreas; Vector: pOTB7; Site\_1: XhoI;
Site\_2: EcoR1; cDNA made by Oligo-dT priming.
Directionally cloned into EcoR1/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Library constructed
by Ling Hong in the laboratory of Gerald M. Rubin
(University of California, Berkeley) using ZAP-CDNA
synthesis kit (Stratagene) and Superscript II RT (Life ; Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 915)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) BE737006 915 bp mRNA EST 15-SEP-2000 601306767F1 NIH\_MGC\_39 Homo sapiens cDNA clone IMAGE:3641081 5' þe tacattgacttccgacaggatctgggctggaagtgggtccatgaacctaagggctactat 120 1 gctttggacaccaattactgcttccgcaacttggaggagaactgctgtgtgcgcccctc 60 DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can ifound through the I.M.A.G.E. Consortium/LLNL at:
Plate: LLCM346 row: e column: 18 CDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DB 139; Length 915; 2; Query Match 38.1%; Score 129.2; DB 139; Lengt Best Local Similarity 73.4%; Pred. No. 3.1e-26; Matches 179; Conservative 0; Mismatches 63; Indels 131 /organism="Homo sapiens" /db\_xref="taxon:9606" Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue Procurement: ATCC High quality sequence stop: 424. Location/Qualifiers 276 g BE737006.1 GI:10150998 Technologies) 279 c Unpublished (1999) mRNA sequence. BE737006 229 human. source LOCUS 220 ORGANISM BASE COUNT 61 REFERENCE AUTHORS TITLE JOURNAL ACCESSION RESULT 8 BE737006 KEYWORDS FEATURES VERSION COMMENT

ORIGIN

ò g ŏ g ŏ

W70801 301 bp mRNA EST 17-JUN-1996 me44c04.rl Scares mouse embryo NbME13.5 14.5 Mus musculus CDNA clone IMAGE:390342 5 similar to 99:X02812\_cds1 TRANSFORMING GROWTH FACTOR BETA 1 PRECURSOR (HUMAN); 9b:M32745 mouse transforming growth factor beta-3 mRNA, complete (MOUSE);, mRNA sequence. T 3'], on equal amounts of mRNA from 2 13.5dpc and 2
14.5dpc embryos [total RNA provided by Minoru Ko, Wayne
State Uniu., from 2 ]; double-stranded cDNA was ligated to
Eco RI adaptors (Pharmacia), digested with Not I and
cloned into the Not I and Eco RI sites of the modified
pT7T3 vector. Library went through one round of
normalization, and was constructed by Bento Soares and 1 (bases 1 to 301)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Gelsel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schallenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson;R. and 4; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Gaps DB 190; Length 301; 4 ; Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu /clone\_lib="Soares mouse embryo NbME13.5 14.5" Score 127.4; DB 190; Lengt Pred. No. 8.1e-26; 0; Mismatches 81; Indels 64 t /organism="Mus musculus" The WashU-HHMI Mouse EST Project High quality sequence stop: 289. Location/Qualifiers /strain="C57BL/6J" /db\_xref="taxon:10090" /clone="IMAGE:390342" M.Fatima Bonaldo. 0

48

Page

g ò g δ g ò 염 ð g ò

195 human. Query Match Best Local AI452742/c LOCUS DEFINITION source BASE COUNT ORIGIN Matches 82 ORGANISM ACCESSION VERSION KEYWORDS REFERENCE AUTHORS JOURNAL FEATURES TITLE COMMENT RESULT SOURCE ŏ q ò g δ g ò ద Bukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mamaalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bass 1 to 560)
Hiller,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rikin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,T.R., Williamson,A., Woldman,P. and Wilson,R. yx90e06.rl Soares melanocyte 2NbHM Homo sapiens cDNa clone IMAGE:269026 5' similar to gb:Y00083 TRANSFORMING GROWTH FACTOR BETA 2 PRECURSOR (HUMAN);contains element OFR repetitive element; High quality sequence stops: 470 Source: IMAGE Consortium, LLNL. This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: 17 Location/Quality sequence stop: 470. 214 178 274 59 aggagaactgctgtgtgcgcccctctacattgacttccgacaggatctgggctggaagt catctgcctcgccttgctgcgtgcccaggacctggagccctgaccatcctgtactatg CTTC-GGGTCACCGTGCTGCGCGCACG-TTTGGAGCCACTGCCCATCGTCTACTACG gcagtgcagacacaacccacagcacggtgctgggactgtacaaccactctgaacctgaag Unpublished (1995)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 /clone\_lib="Soares melanocyte 2NbHM" /sex="Male" 1. .560 /organism="Homo sapiens" /db\_xref="GDB:3878668" /db\_xref="taxon:9606" /clone="IMAGE:269026" Email: est@watson.wustl.edu N36741 N36741.1 GI:1157883 Tel: 314 286 1800 Fax: 314 286 1810 Homo sapiens 335 gctga 339 GCTGA 301 human. source 84 LOCUS ORGANISM TITLE JOURNAL 215 179 35 95 9 155 297 ACCESSION VERSION KEYWORDS REFERENCE AUTHORS

SOURCE

FEATURES

COMMENT

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Anote—"Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from five normalized libraries were mixed, and Ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 5 libraries. The pools consisted of the following libraries and clonelDs: Soares NBHSF pool 1: 309384-310919, 323208-325895 Soares Nb2HP pool 1:
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     so RI
into
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A1452742 396 bp mRNA EST 13-APR-1999 tj45a05.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2144432 3' similar to gb:x02812_cds1 TRANSFORMING GROWTH FACTOR BETA 1 PRECURSOR (HUMAN);contains PTR5.t3 MSR1 repetitive
double-stranded cDNA was size selected, ligated to Eco adapters (Pharmacia), digested with Not I and cloned in the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library constructed by Bento Soares and M.Fatina Bonaldo. RNA from normal foreskin melanocytes (FS374) was kindly provided by Dr. Anthony P. Albino."
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Unpublished (1997)
Contact: Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (infoelmage.llnl.gov) for further information. Seq primer: -40UP from Gibco.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           113 gctactatgccaacttctgctcaggcccttgcccatacctccgcagtgcagacacaaccc 172
                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                         DB 159; Length 560;
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es 64; Indels
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/clone="IMAGE:2144432"
/clone_lib="Soares_NSF_F8_9W_OT_PA_P_S1"
                                                                                                                                                                                                                                                                                   Score 125.2; I
Pred. No. 3.8e-
0; Mismatches
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A1452742
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al Similarity 71.8%;
163; Conservative
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                                                                NbHOT
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 748)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: cgapbs-remail.nh.gov
   Tissue Procurement: M. Bento Soares, Ph.D.
   Tissue Procurement: M. Bento Soares, Ph.D.
   Tissue Procurement: M. Bento Soares and M. Fatima Bonaldo CDNA Library Preparation: Bento Soares and M. Fatima Bonaldo CDNA Library Arrayed by: The J.M.A.G.E. Consortium (LLNL)
   DNA Sequencing by: Incyte Genomics, Inc.
   Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
   http://image.lln.gov
   Plate: LLAM8476 row: h column: 18
   High quality sequence start: 26
   High quality sequence start: 26
   High quality sequence stop: 746.
   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    602117568F1 Soares_mammary_gland_NMLMG Mus musculus cDNA clone IBAGE3737 5', mRNA sequence.
145032-147335, 147720-148103, 148872-149255, 15002 - 150407, 151176-15237 Soares Nb2HF8-9W pool 1: 758280-760583, 772104-774407 Soares NbHRA pool 1: 78230-760581, 320136-322803, 326280-326663 Soares NbPOOL 1: 723720-726407, 739080-740999 Subtraction by Soares and M. Fatima Bonaldo."
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National Institutes of Health, Mammalian Gene Collection (MGC)
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/clone_lib="Soares_mammary_gland_NMLMG"
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/tissue_type="mammary gland"
/lab_host="DH10B"
                                                                                                                                                                                                    Score 124.6; DB 2
Pred. No. 5.3e-25;
0; Mismatches 65
                                                                                                                          88 t
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Best Local Similarity 71.5%;
Matches 163; Conservative
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AA016946 533 bp mRNA EST 21-JAN-1997 mh35a12.r1 Soares mouse placenta 4NbMPl3.5 14.5 Mus musculus cDNA clone IMAGE:444478 B's similar to 9b:X02812_cds1 FRANSFORMING GROWTH FACTOR BETA 1 PRECURSOR (HUMAN); 9b:M32745 mouse transforming growth factor beta-3 mRNA, complete (MOUSE); mRNA sequence. AA016946.1 GI:1478533
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 533)
Marrah., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Gelsel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo." 1 220 c 189 g 150 t
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This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                               tacattgacttccgacaggatctgggctggaagtgggtccatgaacctaagggctactat 120
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Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                               36.5%; Score 123.6; DB 168; Lengt 72.7%; Pred. No. 1.2e-24; ive 0; Mismatches 64; Indels
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/clone_lib="Soares mouse pl
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/organism="Mus musculus"
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/lab_host="DH10B"
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The WashU-HHMI Mouse EST Project
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1 (bases 1 to 379)

Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,M.Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Mateaukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                             T 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT/T3 vector. Library went through one round of normalization, and was constructed by Bento Soares and M.Fatima Bonaldo."
/note="Organ: placenta; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; ist strand cDNA was primed with a Not I - oligo(dT) primer
                                                                                                                                                                                                                                                                                                          5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=RC3-UM0046-290 200-011-a06&t3=2000-02-296t4=1)
                                                                         AW798167 379 bp mRNA EST 16-MAY-2000
RC3-UM0046-290200-011-a06 UM0046 Homo sapiens CDNA, mRNA sequence.
AW798167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Shotgun sequencing of the human transcriptome with ORF expressed
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                                                                                                                                                                                                                                                                                                                                                                                                                                            gccaacttctgctcaggcccttgcccatacctccgcagtgcagacacaacccacagcacg
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                                                                                                                                                                                                                                                                      Length 533;
                                                                                                                                                                                                                                                                                                        80; Indels
                                                                                                                                                                                                                                                                  Score 123; DB 1;
Pred. No. 1.6e-24;
0; Mismatches 80,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                241 caggacctggagccctgaccatcctgtactatgttg 277
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70.0%;
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/dev_stage="Adult"
//dev_stage="Adult"
//dev_stage="Adult"
//note="Organ: uterus; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196 /716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low
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FACTOR BETA 1 PRECURSOR (HUMAN); contains TAR1 repetitive element;;
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1 (bases I to 399)

1 (hases I to 399)

M., Hullman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Polman, M., Rulliamson, A., Wohldman, P. and Wilson, R. Trevaskis, E., Waterston, T. R., Williamson, A., Wohldmann, P. and Wilson, R.

The Washlo-Merck EST Project
Unpublished (1995)

Contact: Wilson RK
Washington University School of Medicine

4444 Porest Park Parky Barkway, Box 8501, St. Louis, MO 63108
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High quality sequence stops: 281
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  283 GCCAACTTCTGCCTCGGGCCCTGCCCTACATTTGGAGCCTGGACAGGAGTACAGCAAG 342
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 122.8; DB 12u; Pred. No. 1.7e-24;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="UM0046"
                                                                                                                                                                                                                                                                                                                                                                                                    stringency conditions."
128 c 98 q 6
                           start: 17
stop: 379.
Seq primer: puc 18 forward
High quality sequence start:
High quality sequence stop: 3
                                                                                 Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 36.2%;
Best Local Similarity 76.3%;
Matches 151; Conservative
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R36467.1 GI:793368
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Fax: 314 286 1810
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tqfb3n.rst

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Fax: +55-11-2707001
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bass 1 to 259)
HCGP http://www.ludwig.org.br/ORESTES.
The FAPESP/LICR Human Cancer Genome Project
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Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  attgacttccgacaggatctgggctggaagtgggtccatgaacctaagggctactatgcc 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             398 ATTGACTTCCGNAAGNACCTGGGCTGGAAGTGGATCCACGGACCCAAGGGCTACNATGCC 339
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                                                                                                                                                                                                                                                                                                                                                                                                                     DB 187; Length 398;
                                                                                                                                                                                                                                                                                                                                                         14 others
                                                                                                                                                                                                                                                                                                                                                                                                                   Score 122.4; DB 187; Lengt
Pred. No. 2.2e-24;
0; Mismatches 93; Indels
                                                                                                         /db_xref="taxon:9606"
/clone="IMAGE:136821"
/clone_lib="Soares placenta Nb2HP"
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                                                              1. .398
/organism="Homo sapiens"
/db_xref="GDB:543039"
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                                                                                                                                                            /sex="Female"
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AW600942.1 GI:7305681
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Best Local Similaritý 65.9%;
Matches 182; Conservative
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TITLE
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SOURCE
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Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Email: capbbs-remail.nih.gov
Email: capbbs-remail.nih.gov
Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
cDNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
Email: asimpsonelludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This sequence in the following URL
(http://www.ludwig.org.br/scripts/gethtm12.pl?tl=RC1&t2=RC1-BN0014-
210100-012-d10_1&t3=2000-01-21&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 258.
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tx932b5.x1 NCI_CGAP_Ut4 Homo sapiens cDNA clone IMAGE:2277105 3/
similar to 9b:X02812_cGa1 TRANSFORMING GROWTH FACTOR BETA 1
PRECURSOR (HUMAN); contains PTR5.t3 PTR5 repetitive element ;, mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      222 CCAACTICTGTGCTGGAGCATGCCCGTATTTATGGAGTTCAGACACTCAGCACAGCAGGG 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  122 ccaacttctgctcaggcccttgcccatacctccgcagtgcagacacaacccacagcacgg 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      182 tgctgggactgtacaacactctgaaccctgaagcatctgcctcgccttgctgcgtgcccc 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     242 aggacctggagccctgaccatcctgtactatgttgggaggaccccaaagtggagcagc 301
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tgfb3n.rst

52

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house mouse.
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                                                                                                                                                                                                                                                                                                                   212
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                                                                                                                                                                                                                                                                                         /note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: Sall; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.48 kb. Life Technologies catalog #:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 867)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BF161473 867 bp mRNA EST 30-OCT-2000 601770461F1 NCI_CGAP_Lu29 Mus musculus cDNA clone IMAGE:3989846
                                                                                                                                                            /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2277105"
/clone_lib="NGI_CGAP_Ut4"
/tissue_type="serous papillary carcinoma, high grade, pooled tumors"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  130 tgetcaggecettgeceatacetecgeagtgeagacacaacceacageaeggtgetggga 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        70 ttccgacaggatctgggctggaagtgggtccatgaacctaagggctactatgccaacttc 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NIH MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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found through the I.M.A.G.E. Consortium/LLNL at:
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0; Mismatches 74;
                  www-bio.llnl.gov/bbrp/image/image.html
                                                   Trace considered overall poor quality Insert Length: 823 Std Error: 0.00 Seq primer: -40UP from Gibco High quality sequence stop: 1. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                      68 t
                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 117.6;
                                                                                                                                                                                                                                                                                                                                                                   88 g
                                                                                                                                                                                                                                                                            /lab_host="DH10B"
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BF161473.1 GI:11041635
                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 34.7%;
Best Local Similarity 69.8%;
Matches 173; Conservative
                                                                                                                                                                                                                                                                                                                                                                     81 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mRNA sequence.
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
image.llnl.gov/image/html/iresources.shtml
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 63)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap,
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                      /strain="CZECH II"
/db_xref="taxon:10090"
/clone="IMAGE:3989846"
/clone=lib="NOILGGAP_Lu29"
/tissue_type="spontaneous tumor, metastatic to mammary.
Stem cell origin."
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Organ: lung; Vector: pCMV-SPORT6; Site_1: SalI; Site_2: NotI; Cloned unidirectionally. Primer: Oligo d Library constructed by Life Technologies. Investigator providing samples: Gilbert Smith, NIH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BF723491 639 bp mRNA EST 03-JAN-2001 mmb325266.yl Soares_NMEBA_Dranchial_arch Mus musculus cDNA clone IMAGE:3972226 5' similar to SW.TGF1_MOUSE P04202 TRANSFORMING GROWTH FACTOR BETA 1 PRECURSOR ; mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        234 cgtgccccaggacctggagccctgaccatcctgtactatgttgggaggaccccaa-ag 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62 CGTCCCCCAGGACCTGGAGCCCCTGACCATCTTGTACTATGTGGGGCAGAACCCCCAAGGG 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          175 agcacggtgctgggactgtacaacactctgaaccc-tgaagcatctgcctcgccttgctg 233
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 AGCACGGTGCTTGGACTATACAACACCCTGAACCCAGGAGGCGTCTGCCTCGCCCATGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 145; Length 867;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         34.2%; Score 115.8; DB
88.6%; Pred. No. 2e-22;
Live 0; Mismatches
                                                                                                                                                                        /organism="Mus musculus"
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/db_xref="taxon:10090"
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http://image.llnl.gov
Plate: LLAM9200 row: i column:
High quality sequence stop: 742.
Location/Qualifiers
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High quality sequence stop: 477.
Location/Qualifiers
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Unpublished (1997)
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/note="Organ: head_neck; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:9606"
/clone_lib="HT0377"
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BE157967/c
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                              0; Gaps
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Clone distribution: MGC clone distribution information can
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Robert Strausberg, Ph.D.
Email: ggapbs r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
GDNA Library Preparation: Life Technologies, Inc.
GDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                                                                                                                                                                                                                                           DB 168; Length 639;
                                                                                                                                                                                                                                          5 others
                                                                                                                                                                                                                                                                                                                                            62; Indels
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http://image.llnl.gov
Plate: LLAM8764 row: h column: 17
High quality sequence stop: 575.
Location/Qualifiers
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Pred. No. 5.3e-22;
0; Mismatches 62
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/clone_lib="NCI_CGAP_Mam1"
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/db_xref="taxon:10090".
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BE377489
BE377489.1 GI:9322854
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70.6%;
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Best Local Similarity
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BE377489
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Tel: +55-11-2704922
Fax: +55-11-2707001
Fax: +55-11-2707001
Fax: +55-11-2707001
Fax: +55-11-2707001
Fax: +55-11-2707001
Fax: Human Cancer Genome
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=MR2-HT0377-150
Seq primer: puc 18 forward
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                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                          /note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: Sall; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigator providing samples: Glibert Smith, NIH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BE157967 175 bp mRNA EST 21-JUN-2000
MR2-HT0377-150200-202-d09 HT0377 Homo sapiens cDNA, mRNA sequence.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 175)
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  \operatorname{Simpson}, \operatorname{A.J.} Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          204 gaaccetgaagcatetgcetegeettgetgegtgeeceaggacetggageeettgeseat 263
                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 GAACCCAGAGGCGTCTCGCCATGCTGCGTCCCCCAGGACCTGGAGCCCCTGACCAT
                                                                                                                                                                                                                                                                                                                                                                       DB 166; Length 684;
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20202663
                                                                                                                                                                                                                                                                                                                                                                    Score 113.6; DB 166; Lengt
Pred. No. 7.9e-22;
0; Mismatches 14; Indels
/tissue_type="tumor, biopsy sample"
/dev_stage="3 months, virgin"
/lab_host="DH10B"
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High quality sequence stop: 175.
Location/Qualifiers
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Best Local Similarity 89.7%;
Matches 122; Conservative
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clonellb="W10190"
/dev_stage="Addult"
/note="Organ: marrow; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196; 716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low
derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 255)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Magai, M.A., da Silva, M. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare Simpson, A.J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=CM2&t2=CM2-MT0190-091200-595-al0&t3=2000-12-09&t4=1)
Seq primer: puc l8 forward
High quality sequence start: 7
High quality sequence stop: 234.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BF901708 255 bp mRNA EST 18-JAN-2001
CM2-MT0190-091200-595-a10 MT0190 Homo sapiens cDNA, mRNA sequence.
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Shotgun sequencing of the human transcriptome with ORF expressed
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                                                                                                                                                                                                                                                                                                                                       136 GCTTTGGACACCAATTACTGCTTCCGCAACTTGGAGGAGAACTGCTGTGTGCGCCCCCTC 77
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                                                                                                                                                                                                                                                                                                                                                                                   sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
                                                                                                                                                                                                               Length 175;
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                                                                                                                                                                                                           Score 112; DB 164;
Pred. No. 1.7e-21;
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0
                                                                                        low stringency conditions."
53 c 45 g 41 t
                                                                                                                                                                                                    33.0%; Score 112; DB 100.0%; Pred. No. 1.7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
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                                                                                                                                                                                                                             Best Local Similarity
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BF901708/c
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AUTHORS
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1552604"
/clone="IMAGE:1552604"
/clone="IMAGE:1552604"
/clone="IMAGE:1552604"
/clone="type="pooled germ cell tumors"
/lab.host="blu08"
/note="Vector: pT773D-Pac (Pharmacia) with a modified polylinker; lst strand cDNA was prepared from 3 pooled germ cell tumors, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo. "I was constructed by a 118 c 154 g 82 t
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CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.lnl.gov/bbrp/image.image.html
Insert Length: 501 Std Error: 0.00
Seq primer: -40ml3 fwd. Erf from Amersham
High quality sequence stop: 141.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 428)
NCI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AA927529 428 bp mRNA EST 17-JUN-1998 om71all.s1 NCI_CGAP_GC4 Homo sapiens CDNA clone IMAGE:1552604 3'
AA927529 AA927529
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                                                                                                                                                      239 GCATTGGACACCAACTATTGCTTCAGTTCCACGGAGAAGAACTGCTGCGGGCGCCAGCTG 180
                                                                                                                                                                                                           61 tacattgacttccgacaggatctgggctggaagtgggtccatgaacctaagggctactat 120
                                                                                                                                                                                                                                        121 gccaacttctg-ctcaggccttgccatacttcgcagtgcagacacaaccagcac 179
                                                                                                                                                                                                                                                                                                                                                                                                                 180 ggtgctgggactgtacaacactctgaaccctgaagcatctgcctcgccttgctgcgtgcc 239
                                                            Gaps
                                                                                                         1 gctttggacaccaattactgcttccgcaacttggaggagaactgctgtgtgcgcccctc 60
                                                                                                                                                                                                                                                                                                                                                               119 GCCAACTICTGCCTCGGGCCCTGCCCATACATTTGGAGCCTGTACACGCAGTACAG-AA 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;;
       Length 255;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D.,
Emmert-Buck, M.D., Ph.D.
                                                          Indels
     Score 112; DB 171;
Pred. No. 1.8e-21;
0; Mismatches 65;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AA927529.1 GI:3076426
  33.0%;
72.1%;
Query Match 33.0
Best Local Similarity 72.1
Matches 173; Conservative
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Unpublished (1997)
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KEYWORDS
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Gaps

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Length Indels 243

23-MAR-2000

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Fax: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
Email: sainpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC1&t2=RC1-BN0014-
210100-012-1h1_effs=2000-01-21&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 218.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 266)
HCGP http://www.ludwig.org.br/ORESTES.
The FAPESP/LICR Human Cancer Genome Project
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                           220 AACATCAGAGCTGGAGCATGCCCGTATTTATGGAGTTCAGACACTCAGCACAGCAGGGTC 161
                                                                                                                                                                                      160 CTGAGCTTATATTATACCATAAGTCCTGAAGCATCTGCTTCTCCTTGCTGCGGGTCCCAA 101
                                                                                                                                                                                                                          244 gacctggagcccctgaccatcctgtactatgttgggaggaccccaaagtggagcagctc 303
                                                                                                                                                                                                                                              100 GATTAGAACCTCTAACCATTCTCTACTACATTGGCATTACACCCAAGATTGAACAGTT 41
                                                                          aacttctgctcaggcccttgcccatacctccgcagtgcagacacaacccacagcacggtg
                                                                                                                                                184 ctgggactgtacaacactctgaaccctgaagcatctgcctcgcctgctgctgctgctgcccag
                                                                                                                                                                                                                                                                                                                                                                                                                              AW600960 266 bp mRNA EST 23-MAR-2
RCI-BN0014-210100-012-h01_1 BN0014 Homo sapiens CDNA, mRNA
 DB 118;
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Pred. No. 6.9e-21;
); Mismatches 55;
Score 110.4; DB 1
Pred. No. 5.2e-21;
0; Mismatches 66
                                                                                                                                                                                                                                                                                                  304 tecaacatggtggtgaagtettgtaaatgtagetga 339
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72.2%;
 32.6%;
69.4%;
                                      Conservative
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ses 143; Conserv
                   Similarity
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 Query Match
Best Local Simi
Matches 150;
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/db_xref="taxon:9606"
/clone_lib="pr0028"
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/dev_stage="Adult"
/note="Organ: denis_drash; Vector: puc18; Site_1: SmaI;
Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the puc18 vector. Reverse transcription of tissue mRNA and CDNA amplification were performed under
                                                       7
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Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
Email: saimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtmil2.pl?tl=RCl&t2=RCl-DT0028-130100-011-hol_Lefs=2000-01-13&t4=1)
Seq primmer: puc 18 forward
High quality sequence stop: 206.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
I (bases 1 to 248)
HCGP http://www.ludwig.org.br/ORESTES.
The FAPESP/LICR Human Cancer Genome Project
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                             237 gececcaggacectggagecetgaceatectgtactatgttgggaggacececaaagtgga 296
                                                                                          58 ctctacattgacttccgacaggatctgggctggaagtgg-gtccatgaacctaagggcta 116
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RCI-DT0028-130100-011-h01_1 DT0028 Homo sapiens CDNA, mRNA
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                   Score 111; DB 13;
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/organism="Homo sapiens"
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/clone_lib="170010"
/dev_stage="Adult"
/note="Organ: epid_tumor; Vector: pucl8; Site_l: Smal;
/note="Organ: epid_tumor; Vector: pucl8; Site_l: Smal;
Site_l: Smal; A mini-library was made by cloning products
Gerived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pucl Revetor. Reverse transcription of tissue mRNA and cDNA amplification were performed under
low stringency conditions."
81 a 102 c 100 g 96 t
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1 (bases I to 379)

10 dases I to 379)

10 dases I to 379)

Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare Simpson, A.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?t1=RC3&t2=RC3-IT0010-11100-011-h02&t3=2000-11-11&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 27
High quality sequence stop: 379.
                                                                                                                                                                                                                                                                                                                                                                                                                    BF769366 379 bp mRNA EST 12-JAN-2001
RC3-IT0010-111100-011-h02 IT0010 Homo sapiens cDNA, mRNA sequence.
BF769366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Shorgun sequencing of the human transcriptome with ORF expressed
321
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
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Fax: +55-11-2707001
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Score 109.8; DB 169; Length 379; Pred. No. 8.4e-21;

32.4%;

Query Match Best Local Similarity

Search completed: October 30, 2001, 10:55:22 Job time: 6180 sec

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Polypeptide sequen Mutant Transformin Sequence of porcin

TGF-beta-3. transforming

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Transforming Growt Human TGF-beta-lik Hybrid TGF-beta 3-Truncated TGF-beta WO9914235 Seq ID N Human TGF-beta 3, Human TGF-beta3 am

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Sequence encoded b Human Transforming Hybrid transformin

Human transforming

Sequence of human

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** / SIDSI/gcgdata/geneseqf/geneseqp/AA1981.DAT:**

** / SIDSI/gcgdata/geneseqf/geneseqp/AA1991.DAT:**

** / SIDSI/gcgdata/geneseqf/geneseqp/AA1999.DAT:**

** / SIDSI/gcgdata/geneseqf/geneseqp/AA1999.DAT:**
         GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
                                                                                                                                                                             412676 segs, 60623988 residues
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Listing first 100 summaries
                                                                  October 30, 2001, 08:48:51
                                              - protein search, using sw model
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AAR39640
AAR92772
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Perfect score:

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Human TGF-Beta2 ex TGF-Beta 1.70eta 2 Simian-human hybri Chimeric simian TG Sequence of mature Platelet-derived h PDGI subunit a. H

Homo sa

human

Recombinant TGF-beta.

Human TGF-beta 1. Human transforming

TGF-betal active

Result No.

Human transforming Human growth facto The mature form of Transforming growt

Human transforming

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TGF-beta 1 amino a TGF-beta 1 c-termin TGF-beta fusion pr TGF-beta fusion pr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           β
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The invention covers hybrid TGF-beta molecules consisting of parts of the human isoforms TGF-betal, TGF-beta2 and TGF-beta3 (see AAQ41599, AAQ41600 and AAQ41601, respectively). The hinge points between parts derived from different parent isoforms are pref. between amino acids 44 and 45, 56 and 57, 79 and 80, 90 and 91, or 22 and 23. The hybrid molecules promote cell migration, inhibit the growth of A375 melanoma cells, accelerate the healing of partial-thickness burn wounds and full-thickness inclaional wounds and increase formation of fibrous granular tissue. See e.g. AAQ41602-Q41607 for pref. hybrids.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 ALDINYCFRNLEENCCVRPLYIDFRQDLGWKWVHEPKGYYANFCSGPCPYLRSADTIHST 60
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             ALDINYCFRNLEENCCVRPLY IDFRQDLGWKWVHEPKGYYANFCSGPCPYLRSADTTHST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New hybrid transforming growth factor-beta molecules - comprise portions of mature TGF-beta isoforms; useful as wound healants, cardioprotective, antiinflammatory and immunosuppressive agents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99.8%; Score 633; DB 14; Length 112; 100.0%; Pred. No. 1.6e-56;
                                                                                                                                                                                                                                                 protein; wound healing; cancer treatment;
                                                Indels
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                                                                                                                                                                                                                       Mature human Transforming Growth Factor-beta3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cerletti N,
                                                                                                                                            AAR39640 standard; Protein; 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 4; Page 24; 48pp; English
                                                                                                                                                                                                                                                               bone repair; growth regulation
                                                                                                                                                                                                                                                                                                                                                                    92EP-0810845.
                                                                                                                                                                                                                                                                                                                                                                                              91EP-0810870
                                                                                                                                                                                               (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cox D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1993-161126/20.
                                                                                                                                                                                                                                                  hTGF-beta3; hybrid
                                                                                                                                                                                                                                                                                                                                                                                                                        GEIGY
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Matches 112; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          112 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 McMaster GK,
                                                                                                                                                                                                                                                                                                                                                                                              11-NOV-1991;
                                                                                                                                                                                                                                                                                         Homo sapiens
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                                                                                                                                                                                             26-AUG-1993
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                                                                                                                                                                                                                                                                                                                 EP542679-A.
                                                                                                                                                                    AAR39640;
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RESULT AAR92772

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Gaps

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Indels

99.8%; Score 633; DB 12; 100.0%; Pred. No. 1.6e-56; ive 0; Mismatches 0;

99.8%, 100.0%; Pro

Conservative

Query Match Best Local Similarity Matches 112; Conserv

Length 112;

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growth factor (TGF) beta-1, TGF beta-2 and TGF beta-3 which are used to growth factor (TGF) beta-1, TGF beta-2 and TGF beta-3 which are used to produce TGF beta-1ike proteins in dimeric form. THE TGF beta-like proteins in dimeric form. THE TGF beta-1ike proteins are in protein proteins of TGF beta-2.3, etc, or bone morphogenic proteins e.g. BMP-2. The TGF beta hybrids were made using a new process of producing dimeric, biologically active TGF beta monomers with folding buffer contg. a mild detergent (CHAPS, CHAPSO or digitionin) and at least one of the columning dimerity sulphoxide). DMSOZ (dimethylsulphone) and DMF (dimethyl formamide). The detergent allows folding of the monomer such that, after dimerisation, the TGF beta-like protein retains biological crivity and remains in soluble form. The method allows relatively high yields of biologically active TGF beta-like proteins in their native dimeric form. TGF-beta like proteins in their native dimeric form. TGF-beta like proteins are multifunctional regulators of cellular activity and a typical use is to stimulate wound healing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          acid-stable; heat-stable; homodimer; mitogenesis; cell proliferation; cell growth; wound; oral mucositis; intestinal mucositis; osteoarthritis; bone disease; bone repair; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Transforming growth factor beta3; TGF-beta3; human; mature protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 ALDINYCFRNLEENCCVRPLYIDFRQDLGWKWVHEPKGYYANFCSGPCPYLRSADTTHST
                                                                                                                                                                                                                                                   Prodn. of dimeric, biologically active transforming growth factor beta - by refolding denatured monomer in buffer contg. mild detergent and specific organic solvents to improve yields
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 VLGLYNTLNPEASASPCCVPQDLEPLTILYYVGRTPKVEQLSNMVVKSCKCS 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99.8%; Score 633; DB 17; Length 112; 100.0%; Pred. No. 1.6e-56; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mature transforming growth factor beta3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW26173 standard; Protein; 112 AA
                                                                                                                                                                                                                                                                                                                     Claim 17; Page 38; 59pp; English.
                                                                             95WO-EP02718
                                                                                                            94EP-0810438
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                                                                                                                                           (CIBA ) CIBA GEIGY AG
                                                                                                                                                                                                          WPI; 1996-116999/12.
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                WO9603432-A1
                                                                              12-JUL-1995;
                                                                                                            25-JUL-1994;
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                                               08-FEB-1996.
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                                                                                                                                                                           Cerletti N;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Non-soluble, monomeric transforming growth factor TGF-beta 3 (AAR92772) was recovered from E. coli LC 137 (DSM 5658) transformants carrying plasmid pPLMu.TGF-beta 3, which includes the coding sequence (AAT17234) for TGF-beta 3. A biologically active, dimeric form of TGF-beta 3 was obtd. by refolding this monomer in detergent-free buffer contg. DMSO and/or DMF. Dimers of TGF-beta 1 (AAR92773) and TGF-beta 2 (AAR92773), and TGF-beta 2 (AAR92773),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 ALDINYCFRNLEENCCVRPLYIDFRQDLGWKWVHEPKGYYANFCSGPCPYLRSADTIHST 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       growth factor
                                                                                                                                                                                                                                                                                                                                                                                                                                               Prodn. of dimeric biologically active transforming growth facto:
by refolding denatured monomer in detergent-free folding buffer
contg. specific organic solvent to improve yield
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 VLGLYNTLNPEASASPCCVPQDLEPLTILYYVGRTPKVEQLSNMVVKSCKCS 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99.8%; Score 633; DB 17; Length 112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Transforming growth factor beta; TGF; regulator; method; proliferation; differentiation; wound healing; solvent.
                                                                                                                           Transforming growth factor type beta; TGF-beta 3; protein renaturation; protein folding.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 1B; Page 34; 54pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAR91958 standard; Protein; 112 AA.
AAR92772 standard; Protein; 112 AA.
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                                                                                                                                                                                                                                                                                                   94EP-0810439
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                                                              (first entry)
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Matches 112; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1996-117000/12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           were also produced.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        112 AA;
                                                                                            Human TGF-beta 3.
                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; AAT17234
                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                        WO9603433-A1
                                                                                                                                                                                                                                                                     12-JUL-1995;
                                                                                                                                                                                                                                                                                                    25-JUL-1994;
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                                                            17-JUL-1996
                                                                                                                                                                                                                                      08-FEB-1996
                                                                                                                                                                                                                                                                                                                                                                   Cerletti N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
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                               AAR92772;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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Gaps 9 9

96WO-US08973 95US-0470837

05-JUN-1996;

12-DEC-1996

06-JUN-1995;

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                                                                                                                                                                                                                                                                                                                                              This sequence represents the mature human transforming growth factor Deta3 (TGF-Deta3). TGF-beta3 is one of five distinct homodimeric TGFbeta4. TGF-beta3 is one of five distinct homodimeric homodimer. All the TGF-beta s are produced as 390-412 amino acid precursors, which undergo proteolytic cleavage to produce mature forms which consist of the C-terminal 112 amino acids. Depending upon cell and tissue type, and the presence of other growth factors, TGF-beta may either stimulate mitogenesis, cell proliferation and growth, or inhibit these processes. Many of the actions of TGF-beta are related to the resultant damage. A crystalline form of TGF-beta3 can be produced by a method of the invention. Crystalline TGF-beta3 is useful in slow release
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          compositions for treatment of conditions such as wounds, oral or
intestinal mucositis, osteoarthritis, bone disease and repair, generally
wherever TGF-beta1 is normally used. The crystalline form is also used
for structure determination in rational drug design. Crystalline
TGF-beta3 shows lower tendency than the dissolved protein to adsorb on
the walls of vials and is more stable against oxidation. Variation of the
properties, e.g. size, of the crystals allows control over the rate at
which active TGF is released in vivo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Crystalline form of transforming growth factor beta-3 - useful in compsns. as slow release form of TGF, e.g. for wound healing, and for structure determn. in rational drug design
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Transforming growth factor-beta fusion protein; wound healing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 VLGLYNTLNPEASASPCCVPQDLEPLTILYYVGRTPKVEQLSNMVVKSCKCS 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 112;
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Pred. No. 1.6e-56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99.8%; Sco. 100.0%; Pred. No. ... 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 artificial skin; surgery recovery time
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                                                                                                                                                                                                                                                                                                                   Example 1; Page 26; 34pp; English.
                                                                                                                                                          Mittl P;
                                                    96WO-EP03140.
                                                                                      95EP-0810484
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Best Local Similarity 100.
Matches 112; Conservative
                                                                                                                                                          Grutter M,
                                                                                                                        (CIBA ) CIBA GEIGY AG.
                                                                                                                                                                                       WPI; 1997-145621/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      112 AA;
                                                                                                                                                                                                             N-PSDB; AAT80110
                                                    17-JUL-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO9639430-A1
                                                                                      25-JUL-1995;
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                  13-FEB-1997
                                                                                                                                                          Arvinte T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
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A novel transforming growth factor-beta (TGF-beta) fusion protein comprises a purification tag and a TGF active fragment. The present sequence represents a specifically claimed TGF active fragment. Additionally, the fusion protein may comprise proteinase-sensitive linker sites and binding domain so the protein sequence may contain some or all of the following elements: purification tag:proteinase site:ECM binding site:proteinase site:TGF-beta. TGF-beta promotes wound healing, and the fusion protein can be used to reduce surgery recovery time and in the preparation of artificial skin. The inclusion of a purification tag facilitates purification of the fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The proteinase site is included to permit cleavage and release of the purification tag after purification if desired. The extracellular matrix binding site facilitates delivery of the fusion protein to the desired site of action. Delivery of the TGF-beta to the site to be treated reduces the amount of TGF-beta required to be administered to be effective and reduces the concentration of circulating TGF-beta which may result in undesirable effects.
                                                                                                                                                                                                                                                                                         Prepn. of transforming growth factor-beta fusion protein - useful to reduce surgery recovery time and to prepare artificial skin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 ALDINYCFRNLEENCCVRPLYIDFRQDLGWKWVHEPKGYYANFCSGPCPYLRSADTTHST 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Growth factor; human; dimer; cysteine knot; cellular inclusion body;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 VLGLYNTLNPEASASPCCVPQDLEPLTILYYVGRTPKVEQLSNMVVKSCKCS 112
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100.0%; Pred. No. 1.6e-56;
iive 0; Mismatches 0;
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100.0%; Pre-
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                                                                                                          CHEUNG D T. HALL F L. NIMNI M E. TUAN T.
                                                                                                                                                                                                                                         WPI; 1997-043065/04.
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Matches 112; Conserv
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                                                                                                                                                                                                                                                          N-PSDB; AAT42773
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                                                                                                                                                                             WULL/) WU L.
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                                                                                                                                                                                                             Cheung DT,
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                                                                                                                                             (NIMN/)
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N-PSDB; AAX15247
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                 25-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10-DEC-1998.
                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                               AAW84209;
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                                                                                                                                                             This invention describes the novel preparation of biologically active dimers of recombinant human growth factors of the cysteine knot family starting from cellular inclusion bodies. Such dimers are are useful in pharmaceutical compositions and the method provides yields of 31-39.7%, in examples, compared with about 10% for the conventional method (see Biochemistry, 28 (1989) 2956). AAY08278-Y08301 are human growth factor protein fragments used in the method of the invention.
                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                       9
                                                                                                                                                                                                                                                                                                               Preparing active growth factor dimers from inclusion bodies in high
                                                                                                                                                                                                                                                                                                     1 ALDINYCFRNLEENCCVRPLYIDFRQDLGWKWVHEPKGYYANFCSGPCPYLRSADITHST
                                                                                                                                                                                                                                                                                     ó
                                                                                                                                                                                                                                                                                                                                        Transforming growth factor-beta-3; TGF-beta-like protein; S-sulphonated TGF-beta-like protein; wound treatment; cancer; bone repair; tissue repair; bone marrow protective agent; cardioprotection; anti-inflammatory; immunosuppressive;
                                                                                                                                                                                                                                                                   Length 112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Schmitz A;
                                                                                                                                                                                                                                                                                     Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              The mature form of transforming growth factor-beta-3.
                                                                                 Weich
                                                                                                                                                                                                                                                                  Score 633; DB 20;
Pred. No. 1.6e-56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Meyhack B,
                                                              (GBFB ) GES BIOTECHNOLOGISCHE FORSCHUNG MBH.
                                                                                Rinas U,
                                                                                                                                                                                                                                                                Ouery Match 99.8%; Score 633; DB Best Local Similarity 100.0%; Pred. No. 1.6 Matches 112; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                       AAW97093 standard; Protein; 112 AA.
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                                                                                Mueller C,
                                                                                                                                             Claim 14; Page 12; 14pp; German.
                          97DE-1048734.
                                            97DE-1048734
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             89GB-0027546
                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                Kaerst U,
                                                                                                WPI; 1999-278785/24
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                                                                                                                                                                                                                                       112 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ulcer; bed sore
                          05-NOV-1997;
                                            05-NOV-1997;
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        06-MAY-1999
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                                                                                Erdmann H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EP891985-A1
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                                                                                                                                                                                                                                         Seguence
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                                                                                                                            yield
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The present sequence represents the mature form of transforming growth factor-beta-3. Dimeric, biologically active TGF-beta-like protein can be produced by subjecting the denatured monomeric form to refolding conditions. The new monomeric S-sulphonated TGF-beta-like protein is useful for the production of the dimeric, biologically active TGF-beta-like protein, which is useful for the treatment of wounds (surface or internal) and cancer in a mammal, in bone and tissue repair, as a bone marrow protective agent, a mediator of cardioprotection, for the production of an anti-inflammatory or immunosuppressive preparation. Treatment is useful for animals, especially humans, and wound treatment (e.g. ulcers, bed sores etc.) is particularly useful for the elderly.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Proteinase site; bone morphogenetic fusion protein; bone binding site; bone morphogenetic protein; transforming growth factor beta; active fragment; wound healing; bone growth; purification tag.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 ALDINYCFRNLEENCCVRPLYIDFRQDLGWKWVHEPKGYYANFCSGPCPYLRSADTTHST 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New bone morphogenetic fusion proteins - comprising a purification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 VLGLYNTLNPEASASPCCVPQDLEPLTILYYVGRTPKVEQLSNMVVKSCKCS 112
Producing biologically active dimeric Transforming Growth Factor-beta - by refolding new monomeric Transforming Growth Factor-beta, useful for treatment of wounds and cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1.6e-56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99.8%; Score 633; DB 20;
100.0%; Pred. No. 1.6e-56;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Transforming growth factor beta active fragment.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW84209 standard; Protein; 112 AA
                                                                                                                         Example 1; Page 30; 32pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98WO-US11189
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 112; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1999-059875/05.
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NIMNI M E.
SHORS E C.
WU L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   112 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hall FL, Han B,
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19-MAR-1999;
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                                                      The present sequence represents a transforming growth factor beta active fragment. The protein can be used in place of a bone morphogenetic active fragment to create the fusion proteins of the invention. When a bone morphogenetic active fragment is used, the fusion proteins are designated bone morphogenetic fusion proteins. The bone morphogenetic fusion proteins. The bone morphogenetic fusion proteins. The bone morphogenetic purification tag, a proteinase site, an ECM/bone binding site, a second proteinase site, and a bone morphogenetic protein active fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "optionally mutated to increase electrostatic interaction between beta hairpin structure and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      optionally mutated to increase electrostatic interaction between beta hairpin structure and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "optionally mutated to increase electrostatic
interaction between beta hairpin structure and
a receptor"
                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                   1 ALDINYCFRNLEENCCVRPLYIDFRQDLGWKWVHEPKGYYANFCSGPCPYLRSADTTHST 60
                                                                                                                                                                                                                                                                                tag and a bone morphogenetic active fragment, used for enhancing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /label- beta_hairpin_loop_1
/note= "mutant optionally comprises one or more
substitutions in these residues"
                                                                                                                                                                                                                                                ;
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substitutions in these residues"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          human transforming growth factor beta 3 monomer; CKGF; mutant; cystine knot growth factor; hairpin loop; infertility.
                                                                                                                                                                                                                                                                                                                61 VLGLYNTLNPEASASPCCVPQDLEPLTILYYVGRTPKVEQLSNMVVKSCKCS 112
                                                                                                                                                                                                                                                                                                                              Length 112;
                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                       99.8%; Score 633; DB 20; 100.0%; Pred. No. 1.6e-56;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human transforming growth factor beta 3 monomer.
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                                                                                                                                                                                                                              100.0%; Preq. ...
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                                  Disclosure; Page 43-44; 64pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             a receptor"
                                                                                                                                                                                                                                                                                                                                                                                                   AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   a receptor
                                                                                                                                                                                                                                                                                                                                                                                                AAY92012 standard; Protein; 112
            wound healing or bone growth
                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                 Best_Local Similarity 100.
Matches 112; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Misc-difference 103..112
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                                                                                                                                                               healing or bone growth.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         41..81
                                                                                                                                                                                     112 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                               19-JUL-2000
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                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                       AAY92012;
                                                                                                                                                                                                                        Query Match
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Mutant cystine knot growth factor (CKGF) proteins comprising one or more mutant subunits and having novel properties or improved pharmacological properties, compared to wild type CKGFs, are claimed. The CKGF approperties, compared to wild type CKGFs, are claimed. The CKGF is superfamily comprises at least four families of growth factors the glycoprotein hormones, the platelet-darived growth factor (PDGF) family, the neurotrophins and the transforming growth factor-beta family; the families are known to be structurally similar (especially comprising the cystines know topology) and it was shown that mutations at certain positions in the CKGF hairpin loops of family members and other members of the CKGF superfamily could significantly alter the biological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             analogues are useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mutant transforming growth factor family proteins or analogues are useful for treatment of ovulatory dysfunction, luteal phase defect, unexplained infertility, time-limited conception and in assisted reproduction.
                                                                                                                                                                                                                                               growth factor proteins comprising one or more for treating or preventing diseases e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Heparin binding; vascular graft; matrix; cell adhesion; growth factor; wound healing; dermal wound; wound healing; TGF-beta 3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 ALDINYCFRNLEENCCVRPLYIDFRQDLGWKWVHEPKGYYANFCSGPCPYLRSADTIHST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99.8%; Score 633; DB 21; Length 112; 100.0%; Pred. No. 1.6e-56;
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                                                                                                                                                                                                                                             New mutant cystine knot growth factor
                                                                                                                                                                                                                                                                                                                                          Claim 223; Page 301; 320pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB35939 standard; protein; 112 AA
                                                                                                                                                                                                                                                                    mutant subunits, useful for treat: hypothyroidism and thyroid cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99.00.
100.08; Pri
                                                                                             (UYMA-) UNIV MARYLAND BALTIMORE.
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                                                                                                                                          Weintraub BD, Szkudlinski MW
                                             98WO-US19772.
99WO-US05908
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              activities of the CKGF
                                                                                                                                                                                             WPI; 2000-283585/24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
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Matches 112;
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McPherron AC;
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                                                                                                                         and cachexia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20-OCT-1986;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TGF-alpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
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                                                                                                                                                                                                                                          providing attachment of a hearin binding peptide (HBP), a peptide comprising a binding domain which binds heparin with high affinity, heparin or heparin-like polymer, and a protein growth factor or peptide fragment which has a domain that binds heparin with low affinity.

Included in the invention is a vascular graft comprising the matrix, which is capable of supporting cell adhesion. The matrix is used for peptides in a controlled manner suitable for wound healing. The matrix or an be used in an article for treating dermal wounds, and in an implantable sterilized composition capable of supporting cell adhesion. The present sequence represents a growth factor protein: The present sequence represents a growth factor protein. The protein is used in an example illustrating that non-heparin-binding growth factors
                                                                                                                                                                                                                                                                                                                                                                                                                                                            can be released in a controlled manner from heparin-based drug delivery systems based on their low affinity for heparin.
                                                                                                   Matrix for controlled release of growth factor for wound healing, has substrate that attaches heparin binding peptide, protein growth factor that bind heparin with low affinity, and heparin or heparin-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gene therapy; growth differentiation factor-8; GDF-8; AIDS; cachexia; neurodegenerative disease; amyotrophic lateral sclerosis; obesity; muscular dystrophy; musculodegenerative disease; tissue repair; muscle wasting disease; neuromuscular disorder; spinal cord injury; traumatic injury; congestive obstructive pulmonary disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 ALDINYCFRNLEENCCVRPLYIDFRQDLGWKWVHEPKGYYANFCSGPCPYLRSADTTHST 60
                                                                                                                                                                                                                             This invention relates to a matrix comprising a substrate capable of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 VLGLYNTLNPEASASPCCVPQDLEPLTILYYVGRTPKVEQLSNMVVKSCKCS 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99.8%; Score 633; DB 22; 100.0%; Pred. No. 1.6e-56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Prec. ...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB73206 standard; Protein; 115 AA.
                                                                                                                                                                                            Example 5; Page 21; 48pp; English.
(ETHZ-) ETH ZURICH & UNIV ZURICH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TGF-beta3 C-terminal sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17-AUG-2000; 2000WO-US22884.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                  Sakiyama SE, Hubbell JA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 99.8
Best Local Similarity 100.
Matches 112; Conservative
                                                                     WPI; 2001-024627/03.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 112 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200112777-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19-AUG-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
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                                                                                                                                                                                                                                                   The present invention relates to growth differentiation factor-8 (GDF-8) coding sequences and proteins. The present sequence is a protein, which was used in a sequence homology comparison with the GDF-8 protein isolated in the present invention. GPF-8 is useful for treating neurodegenerative diseases (e.g. amyotrophic lateral sclerosis and muscular dystrophy), musculodegenerative diseases or in tissue repair due to trauma, obesity and disorders related to abnormal proliferation of adipocytes. GPF-8 is also useful for treating malignancies of the various organ systems, particularly cells in muscle or adipose tissues and in gene therapy for the treatment of cell proliferative or immunological diseases mediated by GDF-8. In addition, GDF-8 is also useful for treating muscle wasting disease, neuromuscular disorder, spinal cord injury, traumatic injury, congestive obstructive pulmonary disease
New substantially purified growth differentiation factor-8 polypeptide,
                               useful for treating muscle wasting disease, obesity, muscular dystrophy, neuromuscular disorder, acquired immunodeficiency syndrome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 ALDTNYCFRNLEENCCVRPLYIDFRQDLGWKWVHEPKGYYANFCSGPCPYLRSADTTHST 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cancer; carcinoma; melanoma; leukaemia; arteriosclerosis; psoriasis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 aldtnycfrnleenccvrplyidfrqdlgwkwvhepkgyyanfcsgpcpylrsadtthst
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99.8%; Score 633; DB 22;
100.0%; Pred. No. 1.7e-56;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Protein with tumour growth inhibitory activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gold LI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAR06548 standard; protein; 202 AA
                                                                                                                                                                                    Example 2; Fig 3; 124pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       87EP-0106772.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               injury, traumatic injury, (COPD), AIDS or cachexia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 112; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (ONCO-) ONCOGENE SCI INC
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                                            Gene product may be used to inhibit growth of tumour cells, to treat proliferative type disorders, burns and other wounds, and may also be used as an immune modulator. Detection of proteins and of TGF-alpha can indicate presence of a tumour. Proteins may be produced from a bacterial or eukaryotic expression
Tissue-derived tumour growth inhibitors - used in diagnosis and treatment of tumours and treatment of proliferative type disorders, burns and wounds
                                                                                                                                           ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Transforming growth factor beta 3 proteins, precursors and mutants - obtd. from polypeptide and antibodies, with optimal therapeutic use due to genetic manipulation of coding sequence
                                                                                                                                                                                     Length 202;
                                                                                                                                          Indels
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                                                                                                                                 3.1e-56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tendijke P, Haley JD;
                                                                                                                   99.8%; Scor.
100.0%; Pred. No. ...
0; Mismatches
                                                                                                                           DB
                                                                                                                                                                                                                                                                                                                                               74. 76
/label= glycosylation
135. 137
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158.160
/label= glycosylation
                                                                                                                                                                                                                                                                                                                                                                      /label= glycosylation
142..144
                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                              Disclosure; Fig 27; 81pp; English.
                                                                                                                                                                                                                                                                                         Transforming Growth Factor beta 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 2; Fig 1; 107pp; English.
                                                                                                                                                                                                                                           AAR20621 standard; Protein; 412
                                                                                                                                                                                                                                                                                                         Human; TGF-beta 3; homodimer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 90US-0543348.
                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                        Matches 112; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (ONCO-) ONCOGENE SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Foulkes JG,
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N-PSDB; AAQ20576.
                                                                                                                                 Best Local Similarity
                                                                                                  202 AA;
                                                                                                                                                                                                                                                                                                                                              Modified-site
                                                                                                                                                                                                                                                                                                                                                             Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                             Modified-site
                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25-JUN-1990;
                                                                                                                                                                                                                                                                          05-MAY-1992
                                                                                                                                                                                                                                                                                                                                                                                                                   WO9200318-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Iwata KK,
                                                                                                   Sequence
                                                                                                                                                                                                                                                           AAR20621;
                                                                                                                          Query Match
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This sequence represents human transforming growth factor-beta 3 (TGF-beta 1. This sequence and the sequence for human TGF-beta 1 (see AAR73596) are claimed within the scope of the invention. The invention is a composition consisting of a TGF-beta protein and an osteogenic color source (OCS) formulated in an acceptable carrier other than a bone morphogenic cofactor. This composition can be used for the restoration of bone deficiency. This provides for the generation of mature bone only where it is required, without the inclusion of a specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Transforming growth factor-beta; Human TGF-beta protein; TGF-beta 1; TGF-beta 3; osteogenic cell source; OCS; bone deficiency; bone-inducing cofactor.
The TGF-beta3 gene sequence was obtained from three shorter overlapping clones derived from human placental, human umbilical cord and A673 cells cDNA libraries, respectively. The predicted amino acid sequence of the gene encoding TGF-beta3 shows extensive homology to TGF-beta1 and beta2. Based on the functional and structural homology, it is likely that TGF-beta3 has therapeutic activity in cancer therapy, wound healing and immunosuppression. See also AAQ22229 and AAR20622.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 ALDINYCFRNLEENCCVRPLYIDFRQDLGWKWVHEPKGYYANFCSGPCPYLRSADTTHST
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                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 VLGLYNTLNPEASASPCCVPQDLEPLTILYYVGRTPKVEQLSNMVVKSCKCS 112
                                                                                                                                                                                                                                                                                                                                                  Score 633; DB 13; Length 412;
Pred. No. 7e-56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                          99.8%; Sco. 100.0%; Pred. No. . . . . . 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAR73598 standard; Protein; 412 AA.
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91US-0790856.
93US-0063841.
93US-0132405.
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                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (GETH ) GENENTECH INC.
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                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
tes 112; Conserv
                                                                                                                                                                                                                                                            412 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12-NOV-1991;
18-MAY-1993;
12-NOV-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo-sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12-NOV-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US5409896-A
                                                                                                                                                                                                                                                            Sequence
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                                                                                                                                                                                                                                                                                                                                                  Query Match
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VLGLYNTLNPEASASPCCVPQDLEPLTILYYVGRTPKVEQLSNMVVKSCKCS 112

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 This method can be used with any of the 5 human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (TGF-beta3). The specification describes a composition for regulating trophoblast invasion which comprises an inhibitor of TGF-beta3, TGF-beta family cytokine receptors, hypoxia inducible factor 1 alpha (HIF-1 alpha) or oxygen tension. The composition is used in methods of diagnosing, monitoring, preventing or treating conditions requiring regulation of trophoblast invasion, especially preeclempsia in pregnant
                                                                                                                                                              Gaps
                                                                                                                                               1 ALDTNYCFRNLEENCCVRPLYIDFRQDLGWKWVHEPKGYYANFCSGPCPYLRSADTTHST 60
                                                                                                                                                                                                                                                                                                                                                                                                                                             trophoblast invasion regulation; inhibitor; HIF-1 alpha;
TGF-beta family cytokine receptor; hypoxia inducible factor 1 alpha;
preeclempsia; pregnanancy; choriocarcinoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence encodes human transforming growth factor-beta 3
                                                                                                                                                                                                                                                                                                                                                                                                                               transforming growth factor-beta 3; TGF-beta3; oxygen tension;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Regulation of trophoblast invasion - by, e.g. transforming growth factor-beta3 inhibitor, useful for detecting or treating
                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                 Amino acid sequence of human transforming growth factor-beta 3.
                                                                                                                                                                                                                       61 VLGLYNTLNPEASASPCCVPQDLEPLTILYYVGRTPKVEQLSNMVVKSCKCS 112
                                                                                       99.8%; Score 633; DB 16; Length 412; 100.0%; Pred. No. 7e-56;
                                                                                                                    Indels
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bone-inducing cofactor. This method can be use TGF-beta's or with TGF-beta from other species.
                                                                                                      Pred. No. 7e-
0; Mismatches
                                                                                                                                                                                                                                                                                                           AAW80417 standard; Protein; 412 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HOSP-) HOSPITAL FOR SICK CHILDREN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (MOUN ) MOUNT SINAI HOSPITAL CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Fig 1; 59pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        preeclempsia in pregnant women
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Post M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98WO-CA00180.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          97US-0039919
                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      women or choriocarcinomas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1998-520837/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lye S,
                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAV63209
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO9840747-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              05-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          07-MAR-1997;
                                                                                                    Best Local Sim;
Matches 112;
                                                                                                                                                                                                                                                                                                                                                                     14-JAN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Caniggia I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17-SEP-1998
                                            Sequence
                                                                                                                                                                                                                                                                                                                                        AAW80417;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                               Human
                                                                                                                                                                                                                                                                              RESULT 16
                                                                                                                                                                                                                                                                                             AAW80417
SS X 8
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This is the amino acid sequence of human transforming growth factor beta-3 (TGF-beta 3, see also AAW7878). The sequence shows homology to human TGF-beta 1 (see AAW78781), porcine TGF-beta 3 (see AAW7878) and bovine TGF-beta 2 (see AAW78784) N-terminal sequences. The invention relates to the recombinant production of TGF-beta. DNA encoding TGF-beta has been isolated and cloned into vectors which are replicated in bacteria and expressed in eukaryotic cells. TGF-beta recovered from transformed cells can be used in known
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 ALDTNYCFRNLEENCCVRPLYIDFRQDLGWKWVHEPKGYYANFCSGPCPYLRSADTTHST 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA encoding transforming growth factor-beta precursor sequence 'useful for analysis to perform manipulations to increase yield of recombinant production of the protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
0
Human transforming growth factor-beta 3 N-terminal sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                         Transforming growth factor-beta 3; TGF-beta 3; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99.4%; Score 630; DB 19; 99.1%; Pred. No. 3.2e-56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Mismatches
                                                                       AAW78782 standard; Protein; 112 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Fig 3; 26pp; English.
                                                                                                                                                                                                                                                                                                  85US-0025423.
85US-0715142.
89US-0389929.
                                                                                                                                                                                                                                                                           85US-0715142.
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                                                                                                                                                                                                                                                                                                                                                    93US-0147364
95US-0454468
                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                    Goeddel DV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 therapeutic applications.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       111; Conservative
                                                                                                                                                                                                                                                                                                                                                                                          (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1998-494840/42.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        112 AA;
                                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                    RMA,
                                                                                                                         21-DEC-1998
                                                                                                                                                                                                                         US5801231-A.
                                                                                                                                                                                                                                                                           22-MAR-1985;
                                                                                                                                                                                                                                                    01-SEP-1998
                                                                                                                                                                                                                                                                                                                 22-MAR-1985;
04-AUG-1989;
                                                                                                                                                                                                                                                                                                                                          04-MAR-1992
                                                                                                                                                                                                                                                                                                                                                   05-NOV-1993
                                                                                                                                                                                                                                                                                                                                                                  30-MAY-1995
                                                                                                                                                                                                                                                                                                    13-MAR-1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seguence
                                                                                                AAW78782;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                   Derynck
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                         AAW78782
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Gaps

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Indels

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99.8%; Score 633; DB 19; Length 412;

Pred. No. 7e-56;

100.0%; Pred. w.

Query Match 99.85
Best Local Similarity 100.0
Matches 112; Conservative

AAR46229

vulnerary.

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growth factor-beta 3 precursor (preTGF-beta 3), deduced from an isolated CDNA clone (see AAV52935). The invention relates to the recombinant production of TGF-beta. Biologically active TGF-beta is defined as being capable of inducing EGF-potentiated anchorage independent growth of target cell lines and/or growth inhibition of neoplastic cell lines. Nucleic acids encoding TGF-beta have been isolated and cloned into vectors which are replicated in bacteria and expressed in eukaryotic cells. TGF-beta recovered from transformed cells is used in known therapeutic applications.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA encoding transforming growth factor-beta precursor sequence useful for analysis to perform manipulations to increase yield of recombinant production of the protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This is a partial amino acid sequence of the human transforming
                                             Transforming growth factor-beta 3; TGF-beta 3; pig.
               Human transforming growth factor-beta 3.
                                                                                                                                                                             /note= "encoded by ATT"
                                                                                                             Location/Qualifiers
93..204
/label= Mat_protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 6; Fig 5; 26pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAR04080 standard; protein; 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99.4%;
99.1%;
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85US-0715142.
89US-0389929.
92US-0845893.
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95US-0454468
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 111; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Goeddel DV;
                                                                                                                                                                                                                                                                                                                                                                                                                             (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1998-494840/42.
N-PSDB; AAV52935.
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                                                                                                                                                              Misc-difference 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           204 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Derynck RMA,
                                                                                                                                                                                                                                                                                                            13-MAR-1987;
22-MAR-1985;
04-AUG-1989;
04-MAR-1992;
05-NOV-1993;
30-MAY-1995;
                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                               22-MAR-1985;
                                                                                                                                                                                                               US5801231-A
                                                                                                                                                                                                                                               01-SEP-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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                                                                                                                              Protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pig TGF-beta-3 (AAQS6925) and human TGF-beta-3 (AAQS6926), and the corresponding amino acid sequences were determined (AAR46227-29, respectively). A genomic fragment corresponding to a human TGF-beta-1 exon (AAQS6924) was also isolated and its amino acid sequence determined (AAR46230). The sequences have been used in the construction of vectors for the expression of recombinant TGF-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 ALDITNYCFRNLEENCCVRPLYIDFRQDLGWKWVHEPKGYYANFCSGPCPYLRSADITHST 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CDNA sequences were determined for human pre-TGF-beta-1 (AAQ56923),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         encoding transforming growth factor-beta for use in therapeutics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
0
                                                                                                                                                                                        TGF-beta-1; TGF-beta-2; transforming growth factor beta-1; transforming growth factor beta-3; recombinant; wound healing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 15; Length 204;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 630; DB 15;
Pred. No. 6.3e-56;
1; Mismatches 0;
                                                       AAR46229 standard; Protein; 204 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW78787 standard; Protein; 204 AA
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87US-0025423.
89US-0389929.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 99.4%;
Best Local Similarity 99.1%;
Matches 111; Conservative 1
                                                                                                                                                                                                                                                                                                                                                           85US-0715142
                                                                                                                                                                                                                                                                                                                                                                                                                                         92US-0845893
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                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Goeddel DV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleic acid sequences diagnostic probes, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1994-056343/07.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      204 AA;
                                                                                                                                                           Human TGF-beta-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; AAQ56926
                                                                                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                          22-MAR-1985;
                                                                                                                                                                                                                                                                                                                                                                                                                        04-AUG-1989;
                                                                                                                         09-JUL-1994
                                                                                                                                                                                                                                                                                        US5284763-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Derynk RMA,
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                                                                                                                                                                                                                                                                                                                          08-FEB-1994
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Sequence

AAW78787;

AAW78787 ID AAW7 XX AC AAW7 XX DT 21-E

RESULT 19

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                                                                                 Gaps
                                                               1 ALDTNYCFRNLEENCCVRPLYIDFRQDLGWKWVHEPKGYYANFCSGPCPYLRSADTTHST
                                ;
0
                                                                                                                          61 VLGLYNTLNPEASASPCCVPQDLEPLTILYYVGRTPKVEQLSNMVVKSCKCS 112
Length 204;
                                                                                                                                            Score 630; DB 19; Length 2
Pred. No. 6.3e-56;
1; Mismatches 0; Indels
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Transforming growth factor beta-3 (TGF beta 3); tumour cells; growth inhibition.
                                          Misc-difference
                                                                                                                                                                                                                                                                                                                                                               413
         Cleavage-site
                                                                                                                             25-JUN-1991;
                                                                                                                                              25-JUN-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31-MAY-1989
                                                                                           WO9200318-A
                                                                                                             09-JAN-1992
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                                                                                                                                                                                                                                                                                                                                                                 Sequence
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                          Region
                                                                   Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             δλ
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                                                                                                                                                                             Nucleotide sequence encoding transforming growth factor beta-3 used as a probe, or to produce TGF beta 3, for inhibiting growth of certain normal and neoplastic cells, eg A549.
                                                                                                                                                                                                                             This sequence represents porcine transforming growth factor-beta 3 (TGF-beta 3) polypeptide. The corresponding nucleic acid sequence of this subtype is useful as a probe or to produce this protein for normal and neoplastic cell growth inhibition. It differs from human TGF-beta 3 at several AA positions.
                                                                                                                                                                                                                                                                                                                                                     Gaps
                        Transforming growth factor beta-3 (TGF beta 3); tumour cells; growth inhibition.
                                                                                                                                                                                                                                                                                                                                             1 ALDTNYCFRNLEENCCVRPLYIDFRQDLGWKWVHEPKGYYANFCSGPCPYLRSADTTHST 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
0
                                                                                                                                                                                                                                                                                                                                                                               61 VLGLYNTLNPEASASPCCVPQDLEPLTILYYVGRTPKVEQLSNMVVKSCKCS 112
                                                                                                                                                                                                                                                                                                                                                                                        Score 630; DB 11; Length 457;
Pred. No. 1.6e-55;
1; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mutant Transforming Growth Factor beta-3 coding sequence.
        sequence of porcine TGF-beta 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /label= glycosylation
135..137
/label= glycosylation
142..144
/label= glycosylation
158..160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                               Disclosure; Fig. 5; 61pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                          AAR22038 standard; Protein; 413
                                                                                                                                                                                                                                                                                                            99.4%;
ilarity 99.1%;
Conservative
                                                                                  88WO-US01945
                                                                                                   88WO-U001945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              rGF-beta 3; homodimer; ss
                                                                                                                                     Goeddel DV;
                                                                                                                    (GETH ) GENENTECH INC.
                                                                                                                                                    WPI; 1990-007474/01.
N-PSDB; AAQ02819.
                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 111; Conserv
                                                                                                                                                                                                                                                                                    457 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Modified-site
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                                                                                  08-JUN-1988;
                                                                                                   08-JUN-1988;
        Polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             05-MAY-1992
                                                WO8912101-A.
                                                                 14-DEC-1989
                                                                                                                                     Dernyck RM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic.
                                                                                                                                                                                                                                                                                    Sequence
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Region
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                                                                                                                                                                                                                                                                                                                                                                                               406
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Muderak
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This sequence has been compiled from the description of a mutant TGF-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
                                                                                              /note= "amino acids 301-403 of TGF-beta3 precursor"
                                                                                                                                                                                                                      "amino acids 405-412 of TGF-beta3 precursor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 ALDTNYCFRNLEENCCVRPLYIDFRQDLGWKWVHEPKGYYANFCSGPCPYLRSADTTHST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Transforming growth factor beta 3 proteins, precursors and mutants - obtd. from polypeptide and antibodies, with optimal therapeutic use due to genetic manipulation of coding sequence
                                                                                                                                             /note= "wild-type = Met; may be substituted by
any other amino acid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 413;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 627; DB 13;
Pred. No. 2.8e-55;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Haley JD;
                  297..300 /
/label= Factor_Xa_site
/label= glycosylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Iwata KK, Foulkes JG, Tendijke P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ¥.
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                                                                                                                                                                                                                                                                                                                                                                             91WO-US04541.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 98.9%;
Best Local Similarity 99.1%;
Matches 111; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                          90US-0543348.
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                                                                                                                                                                                                 .413
                                                                   ..404
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                                                                                                                                                                                                                              /note=
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N-PSDB; AAQ22229.
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Tue Oct

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CDNA sequences were determined for human pre-TGF-beta-1 (AAQ56923),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic acid sequences diagnostic probes, and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1994-056343/07
                                                                                                                                                           112 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; AAQ56925
                                                                                                                                                                                                                                                                                                                                                                                Pig TGF-beta-3.
                                                                                                                                                                                                                                                                                                                                                             09-JUL-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22-MAR-1985;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22-MAR-1985;
13-MAR-1987;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              04-AUG-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       04-MAR-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Sus scrofa
                                                                                                                                                                                                                                                                                                                                                                                                                    vulnerary.
                                                                                                                                                                                                                                                                                                                                            AAR46228;
                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                        24
                                                                                                                                                                                                                                                                                                                 AAR46228
  g
                                                                                                                                                                                                                                                                                                                                  δλ
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                                                                                                                                                              This sequence is that of porcine transforming growth factor-beta 3 (TGF-beta 3) polypeptide. It differs from human TGF-beta 1 sequence at positions 9-11,13,19,40,45,52,55,66,66,60,63,76,68,71,75,82,87,95 and 96. Nucleic acid sequence encoding subtype 3 of TGF-beta (TGF-beta 3) is useful as a probe or to produce TGF-beta 3 for both normal and neoplastic cell growth inhibition.
                                                                                                           Nucleotide sequence encoding transforming growth factor beta-3 used as a probe, or to produce TGF beta 3, for inhibiting growth of certain normal and neoplastic cells, eg A549.
                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                        1 ALDINYCFRNLEENCCVRPLYIDFRQDLGWKWVHEPKGYYANFCSGPCPYLRSADTTHST
                                                                                                                                                                                                                                                                             ó
                                                                                                                                                                                                                                                                                                                                61 VLGLYNTLNPEASASPCCVPQDLEPLTILYYVGR¶PKNEQLSNMVVKSCKCS 112
                                                                                                                                                                                                                                                                                                                                           vlglyntlnpeasaspccvpqdlepltilyyvgrtavegisnmvvksckcs 112
                                                                                                                                                                                                                                                          97.9%; Score 621; DB 11; Length 112; 98.2%; Pred. No. 2.6e-55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pig transforming growth factor-beta 3 N-terminal sequence.
                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Transforming growth factor-beta 3; TGF-beta 3; pig.
                                                                                                                                                                                                                                                                          1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                               AAW78783 standard; Protein; 112 AA
                                                                                                                                                Disclosure; Fig. 3; 61pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              87US-0025423.
85US-0715142.
89US-0389929.
92US-0845893.
93US-0147364.
                  88WO-US01945
                                    88WO-UO01945
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                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Goeddel DV;
                                                       (GETH ) GENENTECH INC.
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                                                                         Goeddel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1998-494840/42.
                                                                                          WPI; 1990-007474/01.
                                                                                                                                                                                                                                                                 Best Local Similarity
Matches 110; Conserv
                                                                                                                                                                                                                               112 AA;
                  08-JUN-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Derynck RMA,
                                     08-JUN-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22-MAR-1985;
                                                                         RW,
                                                                                                                                                                                                                                                                                                                                                                                                                                   21-DEC-1998
14-DEC-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US5801231-A.
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05-NOV-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-SEP-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sus scrofa
                                                                                                                                                                                                                                                                                                                                                                                                                 AAW78783;
                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                          Query Match
                                                                         Dernyck
                                                                                                                                                                                                                                                                                                                                                                                     AAW78783
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beta-3 (TGF-beta 3, see also AAW78786). The sequence shows homology to human TGF-beta 3 (see AAW78781), human TGF-beta 3 (see AAW78781), human TGF-beta 3 (see AAW78781) invention TGF-beta 2 (see AAW78784) N-terminal sequences. The invention relates to the recombinant production of TGF-beta. DNA encoding TGF-beta has been isolated and cloned into vectors which are replicated in bacteria and expressed in eukaryotic cells. TGF-beta recovered from transformed cells can be used in known
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 aldtnycfrnleenccvrplyidfrqdlgwkwvhepkgyyanfcsgpcpylrsadtthss 60
      precursor sequence -
to increase yield of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 ALDINYCFRNLEENCCVRPLYIDFRODLGWKWVHEPKGYYANFCSGPCPYLRSADTTHST
                                                                                                                                                                                     This is the amino acid sequence of pig transforming growth factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       encoding transforming growth factor-beta for use in therapeutics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               transforming growth factor beta-3; recombinant; wound healing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 VLGLYNTLNPEASASPCCVPQDLEPLTILYYVGRTPKVEQLSNMVVKSCKCS 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TGF-beta-1; TGF-beta-3; transforming growth factor beta-1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 621; DB 19;
Pred. No. 2.6e-55;
1; Mismatches 1;
DNA encoding transforming growth factor-beta useful for analysis to perform manipulations recombinant production of the protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Fig 5; 25pp; English.
                                                                                                                            Disclosure; Fig 3; 26pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAR46228 standard; Protein; 456
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87US-0025423.
89US-0389929.
92US-0845893.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           97.9%;
98.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 98.2
Matches 110; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                           therapeutic applications.
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Tue Oct 30 12,56:42,2001

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345 aldtnycfrnleenccvrplyidfrqdlgwkwyhepkgyyanfcsgpcpylrsadtths 404
pig TGF-beta-3 (AAQ56925) and human TGF-beta-3 (AAQ56926), and the corresponding amino acid sequences were determined (AAR46227-29, respectively). A genomic fragment corresponding to a human TGF-beta-1 exon (AAQ56924) was also isolated and its amino acid sequence determined (AAR46230). The sequences have been used in the construction of vectors for the expression of recombinant TGF-
                                                                                                                                                             Gaps
                                                                                                                                                                                   9
                                                                                                                                                                                  ALDINYCFRNLEENCCVRPLYIDFRQDLGWKWVHEPKGYYANFCSGPCPYLRSADTTHS#
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA encoding transforming growth factor-beta precursor sequence - useful for analysis to perform manipulations to increase yield of recombinant production of the protein
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                                                                                                                                                                                                                           Length 456;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'note= "alternative N-terminal Met residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'note= "alternative N-terminal Met residue"
                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                Transforming growth factor-beta 3; TGF-beta 3; pig.
                                                                                                                                                            1;
                                                                                                                                  Score 621; DB 15;
Pred. No. 1.3e-54;
1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "encoded by AAC"
                                                                                                                                                                                                                                                                                                                                                                                         Pig transforming growth factor-beta 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers 345..456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /label= Mat_protein
                                                                                                                                                                                                                                                                                                                  AAW78786 standard; Protein; 456 AA
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85US-0715142.
89US-0389929.
                                                                                                                                   97.98;
98.28;
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93US-0147364
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                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                 Query Match
Best Local Similarity 98.2
Matches 110; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Goeddel DV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1998-494840/42.
                                                                                                  AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Misc-difference 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAV52934.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Misc-difference
                                                                                                456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13-MAR-1987;
22-MAR-1985;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Derynck RMA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22-MAR-1985;
                                                                                                                                                                                                                                                                                                                                                                  21-DEC-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Sus scrofa
                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                          AAW78786;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protein
                                                                          beta.
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Tissue-derived growth inhibitor and corresponding genes - useful for detection of tumours, inhibition of tumour growth, treatment of proliferative disorders and healing of burns and wounds.
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         This is the amino acid sequence of the porcine transforming growth factor-beta 3 precursor (preTGF-beta 3), deduced from isolated CDNA sequences (see AAV52934). The invention relates to the recombinant production of TGF-beta. Biologically active TGF-beta is defined as being capable of inducing EGF-potentiated anchorage independent growth of target cell lines and/or growth inhibition oneoplastic cell lines. Nucleic acids encoding TGF-beta have been isolated and cloned into vectors which are replicated in bacteria and expressed in eukaryotic cells. TGF-beta recovered from transformed cells is used in known therapeutic applications.
                                                                                                                                                                                                                                                                                 1 ALDINYCFRNLEENCCVRPLYIDFRQDLGWKWVHEPKGYYANFCSGPCPYLRSADITH$T
                                                                                                                                                                                                                                                     ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tumour growth inhibitor; carcinoma; melanoma; leukaemia;
arteriosclerosis; inflammation; psoriasis; therapy; vulnerary;
                                                                                                                                                                                                                                                                                                                                          Length 456;
                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                      Score 621; DB 19;
Pred. No. 1.3e-54;
1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tissue-derived tumour growth inhibitor-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "peptide CM-1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Stephenson JR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR86770 standard; Protein; 112 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Fig 29; 83pp; English.
                                                                                                                                                                                                                       97.98;
98.28;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LI, Iwata KK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1996-000991/01.
                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                            456 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; AAT06496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      immunomodulator.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20-OCT-1987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20-OCT-1986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12-JUN-1996
                                                                                                                                                                                                                      Query Match
Best Local Simi
Matches 110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EP684260-A2
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                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAR86770;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gold
                                                                                                                                                                                                                                                                                                                                                                                                                                     AAR86770
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However, amino acids 54-93 of the TGI precursor are not provided in the specification. TGI, or its 205 amino acid precursor, can be used to inhibit the growth of human tumour cells, e.g. carcinoma, melanoma or leukaemia cells, in the treatment of proliferative disorders e.g. arteriosclerosis, inflammation and psorliferative disorders e.g. arteriosclerosis, inflammation and healing. The proteins can also be used as immunomodulators. Although the proteins can also be used as immunomodulators. Although the proteins disorder growth inhibitory activity, they are not transforming growth factor-beta-1 or -beta-2. The 20-amino acid peptide CM-1 (as featured) inhibits the growth of human tumour cells but not of a mink lung cell line.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              psoriasis.
                                                                                                                                                                                                                                                                                                                                                                                                                       AAR08264;
                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo
                                                                                                                                                                                                                                                                                                                                                                                  AAR08264
                                                                                                                                                                                                                                                                                                                                                                    RESULT
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0
                                                                                                                                                            Gaps
                                                                                                                                                                                    9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              corresponding genes - useful for
tumour growth, treatment of
of burns and wounds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    residues 54-93 of the precursor protein are not specified "
e.g. arteriosclerosis, inflammation and psoriasis, or for the treatment of burns to facilitate wound healing. TGI can also be used as an immunomodulator. Although the protein has tumour around inhibitory activity, it is not transforming growth factor-beta-1 or -beta-2. The peptide CM-1 (as featured) inhibits the growth of human tumour cells but not of a mink lung cell line.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The sequence represents the precursor of tumor growth inhibitor (TGI) (see AAR86770), which is produced by recombinant DNA methods.
                                                                                                                                                                                1 ALDINYCFRNLEENCCVRPLYIDFRQDLGWKWVHEPKGYYANFCSGPCPYLRSADITHST
                                                                                                                                                                                               .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "tumour growth inhibitor (see AAR86770)
                                                                                                                                                                                                                                                                                                                                                                                                                             Tumour growth inhibitor; carcinoma; melanoma; leukaemia;
arteriosclerosis; inflammation; psoriasis; therapy; vulnerary;
                                                                                                                                                                                                                                  61 VLGLYNTLNPEASASPCCVPQDLEPLTILYYVGRTPKVEQLSNMVVKSCKCS 112
                                                                                                                                                                                                                                                 97.8%; Score 620; DB 17; Length 112; 98.2%; Pred. No. 3.3e-55; Live 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "tumour growth inhibitor precursor" 53..54 /note= "residues 54-93 of the precursor pr
                                                                                                                                                                                                                                                                                                                                                                                                      Tissue-derived tumour growth inhibitor-1 precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "peptide CM-1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tissue-derived growth inhibitor and detection of tumours, inhibition of proliferative disorders and healing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
1..165
                                                                                                                                                                                                                                                                                                                             A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Stephenson JR;
                                                                                                                                                                                                                                                                                                                         AAR86771 standard; Protein; 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 4; Fig 29; 83pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     87EP-0109866
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                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                           Best_Local Similarity 98.2
Matches 110; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (ONCO-) ONCOGENE SCI INC
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62..81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1996-000991/01.
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                                                                                        112 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; AAT06496.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         immunomodulator.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20-OCT-1987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20-0CT-1986;
                                                                                                                                                                                                                                                                                                                                                                            12-JUN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EP684260-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29-NOV-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gold LI,
                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                   AAR86771;
                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Peptide
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Foulkes JG;
                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                   carcinoma; melanoma; leukaemia; arteriosclerosis; inflammation;
                                                                                                1 ALDINYCFRNLEENCCVRPLYIDFRQDLGWKWVHEPKGYYANFCSGPCPYLRSADTTHST
                                                                        ö
                                                                                                                                                    Length 165;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gold LI,
                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Franco R,
                                         Score 620; DB 17;
Pred. No. 5.1e-55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         142..144
/label= n-glycosylation site
158..160
/label= N-glycosylation site.
                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                    74..76
/label= N-glycosylation
0..137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /label- N-glycosylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tendijke P,
                                                                                                                                                                                                                                                        AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                        412
                                         97.8%;
98.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              89US-0353410.
85US-0725003.
86US-0847931.
86US-0992121.
                                                                                                                                                                                                                                                     AAR08264 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    90WO-US02753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    88US-0183224
                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Iwata KK, Stephenson JR,
                                        Query Match 97.8
Best Local Similarity 98.2
Matches 110; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (ONCO-) ONCOGENE SCI INC
                                                                                                                                                                                                                                                                                                                                        Tumour growth inhibitor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1990-375949/50.
N-PSDB; AAQ06845.
165 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Modified-site
                                                                                                                                                                                                                                                                                                            05-MAR-1991
                                                                                                                                                                                                                                                                                                                                                                                                             sapiens
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19-APR-1985;
07-APR-1986;
20-OCT-1986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17-MAY-1990;
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20-APR-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO9014360-A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleotide sequence encoding transforming growth factor beta-3 used as a probe, or to produce TGF beta 3, for inhibiting growth of certain normal and neoplastic cells, eg A549.
                                                                                                                                                                                                                                                                                                                                                                                              A plasmid carrying DNA encoding the TGI was isolated from a human cDNA library prepd. from the DNA of a chronic myelocytic leukaemia cell line (K562). The sequence can be used to produce the TGI by recombinant techniques. The protein may also be isolated from human umbilical cord and placental tissues. It can be used to inhibit tumour cell growth, to treat burns, to facilitate the healing of wounds or to treat proliferative disorders. The protein and Abs raised to it can be used for detection and typing of tumours. The Abs can also be used to inhibit the activity of the TGI.
                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                             1 ALDINYCFRNLEENCCVRPLYIDFRQDLGWKWVHEPKGYYANFCSGPCPYLRSADTTHST 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Transforming growth factor beta-3 (TGF beta 3); tumour cells; growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequence is that of human transforming growth factor-beta 3
                                                                                                                                                                                                                                                                                                                                                 ó
Tissue-derived tumour growth inhibitors - comprise specified protein sequences used to detect, and treat tumours, burns and
                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 VLGLYNTLNPEASASPCCVPQDLEPLTILYYVGRTPKVEQLSNMVVKSCKCS 112
                                                                                                                                                                                                                                                                                                          Score 617; DB 11; Length 412;
Pred. No. 2.9e-54;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Fig. 3; 61pp; English.
                                                              Claim 10; Fig 41; 190pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR04077 standard; protein; 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence of human TGF-beta 3.
                                                                                                                                                                                                                                                                                                             Query Match 97.3%;
Best Local Similarity 97.3%;
Matches 109; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            88WO-UO01945
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Goeddel DV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1990-007474/01.
                                                                                                                                                                                                                                                              412 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          08-JUN-1988;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31-MAY-1989
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              inhibition.
                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAR04077;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This
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Sequence

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                              Gaps
                                                                          1 ALDINYCFRNLEENCCVRPLYIDFRODLGWKWVHEPKGYYANFCSGPCPYLRSADTTHST 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New hybrid transforming growth factor-beta molecules - comprise portions of mature TGF-beta isoforms; useful as wound healants, cardioprotective, antiinflammatory and immunosuppressive agents
                              ;
                                                                                                                                 61 VLGLYNTLNPEASASPCCVPQDLEPLTILYYVGRTPKVEQLSNMVVKSCKCS 112
 Length 112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "amino acids 45-112 of hTGF-beta3"
                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "amino acids 1-44 of hTGF-beta1"
                                                                                                                                                                                                                                                                                                                                          hTGF-betal; hTGF-beta3; hybrid protein; wound healing;
                                                                                                                                                                                                                                                                                                               Transforming Growth Factor-betal(44/45)beta3 hybrid.
                                                                                                                                                                                                                                                                                                                                                           cancer treatment; bone repair; growth regulation.
Score 612; DB 11;
Pred. No. 2.1e-54;
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                              1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 8; Page 26-27; 48pp; English.
                                                                                                                                                                                                                        AAR39642 standard; Protein; 112 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cerletti N,
 96.5%;
97.3%;
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                                                                                                                                                                                                                                                                                   (first entry)
                              Matches 109; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                               45..112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1993-161126/20.
             Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        McMaster GK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 03-NOV-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11-NOV-1991;
                                                                                                                                                                                                                                                                                  26-AUG-1993
                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EP542679-A.
                                                                                                                                                                                                                                                     AAR39642;
 Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
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1 ALDTNYCFRNLEENCCVRPLYIDFRQDLGWKWVHEPKGYYANFCSGPCPYLRSADTTHST
                                                                                                               61 vlglyntlnpeasaspccvpqdlepltilyyvgrtpkveqlsnmvvksckcs 112
                                                                                         61 VLGLYNTLNPEASASPCCVPQDLEPLTILYYVGRTPKVEQLSNMVVKSCKCS 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Prodn. of dimeric, biologically active transforming growth beta - by refolding denatured monomer in buffer contg. mild detergent and specific organic solvents to improve yields
                                                                                                                                                                                                                                                                                                                                                                                                         Transforming growth factor beta; TGF; regulator; method; proliferation; differentiation; wound healing; solvent.
                                                                                                                                                                                                                                                                                                                                                                 Human TGF-beta-like protein, TGF-beta-1-3.
                                                                                                                                                                                                                                       AAR91959 standard; Protein; 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (CIBA ) CIBA GEIGY AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1996-116999/12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; AAT15465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                        10-JUN-1996
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                                                                                                                                                                                                                                                                               AAR91959;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Peptide
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                                                                                                                                                                                                                   AAR91959
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                                                                                     9
                                                 Gaps
                                                                                                      1 ALDTNYCFRNLEENCCVRPLYIDFRQDLGWKWVHEPKGYYANFCSGPCPYLRSADTTHST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Prodn. of dimeric biologically active transforming growth factor by refolding denatured monomer in detergent-free folding buffer contg. specific organic solvent to improve yield
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   45..112
/note= "amino acids 45-112 of human TGF-beta3"
                                                                                                                                                                  61 VLGLYNTLNPEASASPCCVPQDLEPLTILYYVGRTPKVEQLSNMVVKSCKCS 112
                                                                                                                                                                                          1..33
/note= "amino acids 1-44 of human TGF-betal"
    Length 112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Transforming growth factor type beta; TGF-beta 1; TGF-beta protein renaturation; protein folding.
                                            Indels
  DB 14;
Score 595; DB 14,
Pred. No. 1.1e-52
                                          5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 10; Page 36-37; 54pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                               AAR92775 standard; Protein; 112 AA
93.8%;
92.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95WO-EP02719
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                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                          Matches 104; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1996-117000/12.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Hybrid TGF-beta 1-3.
                   Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic
                                                                                                                                                                                                                                                                                                                                                        AAR92775;
  Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Key
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AAR9277
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/note= "N-terminal 44 amino acids

Location/Qualifiers

AA

(first entry)

TGF-beta-1"

45..112

amino acids of

/note= "C-terminal 68 TGF-beta-3"

94EP-0810438 95WO-EP02718

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AAR91959 is transforming growth factor (TGF) beta-like protein, TGF-beta-1-3. TGF beta-1-3 is a hybrid of TGF-1 and TGF-3. TGF beta bybrids were made using a new process of producing dimeric, biologically active TGF beta-like proteins. The new process involves treating denatured TGF beta-like proteins. The new process involves treating denatured TGF beta-like proteins. The new process involves treating denatured TGF beta-like proteins at least one of the solvents DMSO (dimethyl sulphoxide), DMSOS (dimethylsulphone) and DMF (dimethyl formamide). The detergent allows folding of the monomer such that, after dimerisation, the TGF beta-like protein retains biological activity and remains in soluble form. The method allows relatively high yields of biologically active TGF beta-like proteins in their native dimeric form. TGF-beta like proteins are multifunctional by allows the protein activity and a typical use is to stimulate wound
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 595; DB 17;
Pred. No. 1.1e-52;
Claim 17; Page 40-41; 59pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     93.8%;
92.9%;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Seguence
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Gaps

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Query Match 93.8 Best Local Similarity 92.9 Matches 104; Conservative

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Gaps

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Indels

3;

Mismatches

5;

Conservative

Matches 104;

61 VLGLYNTLNPEASASPCCVPQDLEPLTILYYVGRTPKVEQLSNMVVKSCKCS 112

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention covers hybrid TGF-beta molecules consisting of parts of the human isoforms TGF-beta1, TGF-beta2 and TGF-beta3 (see AAQ41599, AAQ41601, respectively). The hinge points between parts derived from different parent isoforms are pref. between amino acids 44 and 45, 56 and 57, 79 and 80, 90 and 91, or 22 and 23. Of the 30 possible hybrids using these hinge points and one part each from two of the isoforms, 6 are preferred including the hybrid TGF-beta2(44/45)beta3. The hybrid molecules promote cell migration, inhibit the growth of A375 melanoma cells, accelerate the healing of partial-thickness burn wounds and full-thickness incisional wounds and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cardioprotective, antiinflammatory and immunosuppressive agents etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New hybrid transforming growth factor-beta molecules - comprise portions of mature TGF-beta isoforms; useful as wound healants,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
61 vlg1yntlnpeasaspccvpqdlepltilyyygrtpkveq1snmvvksckcs 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 112;
                                                                                                                                                                                                                                                                                                                            45..112
/note= "amino acids 45-112 of hTGF-beta3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                           /note= "amino acids 1-44 of hTGF-beta2"
                                                                                                                                                                                                       hTGF-beta2; hTGF-beta3; hybrid protein; wound healing;
                                                                                                                                                                          Transforming Growth Factor-beta2(44/45)beta3 hybrid.
                                                                                                                                                                                                                         cancer treatment; bone repair; growth regulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 591; DB 14;
Pred. No. 2.7e-52;
7; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            increase formation of fibrous granular tissue.
See AAQ41602-Q41607 for the most pref. hybrids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kuhla J;
                                                                                                                                                                                                                                                                                   Socation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 8; Page 29-30; 48pp; English.
                                                                                  AAR39644 standard; Protein; 112 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cerletti N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       93.2%;
91.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                    92EP-0810845.
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                                                                                                                                                (first entry)
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Best Local Similarity 91.1
Matches 102; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GEIGY AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cox D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1993-161126/20.
N-PSDB; AAQ41605.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         112 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            McMaster GK,
                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (CIBA ) CIBA
                                                                                                                                                                                                                                                                                                                                                                                                                                  03-NOV-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                11-NOV-1991;
                                                                                                                                              26-AUG-1993
                                                                                                                                                                                                                                                                                                                                                                                                     19-MAY-1993
                                                                                                                                                                                                                                                                                                                                                                         EP542679-A.
                                                                                                                 AAR39644;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                              Region
                                                                                                                                                                                                                                                                                                                             Region
                                                                    AAR39644
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AAR91960 is transforming growth factor (TGF) beta-like protein, TGF-beta-2-3. TGF beta-2-3 is a hybrid of TGF-2 and TGF-3. TGF beta bybrids were made using a new process of producing dimeric, biologically active TGF beta-like proteins. The new process involves treating denatured TGF beta-like proteins. The new process involves treating denatured TGF beta-like proteins. The new process involves treating denatured TGF beta-like protein a least one of the solvents DMSO (dimethyl sulphoxida), DMSO2 (dimethylsulphone) and DMF (dimethyl formamide). The detergent allows folding of the monomer such that, after dimerisation, the TGF beta-like protein retains biological activity and remains in soluble form. The method allows relatively high yields of biologically active TGF beta-like proteins in their native dimeric form. TGF-beta like proteins are multifunctional regulators of cellular activity and a typical use is to stimulate wound
                              9
 9
               1 ALDTNYCFRNLEENCCVRPLYIDFRQDLGWKWVHEPKGYYANFCSGPCPYLRSADTTHST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Prodn. of dimeric, biologically active transforming growth factor beta - by refolding denatured monomer in buffer contg. mild detergent and specific organic solvents to improve yields
                                                                          61 VLGLYNTLNPEASASPCCVPQDLEPLTILYYVGRTPKVEQLSNMVVKSCKCS 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 112;
                                                                                                                                                                                                                                                                                            rowth factor beta; TGF; regulator; method; differentiation; wound healing; solvent.
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                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "C-terminal 68 amino acids TGF-beta-3"
                                                                                                                                                                                                                                                                                                                                                                                                   /note= "N-terminal 44 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 591; DB 17;
Pred. No. 2.7e-52;
                                                                                                                                                                                                                                                            Human TGF-beta-like protein, TGF-beta-2-3.
                                                                                                                                                                                                                                                                                          Transforming growth factor beta; TGF;
                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                 TGF-beta-2"
                                                                                                                                                                     Ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 17; Page 43; 59pp; English.
                                                                                                                                                                 AAR91960 standard; Protein; 112
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91.1%;
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                                                                                                                                                                                                                              (first entry)
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                        proliferation;
                                                                                                                                                                                                                                                                                                                                        Homo sapiens
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tgfb3p.rag

Matches

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The invention covers hybrid TGF-beta molecules consisting of parts of the human isoforms TGF-beta1, TGF-beta2 and TGF-beta3 (see AAQ41509, AAQ41600 and AAQ41601, respectively). The hinge points between parts derived from different parent isoforms are pref. between amino acids 44 and 45, 56 and 57, 79 and 80, 90 and 91, or 22 and 23. Of the 30 possible hybrids using these hinge points and one part each from two of the isoforms, 6 are preferred including the hybrid TGF-beta3(44/45)beta2. The hybrid molecules promote cell migration, inhibit the growth of A375 melanoma cells, accelerate the healing of partial-thickness burn wounds and full-thickness incisional wounds and increase formation of fibrous granular tissue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 ALDITNYCFRNLEENCCVRPLYIDFRQDLGWKWVHEPKGYYANFCSGPCPYLRSADTTHST 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New hybrid transforming growth factor-beta molecules - comprise portions of mature TGF-beta isoforms; useful as wound healants, cardioprotective, antiinflammatory and immunosuppressive agents etc.
   1 aldaaycfrnvqdncclrplyidfkrdlgwkwihepkgynanfcsgpcpylrsadtthst
                                     ch 91.0%; Score 577; DB 14; Length 112; 1 Similarity 88.4%; Pred. No. 6.9e-51; 99; Conservative 7; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "amino acids 45-112 of hTGF-beta2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                1..44
/note= "amino acids 1-44 of hTGF-beta3"
45..112
                                                                                                                                                                                                                                                                                                                              hTGF-beta2; hTGF-beta3; hybrid protein; wound healing; cancer treatment; bone repair; growth regulation.
                                                                                                                                                                                                                                                                                          Transforming Growth Factor-beta3(44/45)beta2 hybrid.
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                                                                                                                                                                             Ä.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cerletti N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 8; Page 32; 48pp; English.
                                                                                                                                                                         AAR39646 standard; Protein; 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        92EP-0810845.
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                                                                                                                                                                                                                                                     (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1993-161126/20.
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                                                                                                                                                                                                                                                     26-AUG-1993
                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11-NOV-1991;
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Best Local S
Matches 99
                                                                                                                                                                                                             AAR39646;
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 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                 1 ALDINYCFRNLEENCCVRPLYIDFRQDLGWKWVHEPKGYYANFCSGPCPYLRSADTTHST 60
                                                         Prodn. of dimeric biologically active transforming growth factor by refolding denatured monomer in detergent-free folding buffer contg. specific organic solvent to improve yield
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                                                                                                          61 VLGLYNTLNPEASASPCCVPQDLEPLTILYYVGRTPKVEQLSNMVVKSCKCS 112
                                                                                                                                  Transforming growth factor type beta; TGF-beta 2; TGF-beta 3; protein renaturation; protein folding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "amino acids 1-44 of human TGF-beta2"
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 3;
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Pred. No. 2.7e-52;
7; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                               AAR92776 standard; Protein; 112 AA
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91.1%;
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                                                                                                                                                                                                                                                                                                                                                               Hybrid TGF-beta 2-3
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Synthetic

Protein Protein

AAR92776;

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ALDINYCFRNLEENCCVRPLYIDFRQDLGWKWVHEPKGYYANFCSGPCPYLRSADTTHST 

Sequence

Query Match Best Local S

Matches

1 aldtnycfrnleenccvrplyidfrqdlgwkwvhepkgyyanfcagacpylwssdtqhsr 60

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AAR91961 is transforming growth factor (TGF) beta-like protein, TGF-beta-3-2. TGF beta-3-2 is a hybrid of TGF-3 and TGF-2. TGF beta hybrids were made using a new process of producing dimeric, blologically active TGF beta-like proteins. The new process involves treating denatured TGF beta monomers with folding buffer contg. a mild detergent (CHAPS, CHAPSO or digitonin) and at least one of the solvents DMSO (dimethyl sulphoxide), DMSO2 (dimethylsulphone) and DMF (dimethyl formamide). The detergent allows folding of the monomer buch that, after dimerisation, the TGF beta-like protein retains blological activity and remains in soluble form. The method allows relatively high yields of biologically active TGF beta-like proteins in their native dimeric form: TGF-beta like proteins are multifunctional requirators of cellular activity and a typical use is to stimulate wound
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Prodn. of dimeric, biologically active transforming growth factor
beta - by refolding denatured monomer in buffer contg. mild detergent and specific organic solvents to improve yields
                                                                                                                                                                                                                     method;
                                                                                                                                                                                                                 Transforming growth factor beta; TGF; regulator; method
proliferation; differentiation; wound healing; solvent.
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                                                                                                                                                                                                                                                                                                                  /note= "N-terminal 44 amino acids TGF-beta-3"
                                                                                                                                                                                                                                                                                                                                                                  amino acids
                                                                                                                                                                                      Human TGF-beta-like protein, TGF-beta-3-2.
                                                                                                                                                                                                                                                                                                                                                            /note= "C-terminal 68
TGF-beta-2"
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                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                 AAR91961 standard; Protein; 112 AA.
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N-PSDB; AAT15467.
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                                                                                                                               AAR91961;
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                                                                                                                                                                                                                                                                                                      Peptide
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                                                                       37
                                                                                                                                                                                                                                                                                          Key
                                                                                        AAR91961
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growth factor-beta, TGF-beta 3 (see also AAR92777), is composed of the N-terminal portion of TGF-beta 3 (see also AAR92777), is composed of the portion of TGF-beta 2 (see also AAR92774). It was produced by E. coli LC37 transformants carrying plasmid ppLMu-TGF-beta3/44/45) beta2, which includes a coding sequence (AAT17239) for the hybrid. A lologically active, dimeric form of TGF-beta3-z was oblid. By refolding the monomer in detergent-free buffer contg. DMSO and/or DMF. Hybrid dimers TGF-beta 1-3 (AAR92775) and TGF-beta 2-3 (AAR92776) were
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 ALDINYCFRNLEENCCVRPLYIDFRQDLGWKWVHEPKGYYANFCSGPCPYLRSADTTHST 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A recombinant, non-soluble, monomeric hybrid of human transforming
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              growth factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Prodn. of dimeric biologically active transforming growth factor by refolding denatured monomer in detergent-free folding buffer contg. specific organic solvent to improve yield
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
/note= "amino acids 45-112 of human TGF-beta2"
                                                                                                                                                                                                Transforming growth factor type beta; TGF-beta 2; TGF-beta 3; protein renaturation; protein folding.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 577; DB 17;
Pred. No. 6.9e-51;
7; Mismatches 6;
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                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                              AA.
                                                                                         AAR92777 standard; Protein; 112
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Best Local Similarity 88.4%;
Matches 99; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1996-117000/12.
                                                                                                                                                                         Hybrid TGF-beta 3-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               similarly produced.
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                                                                                                                                                                                                                                                                                                                                                                                                 12-JUL-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                           25-JUL-1994;
                                                                                                                                             17-JUL-1996
                                                                                                                                                                                                                                                                                                                                                                       08-FEB-1996,
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                                                                                                                                                                                                                                       Synthetic
                                                                                                                     AAR92777;
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Score 577; DB 17; Length 112; Pred. No. 6.9e-51; 7; Mismatches 6; Indels -

91.0%; ilarity 88.4%; Conservative 7

Query Match Best Local Similarity

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Matches

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1 ALDINYCFRNLEENCCVRPLYIDFRQDLGWKWVHEPKGYYANFCSGPCPYLRSADTTHST 60

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WPI; 1999-244023/20
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                                                                                          15-SEP-1998;
                                                                                                            16-SEP-1997;
                                     Unidentified
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                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Growth factor; GF; persephin; neuron growth; cellular degeneration;
peripheral neuropathy; amyotrophic lateral sclerosis; ischemic stroke;
Alzheimer's disease; Parkinson's disease; Huntington's disease; trauma;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15 CCVRPLYIDFRQDLGWKWVHEPKGYYANFCSGPCPYLRSADTTHSTVLGLYNTLNPEASA
                                                                                                                                                                                                                                                                                Recombinant truncated transforming growth factor-beta analogues capable of inducing an anti-proliferative effect in mammalian epithelial cells in vitro
                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
                                                                                                                                                                                                                                                                                                                                    This sequence is an example of a highly generic protein (see AAR11954). It can be used to control proliferation of tumour ce or for enhancing growth rate of T and B-lymphocytes in immunosuppressed patients. The first 5 N-terminal residues can
61 vlslyntinpeasaspccvsqdlepltilyyigktpkieqlsnmivksckcs 112
                                                                                                                                                                                                                                                                                                                                                                                                                              Length 98;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                      9.7e-49;
                                                                                                                                                                                                                                                                                                                                                                                                                              DB 12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Pred. No. 9.7 ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                              Score 555;
                                                                                                                  Transforming Growth Factor beta; AIDS.
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                                                                                                                                                                                                                                                                                                                   Claim 12; Page 27; 42pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                             87.5%;
                                            AAR11944 standard; Protein;
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                                                                                                                                                                                                                            (CREA-) CREATIVE BIOMOLECUL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY16699 standard; Peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 87.5
Best Local Similarity 100.
Matches 98; Conservative
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                                                                                                 Truncated TGF-beta #3
                                                                                                                                                                                                                                                               WPI; 1991-148530/20.
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                                                                                23-JUL-1991
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                                                                                                                                                                       02-MAY-1991
                                                                                                                                    Synthetic.
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                                                              AAR11944;
                                                                                                                                                                                                                                              Cohen CM;
                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
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ID AAY1
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DT 17-A
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KW Grow
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The invention relates to a novel isolated and purified growth factor (GF) that comprises persephin or a fragment or a conservatively substituted variant. The persephin GF polypeptides can promote the survival and growth of neurons and non-neuronal cells. The persephin GF polypeptides or polynucleotides can be used for preventing or treating cellular degeneration or insufficiency, e.g. neuronal degeneration resulting from peripheral neuropathy, amyotrophic lateral sclerosis, Alsheimer's disease, Parkinson's disease, Huntington's disease, ischemic stroke, acute brain injury, acute spinal cord injury, nervous system tumours, acute brain injury, acute spinal cord injury, nervous system tumours, consulting from eosinopenia, anemias, thrombocytopenia, or stem cell insufficiences, cardiac muscle degeneration or insufficiency resulting from eosinopenia, anemias, thrombocytopenia, or stem cell insufficiences, cardiac muscle degeneration or insufficiency resulting from eosinopenia, anemias, thrombocytopenia, or stem cell insufficiences, cardiac muscle degeneration or insufficiency resulting from eosinopenia, and injury, exposure to be used for treating agents and damage caused by infectious agents. The GF can also be used for condition mediated by expression of persephin by a population of cells.

The products can also be used for detection and diagnosis.
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brain injury; spinal cord injury; nervous system tumour; infection; multiple sclerosis; cardiac muscle degeneration; injury;neurotoxin; metabolic disease; diabetes; renal dysfunction; neurturin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated persephin growth factor nucleic acids used to, e.g. promote neuronal growth
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Klein R, Kotzbauer PT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 176-177; 222pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                              98WO-US19163.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           97US-0931858
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Desauvage F, Johnson EM,
Lampe PA, Milbrandt JD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 100.
Matches 98; Conservative
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The invention relates to mutant TGF-beta (transforming growth factorbeta) superfamily members. These mutants comprise one or more amino acid substitutions in the base region of the finger 2 subdomain, and a cretarinal residue selected from Arg, Ile, Ieu, Ser and Ala. In the finger 2 subdomain, basic residues (e.g., Glu, Ser, Iys), or residues containing an amide group (e.g., Gln, Asp), are substituted with acidic containing an amide group (e.g., Glu, Asp), are substituted with acidic residues (e.g., Thr). TGF-beta superfamily proteins containing a hydroxyl group (e.g., Ser, Thr). TGF-beta superfamily proteins regulate developmental content or proteins such as the osteogenic proteins (OPS), bone morphogenetic proteins such as the osteogenic proteins (OPS), compassed by the invention are the finger 2 subdomain mutants of human osteogenic protein- (OP-1) (AAB09576-B09615). Mutant TGF-beta proteins care used for inducing tissue morphogenesis in bon- non-mineralised skeletal tissue, dental tissue, connective tissue, brain, liver and nerve consective dental tissue, connective tissue, brain, liver and nerve connective tissue can be used in conjunction with a biocompatible matrix e.g., collagen, hydroxyapatite or carboxymethylcellulose for regenerating bone, cartilage and/or other mineralised skeletal or regenerating band intervertebral discs. The OP-1 mutants can be used to repair capsule and intervertebral discs. The OP-1 mutants can be used to repair connective fissues e.g., ligament, tendon, muscle, fibrocartilage, discassed or damaged mammalian tissue mediated tissue damaged mammalian tissue end to prevent or substantially file to reponse mediated tissue damaged and and substantially filesues e.g., ligament endon to prevent or substantially filesues e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tissue formation following an injury. Compared to the wild-type TGF-beta superfamily members, the mutant proteins have improved in vitro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Transforming growth factor-beta superfamily member mutant induces tissue morphogenesis in e.g. bone, non-mineralized skeletal tissue, dental tissue and connective tissue and comprises a substitution in a region of the finger 2 domain -
TGF-beta superfamily; transforming growth factor-beta; developmental regulation; finger 2 subdomain; basic region; protein refolding; stability; solubility; osteogenic protein; OP; bone morphogenetic protein; BMP; growth/differentiation factor; GDF; inhibin; tissue morphogenesis; regeneration; bone; dental tissue; connective tissue; cartilage; vulnerary.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                refolding properties in a pH range of 6-9, increased solubility in aqueous solution and improved stability and/or activity. Sequences AAB09519-B09542 and AAB09553-B0958 represent a variety of wild-type TGF-beta superfamily proteins referred to in the specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 14; Page 141; 162pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             McCartney J;
                                                                                                                                                                                                                                                                                                                                                                            99WO-US23371.
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99US-0374958
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                                                                                                                                                                                                      Homo sapiens.
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15 CCVRPLYIDFRQDLGWKWVHEPKGYYANFCSGPCPYLRSADTTHSTVLGLYNTLNPEASA 74

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SPCCVPQDLEPLTILYYVGRTPKVEQLSNMVVKSCKCS 112 75

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The present invention describes a tumour growth factor beta (TGF-beta)

Superfamily chimeric protein (I) derived from at least 2 different

members of the superfamily comprising a dimer with one monomer that

contains a finger 2 domain derived from a first family member and a

finger 1 domain and heel domain, both derived from a second family

member. The monomer further comprises a conserved c-terminal cysteine

skeleton. (I) has osteogenic, proliferative and antiinflammatory

cutivities. The TGF-beta superfamily chimeric proteins (I) are useful

cotivities. The TGF-beta superfamily chimeric proteins (I) are useful

crimicalised skeletal tissue, dental tissue, connective tissue,

non-mineralised skeletal tissue, dental tissue, connective tissue,

brain, liver and nerve and for inducing the proliferation and

differentiation of uncommitted progenitor cells in a tissue-specific

manner to support new tissue formation. AAA29807 and AAB02748

to AAB02824 represent sequences used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel TGF-beta superfamily mutant chimeric protein, useful for inducing tissue morphogenesis in e.g. bone, comprises a dimer consisting of one monomer containing domains from two family members
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                       Tumour growth factor beta; TGF-beta; morphogenic protein; BMP; OP; bone morphogenic protein; osteogenic protein; mutant; modified; finger 2 sub-domain; finger 1 domain; heel domain; chimeric protein; osteogenic; proliferative; antiinflammatory; tissue morphogenesis; tissue repair; regeneration; proliferation; differentiation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                     Human TGF-beta3 amino acid sequence SEQ ID NO:42.
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100.0%; Pred. No. 9.7e-49;
tive 0; Mismatches 0;
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AAB02787 standard; Protein; 98
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99US-0374936.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     (STYC ) STRYKER CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2000-303776/26.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             present invention.
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                                                                                                                                                                                                                                                                                     WO200020591-A2.
                                                                                                                                                                                                                                                    Homo sapiens.
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16-AUG-1999;
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75 SPCCVPQDLEPLTILYYVGRTPKVEQLSNMVVKSCKCS 112 

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Superfamily members. These sequences can be used to form novel fusion superfamily members. These sequences can be used to form novel fusion proteins. Owner proteins copmrise biologically active TGF-beta family member fusion proteins competent to refold under suitable refolding conditions. The fusion proteins comprise; (1) a TGF-beta family protein conditions. The fusion proteins comprising finger 1, finger 2 and heel subdomains; and (2) a heterologus leader sequence domain operatively linked to the C-terminal domain. Truncations, heterodimers and mutants of these fusion proteins and methods of purifying the heterodimers are also claimed. The TGF-beta family proteins can be used to induce the full cascade of morphogenic events which culminate in skeletal tissue full cascade of morphogenic events which culminate in skeletal tissue seful in the binding cartilage and endochoronal bone formation. They are useful in the binding of fibrin and fibronectin to the implanted matrix, chemotaxis of cells, proliferation of fibricals invasion, bone formation into chondroblasts, cartilage formation, vascular invasion, bone formation in remodeling, and bone marrow differentiation. The proteins have improved physical properties such as solubility and stability, improved target in caractivity, including altered receptor binding and improved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A biologically active TGF-beta family member fusion protein competent to refold, comprising a C-terminal linked TGF-beta family protein
                                                                                                                                                                           finger domain; heel region; BMP; TGF-beta family; protein refolding; fusion protein; osteopathic; antibacterial; cytostatic.
                                                                                                                                       TGB-beta 3 finger-1-heel-finger-2 sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 138-139; 160pp; English.
                                                                                                                                                                                                                                                                     Location/Qualifiers
                                AAY92556 standard; peptide; 98 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          McCartney J;
                                                                                                                                                                                                                                                                                                                                                       65..94
/label= finger_2
                                                                                                                                                                                                                                                                                     2..29
/label= finger_1
                                                                                                                                                                                                                                                                                                                        35..62
/label= heel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99WO-US23372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98US-0103418.
99US-0375333.
                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         targeting capabilities.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tai M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (STYC ) STRYKER CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2000-303743/26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98 AA;
                                                                                                                                                                                                                                                                                                                                                                                                            WO200020449-A2
                                                                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 07-OCT-1998;
16-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Oppermann H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                07-0CT-1999;
                                                                                                        10-AUG-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                               13-APR-2000
                                                                     AAY92556;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                     Domain
                                                                                                                                                                                                                                                                                                                      Region
                                                                                                                                                                                                                                                                                                                                                         Domain
RESULT 43
                    AAY92556
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45..112 /note= "amino acids 45-112 of hTGF-beta2"

Kuhla J;

Cerletti N,

Cox D,

McMaster GK,

WPI; 1993-161126/20. N-PSDB; AAQ41602.

(CIBA ) CIBA GEIGY AG.

92EP-0810845. 91EP-0810870

03-NOV-1992; 11-NOV-1991;

19-MAY-1993 EP542679-A.

/note= "amino acids 1-44 of hTGF-betal"

Location/Qualifiers

Homo sapiens

Region Region

hTGF-betal; hTGF-beta2; hybrid protein; wound healing; cancer treatment; bone repair; growth regulation.

Growth Factor-betal(44/45)beta2 hybrid.

Transforming 26-AUG-1993

(first entry)

AAR39641 standard; Protein; 112 AA.

AAR39641;

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The invention covers hybrid TGF-beta molecules consisting of parts of the human isoforms TGF-beta1, TGF-beta2 and TGF-beta3 (see AAQ4159), AAQ41600 and AAQ41601, respectively). The hinge points between parts derived from different parent isoforms are pref. between amino acids 44 and 45, 56 and 57, 79 and 80, 90 and 91, or 22 and 23. Of the 30 possible hybrids formed using these hinge points and one part each from two of the isoforms, 6 are preferred including the hybrid TGF-beta1(44/45)beta2. The hybrid molecules promote cell migration, inhibit the growth of A375 melanoma cells, accelerate the healing of partial-thickness burn wounds and full-thickness incisional wounds and full-thickness incisional wounds and increase formation of fibrous granular tissue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New hybrid transforming growth factor-beta molecules - comprise portions of mature TGF-beta isoforms; useful as wound healants, cardioprotective, antiinflammatory and immunosuppressive agents etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 ALDINYCFRNLEENCCVRPLYIDFRQDLGWKWVHEPKGYYANFCSGPCPYLRSADTIHST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 539; DB 14;
Pred. No. 4.6e-47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              85.0%; Sco...
81.2%; Pred. No. ...
... 12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 8; Page 25-26; 48pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    112 AA;
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Best Local Si
Matches 91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Seguence
A PART OF THE FERRICA STANDARD STANDARD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    δ
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Query Match Best Local 8

Best Loc Matches

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A substantially pure polypeptide composition having AA sequence given in AAP80462 is claimed. Also claimed is a polypeptide comprising AA sequence of at least eight AAS included in the sequence in AAP80462. The eight polypeptide (designated TGF-beta2) may be used in the treatment of hormonally responsive carcinomas. The TGF-beta2 and fragments can also be used in diagnostics.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 ALDTNYCFRNLEENCCVRPLYIDFRQDLGWKWVHEPKGYYANFCSGPCPYLRSADTTHST 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence from which new transforming growth factor polypeptide(s)
61 VLGLYNTLNPEASASPCCVPQDLEPLTILYYVGRTPKVEQLSNMVVKSCKCS 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New transforming growth factor polypeptide(s) - used for treating hormonally responsive carcinoma(s), prodn. antibodies and in diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGF-beta2; biologically active protein production.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          84.4%; Score 535; DB 9; L
79.5%; Pred. No. 1.2e-46;
ive 14; Mismatches 9;
                                                                                                                                                                                                                                                                                      Carcinoma treatment; tumour treatment.
                                                                                                                  Ā
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lioubin MN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR12403 standard; Protein; 112 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Transforming Growth Factor beta 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 10; Page 14; 17pp; English.
                                                                                                              AAP80462 standard; Protein; 112
                                                                                                                                                                                                                                                                                                                                                                                                       88EP-0107174
                                                                                                                                                                                                                                                                                                                                                                                                                                           87US-0115776.
87US-0046846.
                                                                                                                                                                                         (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 84.4
Best Local Similarity 79.5
Matches 89; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Marquardt H, Ikeda T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1988-316293/45.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    112 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (ONCO-) ONCOGEN.
                                                                                                                                                                                                                                                                                                                                                                                                       04-MAY-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                             30-OCT-1987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 04-MAY-1987;
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                                                                                                                                                                                                                                                     are derived
                                                                                                                                                                                                                                                                                                                          EP290012-A.
                                                                                                                                                    AAP80462;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAR12403;
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                                                                             RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention covers hybrid TGF-beta molecules consisting of parts of the human isoforms TGF-beta1, TGF-beta2 and TGF-beta3 (see AAQ1599, AAQ41600, and AAQ41601, respectively). The hinge points between parts derived from different parent isoforms are pref. between amino acids 44 and 45, 56 and 57, 79 and 80, 90 and 91, or 22 and 23. Of the 30 possible hybrids using these hinge points and one part each from two of the isoforms, 6 are preferred including the hybrid TGF-beta3 (44/45)beta1. The hybrid molecules promote cell migration, inhibit the growth of A375 melanoma cells, accelerate the healing of partial-thickness burn wounds and full-thickness incisional wounds and full-takes formation of fibrous granular tissue. See AAQ41602-Q41607 for the most pref. hybrids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 ALDINYCFRNLEENCCVRPLYIDFRQDLGWKWVHEPKGYYANFCSGPCPYLRSADTTHST 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 aldtnycfrnleenccvrplyidfrqdlgwkwvhepkgyyanfclgpcpyiwsldtgysk 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New hybrid transforming growth factor-beta molecules - comprise portions of mature TGF-beta isoforms; useful as wound healants, cardioprotective, antiinflammatory and immunosuppressive agents etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
0
             61 VLGLYNTLNPEASASPCCVPQDLEPLTILYYVGRTPKVEQLSNMVVKSCKCS 112
                               61 vlslyntinpeasaspccvsqdlepltilyyjgktpkieglsnmivksckcs 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "amino acids 45-112 of hTGF-betal"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "amino acids 1-44 of hTGF-beta3"
45..112
                                                                                                                                                                                                                                                                                                  hTGF-betal; hTGF-beta3; hybrid protein; wound healing; cancer treatment; bone repair; growth regulation.
                                                                                                                                                                                                                                                                 Transforming Growth Factor-beta3(44/45)betal hybrid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 538; DB 14;
Pred. No. 5.8e-47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kuhla J;
                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                  ¥Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 8; Page 30-31; 48pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cerletti N,
                                                                                                                                              AAR39645 standard; Protein; 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 92EP-0810845.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 84.9%;
Best Local Similarity 83.9%;
Matches 94; Conservative
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                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cox D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1993-161126/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             112 AA;
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McMaster GK,

03-NOV-1992; 11-NOV-1991;

19-MAY-1993 EP542679-A.

Homo sapiens

Region Region

26-AUG-1993

AAR39645;

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Gaps

; 0

51 VLGLYNTLNPEASASPCCVPQDLEPLTILYYVGRTPKVEQLSNMVVKSCKCS 112

Sequence

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Length 112; Indels

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The invention covers hybrid TGF-beta molecules consisting of parts of the human isoforms TGF-beta1, TGF-beta2 and TGF-beta3 (see AAQ41599, AAQ41601, respectively). The hinge points between parts derived from different parent isoforms are pref. between amino acids 44 and 45, 56 and 57, 79 and 80, 90 and 91, or 22 and 23. The hybrid molecules promote cell migration, inhibit the growth of A375 melanoma cells, accelerate the healing of partial-thickness burn wounds and full-thickness incisional wounds and increase formation of fibrous granular tissue. See e.g. AAQ41602-Q41607 for pref. hybrids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cardioprotective, antiinflammatory and immunosuppressive agents etc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 ALDTNYCFRNLEENCCVRPLYIDFRQDLGWKWVHEPKGYYANFCSGPCPYLRSADTTHST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Prodn. of dimeric biologically active transforming growth factor by refolding denatured monomer in detergent-free folding buffer contg. specific organic solvent to improve yield
                                                                                                               New hybrid transforming growth factor-beta molecules - comprise portions of mature TGF-beta isoforms; useful as wound healants,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 VLGLYNTLNPEASASPCCVPQDLEPLTILYYVGRTPKVEQLSNMVVKSCKCS 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 84.4%; Score 535; DB 14;
Best Local Similarity 79.5%; Pred. No. 1.2e-46;
Matches 89; Conservative 14; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Transforming growth factor type beta; TGF-beta 2; protein renaturation; protein folding.
                     Kuhla J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 1B; Page 31-32; 54pp; English.
                                                                                                                                                                                        Claim 4; Page 22-23; 48pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAR92774 standard; Protein; 112 AA
                       Cerletti N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               95WO-EP02719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  94EP-0810439
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                       Cox D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1996-117000/12.
N-PSDB; AAT17236.
                                                         WPI; 1993-161126/20
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                                                                                                                                                                                                                                                                                                                                                                                                                    112 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human TGF-beta 2.
                                                                            N-PSDB; AAQ41600
                       McMaster GK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO9603433-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25-JUL-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17-JUL-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12-JUL-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          08-FEB-1996.
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                                                                                                                                                                                                                                                                                                                                                                                                                    Sednence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR92774;
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                                                                                                                                                                                                                                                                                                                                                                                                        The TGF-beta2 coding sequence was isolated from the CI-215 human glioma cell line. It was incorporated into an appropriate vector to transform Saccharomyces cerevisale or E.coli. Monomeric TGF-beta1 was purified, denatured and dissolved in 140ml 50mM Tris/HCl pH8. IM NaCl. 5mM EDTA. 2mM reduced glutathione, ImM oxidised glutathione and 33mM Chaps. After 72 hrs at 4 deg C, pH was adjusted to 2.5 and the mixture was conc. 10 times. The conc. soln was diluted to the original vol. with 10mM HCl and conc to a final vol of 10 ml. The supernatant from centrifugation at 5000g for 30 min contained disulphide-linked dimeric TGF-beta2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 ALDINYCFRNLEENCCVRPLYIDFRQDLGWKWVHEPKGYYANFCSGPCPYLRSADTTHŚT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        - by
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 VLGLYNTLNPEASASPCCVPQDLEPLTILYYVGRTPKVEQLSNMVVKSCKCS 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Prodn. of Transforming Growth Factor type-beta-like proteins subjecting denatured monomeric form to refolding conditions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hTGF-beta2; hybrid protein; wound healing; cancer treatment; bone repair; growth regulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 112;
                                                                                                                                                                                                                           Schmitz A, Meyhack B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            84.4%; Score 535; DB 12; 79.5%; Pred. No. 1.2e-46; ive 14; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mature human Transforming Growth Factor-beta2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR39639 standard; Protein; 112 AA
                                                                                                                                                                                                                         Cox D,
                                                                                                                                                                                                                                                                                                                                                                       Example; Page 27; 35pp; English.
                                                                                                           90EP-0810922
                                                                                                                                              89GB-0027546.
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                                                                                                                                                                                                                         McMaster GK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
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                                                                                                                                                                                    (CIBA ) CIBA GEIGY AG
                                                                                                                                                                                                                                                            WPI; 1991-180005/25.
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Best Local Similarity
Matches 89; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      112 AA
                                                                                                                                                                                                                                                                               N-PSDB; AA011994
Homo sapiens
                                                                                                         27-NOV-1990;
                                                                                                                                                06-DEC-1989;
                                                                                                                                                                                                                         Cerletti N,
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                                                                     19-JUN-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19-MAY-1993
                                EP433225-A.
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               Non-soluble, monomeric transforming growth factor TGF-beta 2 (AAR92774) was recovered from E. coli LC 137 (DSM 5658) transformants carrying plasmid ppLMu.TGF-beta 2, which includes the coding sequence (AAT17236) for TGF-beta 2. A biologically active, dimeric form of TGF-beta 2 was obtd. by refolding this monomer in detergentfere buffer contg. DMSO and/or DMF. Dimers of TGF-beta 3 (AAR92772), and hybrid dimers (see also AAR92775-777),
                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                           1 ALDINYCFRNLEENCCVRPLYIDFRQDLGWKWVHEPKGYYANFCSGPCPYLRSADTTHST 60
                                                                                                                                                                                                                                                                                                                               Prodn. of dimeric, biologically active transforming growth factor beta - by refolding denatured monomer in buffer contg. mild detergent and specific organic solvents to improve yields
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                                                                                                                                                                                                                                   84.4%; Score 535; DB 17; Length 112; 79.5%; Pred. No. 1.2e-46; ive 14; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Transforming growth factor beta; TGF; regulator; method; proliferation; differentiation; wound healing; solvent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human transforming growth factor beta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 17; Page 35-36; 59pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAR91957 standard; Protein; 112 AA.
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                                                                                                                                             were also produced
                                                                                                                                                                              112 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAT15463.
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                                                                                                                                                                                Sequence
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Matches
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that, after dimerisation, the TGF beta-like protein retains biological activity and remains in soluble form. The method allows relatively high yields of biologically active TGF beta-like proteins in their native dimeric form. TGF-beta like proteins are multifunctional requiators of cellular activity and a typical use is to stimulate wound healing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              comprises a purification tag and a TGF active fragment. The present sequence represents a specifically claimed TGF active fragment. The present additionally, the fusion protein may comprise proteinase-sensitive linker sites and binding domain so the protein sequence may contain some or all of the following elements: purification tag; proteinase site: GGF betta promotes wound healing, and the fusion protein can be used to reduce surgery recovery time and in the preparation of artificial skin. The inclusion of a purification tag facilitates purification of the fusion protein. The proteinase site is included to permit cleavage and release of the purification tag after purification if desired. The extracellular
                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                 1 ALDTHYCFRNLEENCCVRPLYIDFRQDLGWKWVHEPKGYYANFCSGPCPYLRSADTTHST 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Prepn. of transforming growth factor-beta fusion protein - useful to reduce surgery recovery time and to prepare artificial skin \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A novel transforming growth factor-beta (TGF-beta) fusion protein
                                                                                                                                                                                   ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Transforming growth factor-beta fusion protein; wound healing; artificial skin; surgery recovery time.
                                                                                                                                                                                                                                                                                 61 VLGLYNTLNPEASASPCCVPQDLEPLTILYYVGRTPKVEQLSNMVVKSCKCS 112
                                                                                                                                                                                                                                                                                                  Length 112;
                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IGF active fragment of a TGF-beta fusion protein.
                                                                                                                                                 84.4%; Score 535; DB 17; 79.5%; Pred. No. 1.2e-46;
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                                                                                                                                                                                 14; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 12; Page 47-48; 59pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                AAW08174 standard; Peptide; 112 AA
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                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1997-043065/04.
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                                                                                                                                                                Similarity
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TUAN T.
                                                                                                 112 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
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                                                                                                                                                                                 89;
                                                                                                   Sequence
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Best Local S
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(TUAN/)
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This invention describes the novel preparation of biologically active dimers of recombinant. human growth factors of the cysteine knot family starting from cellular inclusion bodies. Such dimers are are useful in pharmaceutical compositions and the method provides yields of 31.39.7%, in examples, compared with about 10% for the conventional method (see Biochemistry, 28 (1989) 2956). AAYO8278-YO8301 are human growth factor protein fragments used in the method of the invention.
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       the fusion protein to the
                                                                                                                                                           Gaps
                                                                                                                                                                                      9
                                                                                                                                                                                                human; dimer; cysteine knot; cellular inclusion body;
matrix binding site facilitates delivery of the fusion protein to t desired site of action. Delivery of the TGF-beta to the site to be treated reduces the amount of TGF-beta required to be administered be effective and reduces the concentration of circulating TGF-beta which may result in undesirable effects.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Preparing active growth factor dimers from inclusion bodies in high
                                                                                                                                                                                  1 ALDINYCFRNLEENCCVRPLYIDFRQDLGWKWVHEPKGYYANFCSGPCPYLRSADTTHST
                                                                                                                                                           ;
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                                                                                                                                                                                                                                        61 VLGLYNTLNPEASASPCCVPQDLEPLTILYYVGRTPKVEQLSNMVVKSCKCS 112
                                                                                                                                                                                                                                                        Length 112;
                                                                                                                                                          Indels
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                                                                                                                               ; DB 18;
1.2e-46;
                                                                                                                                                                                                                                                                                                                                                                                                                        Human growth factor protein fragment TGF-Beta2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rinas U,
                                                                                                                                                        14; Mismatches
                                                                                                                             84.4%; Score 535; 79.5%; Pred. No. 1
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                                                                                                                                                                                                                                                                                                                                       AAY08300 standard; Protein; 112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97DE-1048734.
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                                                                                                                                                       89; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1999-278785/24.
                                                                                                                                          Local Similarity
                                                                                    112 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Growth factor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pharmaceutical
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                                                                                    Sequence
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                                                                                                                             Query Match
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The present sequence represents the mature form of transforming growth factor-beta-2. Dimeric, biologically active TGF-beta-like protein can be produced by subjecting the denatured monomeric form to refolding conditions. The new monomeric S-sulphonated TGF-beta-like protein is useful for the production of the dimeric, biologically active TGF-beta-like protein, which is useful for the treatment of wounds (surface or internal) and cancer in a mammal, in bone and tissue repair, as a bone marrow protective agent, a mediator of cardioprotection, for the production of an anti-inflammatory or immunosuppressive preparation. Treatment is useful for animals, especially humans, and wound treatment (e.g. ulcers, bed sores etc.) is particularly useful for the elderly.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                Transforming growth factor-beta-2; TGF-beta-like protein; S-sulphonated TGF-beta-like protein; wound treatment; cancer; bone repair; tissue repair; bone marrow protective agent; cardioprotection; anti-inflammatory; immunosuppressive;
61 VLGLYNTLNPEASASPCCVPQDLEPLTILYYVGRTPKVEQLSNMVVKSCKCS 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Producing biologically active dimeric Transforming Growth Factor-beta - by refolding new monomeric Transforming Growth Factor-beta, useful for treatment of wounds and cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 112;
               VLGLYNTLNPEASASPCCVPQDLEPLTILYYVGRTPKVEQLSNMVVKSCKCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Schmitz A;
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                                                                                                                                                                                                     transforming growth factor-beta-2.
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; Pred. No. 1.2e-46;
14; Mismatches 9;
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                                                                                                        AAW97092 standard; Protein; 112
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79.5%;
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                                                                                                                                                                      (first entry)
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Best Local Similarity 79.5
Matches 89; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (NOVS ) NOVARTIS AG
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                                                                                                                                                                                                                                                                                              ulcer; bed sore
                                                                                                                                                                    28-APR-1999
                                                                                                                                                                                                                                                                                                                            Homo sapiens
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                                                                                                                                                                                                    The mature
                                                                                                                                      AAW97092;
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                                                                                        AAW97092
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Gaps

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Indels

Length 112;

84.4%; Score 535; DB 20; 79.5%; Pred. No. 1.2e-46; ive 14; Mismatches 9;

Conservative

Query Match Best Local Similarity Matches 89; Conserv

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ALDINYCFRNLEENCCVRPLYIDFRQDLGWKWVHEPKGYYANFCSGPCPYLRSADTTHST 60

(first entry)

19-JUL-2000

AAY92011;

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The present sequence represents a transforming growth factor beta active fragment. The protein can be used in place of a bone morphogenetic active fragment to create the fusion proteins of the invention. When a bone morphogenetic active fragment is used, the fusion proteins are designated bone morphogenetic fusion proteins. The bone morphogenetic fusion proteins. The bone morphogenetic fusion proteins. The bone morphogenetic purification tag, a proteinase site, an SCM/bone binding site, a second proteinase site, and a bone morphogenetic protein active fragment. The bone morphogenetic fusion proteins can be used for enhancing wound
                                                                                                                                              Proteinase site; bone morphogenetic fusion protein; bone binding site; bone morphogenetic protein; transforming growth factor beta; active fragment; wound healing; bone growth; purification tag.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New bone morphogenetic fusion proteins - comprising a purification tag and a bone morphogenetic active fragment, used for enhancing wound healing or bone growth
                                                                                                                 Transforming growth factor beta active fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Wu L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Shors EC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 42-43; 64pp; English.
                         AAW84208 standard; Protein; 112 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Han B, Nimni ME,
                                                                                                                                                                                                                                                                                                98WO-US11189
                                                                                                                                                                                                                                                                                                                            97US-0868452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 healing or bone growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1999-059875/05.
N-PSDB; AAV99376.
                                                                                                                                                                                                                                                                                                                                                       HALL F L.
HAN B.
NIMNI M E.
SHORS E C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            112 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                 (WULL/) WU L.
                                                                                                                                                                                                                                     WO9855137-A1.
                                                                                                                                                                                                                                                                                               02-JUN-1998;
                                                                                                                                                                                                                                                                                                                          03-JUN-1997;
                                                                                    25-MAR-1999
                                                                                                                                                                                                                                                                  10-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                             Hall FL,
                                                       AAW84208;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
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(SHOR/)
                                                                                                                                                                                                                                                                                                                                                                       (HANB/)
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               AAW84208
RESULT
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                                      Gaps
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     Length 112;
                                      Indels
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Ouery Match

84.4%; Score 535; DB 20;
Best Local Similarity 79.5%; Pred. No. 1.2e-46;
Matches 89; Conservative 14; Mismatches 9;
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1 ALDINYCFRNLEENCCVRPLYIDFRQDLGWKWVHEPKGYYANFCSGPCPYLRSADTTHST 60

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AAY92011 standard; Protein; 112 AA. RESULT 55 AAY92011 ID AAY9

112 AA;

Sequence

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This is the wild type human transforming growth factor beta 2 monomer. Mutants comprise at least one electrostatic charge altering mutation in a beta hairpin loop, resulting in increased bioactivity.

Mutant cystine knot growth factor (CKGF) proteins comprising one or more mutant subunits and having novel properties or improved pharmacological properties, compared to wild type CKGFs, are claimed. The CKGF superfamily comprises at least four families of growth factors: the glycoprotein hormones, the platelet-derived growth factor (PDGF) family, the neurotrophins and the transforming growth factor-beta family; the families are known to be structurally similar (especially comprising the cystine knot topology) and it was shown that mutations at certain positions in the CKGF hairpin loops of family members and other members of the CKGF superfamily could significantly alter the biological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mutant transforming growth factor family proteins or analogues are useful for treatment of ovulatory dysfunction, luteal phase defect, unexplained infertility, time-limited conception and in assisted reproduction.
                                                                                                                                                                                                                                                                                                                                                                        uprionally mutated to increase electrostatic
interaction between beta hairpin structure and
a receptor"

    20
    /note= "optionally mutated to increase electrostatic
interaction between beta hairpin structure and

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "optionally mutated to increase electrostatic
interaction between beta hairpin structure and
a receptor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New mutant cystine knot growth factor proteins comprising one or more mutant subunits, useful for treating or preventing diseases e.g.
                                                                                                                                                                                                                                                                                                             /label= beta_hairpin_loop_1
/note= "mutant optionally comprises one or more
substitutions in these residues"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               or more
                                                                                                                  human transforming growth factor beta 2 monomer; CKGF; mutant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      /label= beta_hairpin_loop_3
/note= "mutant optionally comprises one c
substitutions in these residues"
                                                                                                                                    cystine knot growth factor; hairpin loop; infertility
                                                                                 Human transforming growth factor beta 2 monomer.
                                                                                                                                                                                                                                                                                                                                                                                    /note= "optionally mutated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 208; Page 301; 320pp; English.
                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                              a receptor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothyroidism and thyroid cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (UYMA-) UNIV MARYLAND BALTIMORE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Weintraub BD, Szkudlinski MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98WO-US19772.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Misc-difference 103..112
                                                                                                                                                                                                                                                                                                                                                                                                                                       82..102
                                                                                                                                                                                                                                                                                                                                                                    Misc-difference 41..81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         activities of the CKGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2000-283585/24.
                                                                                                                                                                                                                          Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200017360-A1.
                                                                                                                                                                         Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-MAR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                         Domain
                                                                                                                                                                                                                                                                                                  Domain
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1 ALDINYCFRNLEENCCVRPLYIDFRQDLGWKWVHEPKGYYANFCSGPCPYLRSADTTHST

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This invention relates to a matrix comprising a substrate capable of providing attachment of a heparin binding peptide (HBP), a peptide, comprising a binding domain which binds heparin with high affinity, heparin or heparin-like polymer, and a protein growth factor or peptide fragment which has a domain that binds heparin with low affinity. Included in the invention is a vascular graft comprising the matrix, which is capable of supporting cell adhesion. The matrix is used for delivering low heparin binding affinity growth factor proteins or peptides in a controlled manner suitable for wound healing. The matrix can be used in an article for treating dermal wounds, and in an implantable sterilized composition capable of supporting cell adhesion. The present sequence represents a growth factor protein. The protein is used in an example illustrating that non-heparin-binding growth factors can be released in a controlled manner from heparin-based drug delivery systems based on their low affinity for heparin.
                                        ö
                                                                                                                                                                                                                                                                                                                                                                                               j; vascular graft; matrix; cell adhesion; growth factor;
dermal wound; wound healing; TGF-beta 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matrix for controlled release of growth factor for wound healing, has substrate that attaches heparin binding peptide, protein growth factor that bind heparin with low affinity, and heparin or heparin-like
                                        Gaps
                                                                   ALDINYCFRNLEENCCVRPLYIDFRQDLGWKWVHEPKGYYANFCSGPCPYLRSADITHST 60
                                                                                     ;
0
                                                                                                                                   61 VLGLYNTLNPEASASPCCVPQDLEPLTILYYVGRTPKVEQLSNMVVKSCKCS 112
                                                                                                                                                   Length 112;
                                     Indels
       DB 21;
 ; Score 535; DB 21;
; Pred. No. 1.2e-46;
14; Mismatches 9
                                                                                                                                                                                                                                                        AAB35938 standard; protein; 112 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5; Page 21; 48pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (ETHZ-) ETH ZURICH & UNIV ZURICH.
                                                                                                                                                                                                                                                                                                                                                                                               Heparin binding; vascular graft;
                                                                                                                                                                                                                                                                                                                                                             TGF-beta 2 amino acid sequence.
Query Match 84.4%;
Best Local Similarity 79.5%;
Matches 89; Conservative 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99WO-IB00800.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99WO-IB00800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sakiyama SE, Hubbell JA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-024627/03.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           112 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200064481-A1.
                                                                                                                                                                                                                                                                                                                                                                                                               wound healing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unidentified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22-APR-1999;
                                                                                                                                                                                                                                                                                                                            26-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    02-NOV-2000
                                                                                                                                                                                                                                                                                            AAB35938;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             polymer
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The present invention relates to growth differentiation factor-8 (GDF-8) coding sequences and proteins. The present sequence is a protein, which was used in a sequence homology comparison with the GDF-8 protein lisolated in the present invention. GDF-8 is useful for treating meurodegenerative diseases (e.g. amyotrophic lateral sclerosis and muscular dystrophy), musculodegenerative diseases or in tissue repair to trauma, obesity and disorders related to abnormal proliferation of adipocytes. GDF-8 is also useful for treating malignancies of the various organ systems, particularly cells in muscle or adipose tissues and in gene therapy for the treatment of cell proliferative or immunological diseases mediated by GDF-8. In addition, GDF-8 is also useful for treating muscle wasting disease, neuromuscular disorder, spinal cord injury, treatmatic injury, congestive obstructive pulmonary disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New substantially purified growth differentiation factor-8 polypeptide, useful for treating muscle wasting disease, obesity, muscular dystrophy, neuromuscular disorder, acquired immunodeficiency syndrome
                                                                                                                                                                                                                                                                                                                   Gene therapy; growth differentiation factor-8; GDF-8; AIDS; cachexia; neurodegenerative disease; amyotrophic lateral sclerosis; obesity; muscular dystrophy; musculodegenerative disease; tissue repair; muscle wasting disease; neuromuscular disorder; spinal cord injury; traumatic injury; congestive obstructive pulmonary disease.
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 ALDINYCFRNLEENCCVRPLYIDFRQDLGWKWVHEPKGYYANFCSGPCPYLRSADTTHST 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                  61 VLGLYNTLNPEASASPCCVPQDLEPLTILYYVGRTPKVEQLSNMVVKSCKCS 112
                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 535; DB 22;
Pred. No. 1.2e-46;
4; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (UYJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 2; Fig 3; 124pp; English.
                                                                                                                                                                             AAB73205 standard; Protein; 115
                                                                                                                                                                                                                                                                                     TGF-beta2 C-terminal sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           84.4%;
ilarity 79.5%;
Conservative 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99US-0378238
                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (COPD), AIDS or cachexia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  S, McPherron AC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-211209/21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 89; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 115 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200112777-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Unidentified
                                                                                                                                                                                                                                                11-MAY-2001
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                                                                                                                                                                                                                AAB73205;
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Gaps

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84.4%; Score 535; DB 22; Length 112; 79.5%; Pred. No. 1.2e-46; ive 14; Mismatches 9; Indels

Query Match
Best Local Similarity 79.5
Matches 89; Conservative

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IL1-beta;

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Transforming growth factor-beta 2 (TGF-beta 2) has been found to inhibit inducible nitric oxide synthase (INOS) gene transcription, esp. in interleukin-1-beta (IL1-beta) stimulated rat smooth muscle cells, and a dose which does not inhibit consitutive NOS. TGF-beta 1 (AAR83054) or 2 or their active fragments (esp. derived from the carboxy-terminal 112 amino acids), can be used in the treatment of hypotension, such as that associated with severe inflammation or septic shock.
                                                                                                                                                                                                                                                             303..414
/note= "represents the mature active TGF beta-1 mol."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 ALDINYCFRNLEENCCVRPLYIDFRQDLGWKWVHEPKGYYANFCSGPCPYLRSADTTHST 60
                                                                                                                      macrophage inducible nitric oxide synthase; iNOS; constitutive NOS;
                                                                                                                                      interleukin-1-beta; transforming growth factor-beta; TGF-beta; IL
nitric oxide production; hypotension; inflammation; septic shock;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Treatment of hypotension, esp. in septic shock - by administering transforming growth factor-beta e.g. to inhibit inducible nitric oxide synthase gene transcription
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VLGLYNTLNPEASASPCCVPQDLEPLTILYYVGRTPKVEQLSNMVVKSCKCS 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              84.4%; Score 535; DB 16; 79.5%; Pred. No. 5.1e-46; ive 14; Mismatches 9;
                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AA.
                                                                                      Transforming growth factor-beta 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Fig 18; 52pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAR73597 standard; Protein; 414
                                                                                                                                                                                                                                                                                                                                                                                                                  94WO-US03705.
                                                                                                                                                                                                                                                                                                                                                                                 94WO-US03705.
                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human TGF-beta 2 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                    (HARD ) HARVARD COLLEGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Perrella MA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1995-358443/46.
N-PSDB; AAT05877.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 89; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    414 AA;
                                                                                                                                                                                                        Mammalian sp
                                                                                                                                                                                                                                                                                                             W09526745-A1
                                                                                                                                                                                                                                                                                                                                                                                 05-APR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                  05-APR-1994;
                                                     25-JUN-1996
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                                                                                                                                                                                                                                                                                                                                               12-0CT-1995
                                                                                                                                                                          treatment
                     AAR83055;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAR73597;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                             Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lee M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
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                                                                                                                                                                                                                                             Key
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4 aldaaycfrnvqdncclrplyidfkrdlgwkwihepkgynanfcagacpylwssdtqhsr 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 ALDINYCFRNLEENCCVRPLYIDFRQDLGWKWVHEPKGYYANFCSGPCPYLRSADTTHST 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A new method for treating hypertension comprises administering a transforming growth factor (TGF)-beta to an individual at a dose effective for lowering blood pressure; the TGF-beta may be e.g. mature TGF-beta TGF-beta, TGF-beta, a mature TGF-betal/beta2 hybrid, TGF-betal precursor, a latent TGF-betal precursor, hybrid TGF-betal/TGF-beta2 precursor, a latent TGF-betal complex or a latent TGF-beta1
                                                                                                                                                                                                                                                                                          Hypertension therapy; hypotensive agent; blood pressure modulator.
                                                                                                                                                                                                                                                        hybrid transforming growth factor (TGF) beta-1/beta2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .;
0
                                                   61 VLGLYNTLNPEASASPCCVPQDLEPLTILYYVGRTPKVEQLSNMVVKSCKCS 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 VLGLYNTLNPEASASPCCVPQDLEPLTILYYVGRTPKVEQLSNMVVKSCKCS 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 390;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Use of transforming growth factor (TGF)-beta and their antagonists - for modulating blood pressure, for treating hypertension and hypotension
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Score 535; DB 13;
; Pred. No. 4.8e-46;
14; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                      AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAR83055
ID AAR83055 standard; Protein; 414 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Fig 3; 42pp; English.
                                                                                                                                                     AAR20126 standard; Protein; 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          84.48;
79.58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      91WO-US04449.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      90US-0541221.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (BRIM ) BRISTOL-MYERS SQUIB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 79.5%;
Matches 89; Conservative
                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Comereski CR;
                                                                                                                                                                                                                                                                                                                                                                                 8..21
280..391
                                                                                                                                                                                                                                                                                                                           Monkey and Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1992-024199/03.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       390 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAQ20291.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20-JUN-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20-JUN-1990;
                                                                                                                                                                                                                        16-APR-1992
                                                                                                                                                                                                                                                        Sequence of
                                                                                                                                                                                                                                                                                                                                                                                                                               WO9119513-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-DEC-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oleson FB,
                                                                                                                                                                                     AAR20126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complex.
                                                                                                                                                                                                                                                                                                                                                                             Peptide
                                                                                                                                                                                                                                                                                                                                                                                                 Protein
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Key

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Gaps

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RESULT 59

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Length 414; Indels

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Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Key
Protein
                                                                                                                              Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAR05748
   g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q
                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                This sequence represents human transforming growth factor-beta 2 (TGF-beta 2). The sequences for human TGF-beta 1 (see AAR73596) and human TGF-beta 3 (see AAR73598) are claimed within the scope of the invention. The invention is a composition consisting of a TGF-beta protein and an osteogenic cell source (OCS) formulated in an acceptable carrier other than a bone morphogenic cofactor. This composition can be used for the restoration of bone deficiency. This provides for the generation of mature bone only where it is required, without the inclusion of a specific bone-inducing cofactor. This method can be used with any of the 5 human TGF-beta's or with TGF-beta from other species.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Transforming growth factor-beta; Human TGF-beta protein; TGF-beta 1; TGF-beta 2; TGF-beta 3; osteogenic cell source; OCS; bone deficiency;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 ALDINYCFRNLEENCCVRPLYIDFRQDLGWKWVHEPKGYYANFCSGPCPYLRSADTTHST 60
                                                                                                                                                                                                                          Compsn. for treating skeletal tissue deficiency - comprising transforming growth factor-beta and an osteogenic cell source in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence encoded by human transforming growth factor (TGF) beta-2 precursor 442 cDNA in pPC-21.
                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 VLGLYNTLNPEASASPCCVPQDLEPLTILYYVGRTPKVEQLSNMVVKSCKCS 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 414;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                         Score 535; DB 16;
Pred. No. 5.1e-46;
                                                                                                                                                                                                                                                                                                                                                                                                                  84 4%; Sco... 79.5%; Pred. No. ... 14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cell differentiation; cell proliferation.
                                                                                                                                                                                                                                                             Disclosure; Column 17-20; 19pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers 20..442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAP91899 standard; protein; 442 AA
                                                                                                                 89US-0401906.
91US-0790856.
93US-0063841.
93US-0132405.
                                                                                              93US-0401906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 79.55
Matches 89; Conservative
                 bone-inducing cofactor
                                                                                                                                                                                     Ammann AJ, Rudman CG;
                                                                                                                                                                 (GETH ) GENENTECH INC.
                                                                                                                                                                                                       WPI; 1995-169610/22
                                                                                                                                                                                                                                                                                                                                                                                            414 AA
                                      Homo sapiens
                                                                                             12-NOV-1993;
                                                                                                                 01-SEP-1989;
12-NOV-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23-DEC-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                               12-NOV-1993;
                                                       US5409896-A
                                                                                                                                    18-MAY-1993;
                                                                           25-APR-1995
                                                                                                                                                                                                                                                                                                                                                                                            Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAP91899;
                                                                                                                                                                                                                                               carrier
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61
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PolyA-RNA was isolated from the tamoxifen-treated, human prostatic adenocarcinoma line PC-3 and converted to CDNA. TGF DNA is pref. used for control of the SV40 promoter. and expressed in CHO cells. The simian SQ is also claimed.
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116..144
/note="This entire SQ_is replaced with Asn in simian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 ALDTNYCFRNLEENCCVRPLYIDFRQDLGWKWVHEPKGYYANFCSGPCPYLRSADTTHST 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 VLGLYNTLNPEASASPCCVPQDLEPLTILYYVGRTPKVEQLSNMVVKSCKCS 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 442;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New DNA sequence encoding transforming growth factor beta 2 used for large scale expression in eucaryotic cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Potential glycosylation site"
                                                                                                                                                                                                                                                   /note="Potential glycosylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 84.4%; Score 535; DB 10;
79.5%; Pred. No. 5.5e-46;
live 14; Mismatches 9;
                                                                                                                                                                  /note="Potential glycosylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human TGF-Beta2 precursor; cancer; tumorcide;
                                                                                                                          TGF-beta-2-414"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers 331..442
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ż
/note="Claimed"
                                       /note="Signal"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 4; Fig la; 27pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Webb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human TGF-Beta2-442 precursor.
                                                                                                                                                                                                                                                                                                                                                                                                      88DE-3833897
                                                                                                                                                                                                                                                                                                                                                                                                                                               88US-0234065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 79.5
les 89; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Purchio AF, Madisen L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1989-138796/19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        442 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (ONCO-) ONCOGEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; AAN90767
                                                           Cleavage-site
                                                                                                                                              Modified-site
                                                                                                                                                                                   Modified-site
                                                                                                                                                                                                                           Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           02-NOV-1990
                                                                                                                                                                                                                                                                                                                                                                                                   05-OCT-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                               18-AUG-1988;
                                                                                                                                                                                                                                                                                                                DE3833897-A.
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transforming growth factor (TGF)-beta to an individual at a dose effective for lowering blood pressure; the TGF-beta may be e.g. mature TGF-betal/beta2 hybrid, TGF-betal precursor, a latent TGF-beta2 precursor, hybrid TGF-beta1 beta2 precursor, a latent TGF-beta1 complex or a latent TGF-beta1
                                                                                                                                                                                                                                                                                                                                                                      1 ALDINYCFRNLEENCCVRPLYIDFRODLGWKWVHEPKGYYANFCSGPCPYLRSADTTHST 60
                                                                                                                                                A new method for treating hypertension comprises administering a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGF-betal; TGF-beta2; transforming growth factor; protein; cell differentiation; cell proliferation; CHO; Chinese hamster; ovary; COS; monkey kidney; animal; mammal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20..21
/note= "putative signal sequence cleavage site"
                                                                                                                                                                                                                                                                                                                                                                                                                                               61 VLGLYNTLNPEASASPCCVPQDLEPLTILYYVGRTPKVEQLSNMVVKSCKCS 112
                                                                                                                                                                                                                                                                                                            84.4%; Score 535; DB 13; Length 442; 79.5%; Pred. No. 5.5e-46;
                                                         Use of transforming growth factor (TGF)-beta and their antagonists - for modulating blood pressure, for treating hypertension and hypotension
                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                           6
                                                                                                                                                                                                                                                                                                                                         14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'note= "signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "mature peptide"
                                                                                                                                                                                                                                                                                                                             Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR79922 standard; Protein; 442 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human transforming growth factor-2
                                                                                                                   Disclosure; Fig 2; 42pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     89EP-0104223
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88US-0285140.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 331..442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Madisen L, Purchio AF,
                1992-024199/03.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1995-346094/45.
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                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                  442 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAT04116
                              N-PSDB; AAQ20290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cleavage-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16-DEC-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14-DEC-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28-MAY-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-DEC-1989;
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                                                                                                                                                                                                                                                                                                                                         89;
                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAR79922;
                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                        complex.
                                                                                                                                                                                                                                                                                                                              Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64
                                                                                                                                                                                                                                                                                                                                         Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 ALDTNYCFRNLEENCCVRPLYIDFRQDLGWKWVHEPKGYYANFCSGPCPYLRSADTTHST 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                      TGF-Beta2 may be used in treatment of tumors at effective doses, and may also be useful in augmenting wound healing by stimulating cell proliferation. The growth factor can be produced at high levels from a CHO expression system.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hypertension therapy; hypotensive agent; blood pressure modulator.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     human transforming growth factor (TGF) beta-2-442.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 VLGLYNTLNPEASASPCCVPQDLEPLTILYYVGRTPKVEQLSNMVVKSCKCS 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cloning and expression of transforming growth factor beta 2 used for treatment of tumors or for augmenting wound healing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 442;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 535; DB 11;
Pred. No. 5.5e-46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14; Mismatches
/label=Sinal peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR20125 standard; Protein; 442 AA.
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                                                                                                                                                                                                                                                                                                         Claim 1; Fig la; 58pp; English.
                                                                                                                                                                                          Webb
                                                                                                                                                                                                                                                                                                                                                                                                                                                           84.48;
79.58;
                                                                                     89EP-0403480.
                                                                                                                88US-0285140.
89US-0446020.
                                                                                                                                                             (ONCO-) ONCOGEN LTD PARTNER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oleson FB, Comereski CR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 79.5
nes 89; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4..19
                                                                                                                                                                                         Madisen L,
                                                                                                                                                                                                                    WPI; 1990-203127/27
                                                                                                                                                                                                                                                                                                                                                                                                                442 AA;
                                                                                                                                                                                                                                   N-PSDB; AAQ05126
                                                                                     14-DEC-1989;
                                                                                                                 16-DEC-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20-JUN-1991;
                                                                                                                                                                                         Purchio AF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
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                                                                                                                               05-DEC-1989
                                                        04-JUL-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO9119513-A
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                           EP376785-A
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Sequence

Query Match

Matches

P

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g

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AAR20125;

63

RESULT 6 AAR20125

Peptide Protein

Key

; 0

Gaps

; 0

391 AA;

Sequence

g

- nsed

Gaps

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PolyA-RNA was isolated from the tamoxifen-treated, human prostatic adenocarcinoma line PC-3 and converted to cDNA. TGF DNA is pref. used for control of the SV40 promoter. and expressed in CHO cells.
                                                                                                                                                                                                                         1 ALDINYCFRNLEENCCVRPLYIDFRQDLGWKWVHEPKGYYANFCSGPCPYLRSADTTHST 60
                                                                                                                                                                                       .;
0
               precursor
                                                                                                                                                                                                                                                       This sequence is expressed in a host cell, preferably a COS or CHO cell, so the host cell produces active TGF-beta2. produced TGF-beta2 protein can be used to regulate cellular differentiation and proliferation.
                                                                                                                                                              84.4%; Score 535; DB 16; Length 442;
llarity 79.5%; Pred. No. 5.5e-46;
Conservative 14; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                             Sequence encoded by human transforming growth factor (TGF)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New DNA sequence encoding transforming growth factor beta
used for large scale expression in eucaryotic cells
            Hybrid transforming growth factor beta-1/TGF-beta-2 to produce biologically active, mature TGF-beta-2
                                                                                                                                                                                                                                                                                                                                                                                                                                            Cell differentiation; cell proliferation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                       AAP91900 standard; protein; 391 AA
                                             Disclosure; Fig.1a; 52pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ž
                                                                                                                                                                                                                                                                                                                                                                                                                        beta-1/TGF-beta-2 precursor DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30..391
/note="Claimed"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 10; Fig 1b; 27pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Signal"
279..291
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         88DE-3833897
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Madisen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1989-138796/19.
                                                                                                                                                              Query Match
Best Local Similarity
Matches 89; Conserv
                                                                                                                            442 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAN90768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (ONCO-) ONCOGEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        05-OCT-1988;
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                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                               AAP91900;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Peptide
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                                                       TGF-beta may be used in vivo to prevent formation of synctia and inhibit HIV infection. {\tt TGF} may also be used with other HIV treatments (AZI, soluble CD4 etc.).
                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 ALDINYCFRNLEENCCVRPLYIDFRQDLGWKWVHEPKGYYANFCSGPCPYLRSADTIHST 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 VLGLYNTLNPEASASPCCVPQDLEPLTILYYVGRTPKVEQLSNMVVKSCKCS 112
                                                                                                 Length 391;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 390;
                       10; Indels
                                                                                                                                                                                                                              Human Transforming growth factor from TGF-Beta2-442 cDNA.
                                                                                                                                                                                                                                                   HIV; AIDS; SIV; vaccine; AZT; CD4; cytokines; growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 83.9%; Score 532; DB 11;
79.5%; Pred. No. 9.6e-46;
live 13; Mismatches 10;
Score 533; DB 10;
Pred. No. 7.6e-46;
                     13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                              Purchio A;
                                                                                                                                                                                                                                                                                    Location/Qualifiers 279..390
                                                                                                                                                                AAR05665 standard; protein; 390 AA.
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84.1%;
79.5%;
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                                                                                                                                                                                                           (first entry)
           Local Similarity 79.5
les 89; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best_Local Similarity 79.53
Matches 89; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                              Brankovan V, Lioubin M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1990-068723/10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   390 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAQ03510
                                                                                                                                                                                                          14-AUG-1990
                                                                                                                                                                                                                                                                                                                                                              25-AUG-1989;
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                                                                                                                                                                                                                                                               factors; ds.
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 Query Match
                                                                                                                                                                                     AAR05665;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                              Peptide
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                     Matches
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RESULT 67

Tue Oct 30 12:56:42 2001

AAR05666

Peptide

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Transforming growth factor; TGF; TGF-beta; TGF-5 beta; simian; Simian virus 40; SV40; expression vector; Chinese Hamster ovary; CHO; vascular endothelial cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGF-Beta2 may be used in treatment of tumors at effective doses, and may also be useful in augmenting wound healing by stimulating cell proliferation. The growth factor can be produced at high levels from a CHO expression system.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 ALDINYCFRNLEENCCVRPLYIDFRODLGWKWVHEPKGYYANFCSGPCPYLRSADTTHST
                                                                                                                                                                                                                                              Cloning and expression of transforming growth factor beta 2 - used for treatment of tumors or for augmenting wound healing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 VLGLYNTLNPEASASPCCVPQDLEPLTILYYVGRTPKVEQLSNMVVKSCKCS 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 390;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         pre-pro-protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                          83.9%; Score 532; DB 11;
79.5%; Pred. No. 9.6e-46;
iive 13; Mismatches 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "N-glycosylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "N-glycosylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'note= "N-glycosylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "Mature TGF-5 beta"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1..29
/note= "Signal peptide,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /nocc
30..278
/~~+e= "Pro-protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGF-beta 1/beta 2 chimeric protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAR27522 standard; Protein; 390 AA
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                                                                                                                                                                                                                                                                                          Claim 15; Fig 1b; 58pp; English
                                                                                                                                                                         Webb
                                                                   89EP-0403480.
                                                                                              88US-0285140.
89US-0446020.
                                                                                                                                            (ONCO-) ONCOGEN LID PARTNER.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                      Madisen L,
                                                                                                                                                                                                   WPI; 1990-203127/27.
N-PSDB; AAQ05127.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 89; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                               390
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                                                                                                                                                                        Purchio AF,
                                                                   14-DEC-1989;
                                                                                              16-DEC-1988;
05-DEC-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10-MAR-1993
                                       04-JUL-1990
            EP376785-A.
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qq
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TGF-beta may be used in vivo to prevent formation of synctia and inhibit HIV infection. TGF may also be used with other HIV treatments (AZI, soluble CD4 etc.).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 ALDTNYCFRNLEENCCVRPLYIDFRQDLGWKWVHEPKGYYANFCSGPCPYLRSADTTHST 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human TGF-Beta2 expressed by TGF-Beta1/TGF-Beta2 hybrid precursor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Compsns. contg. transforming growth factor beta - used for inhibitions of HIV infection and replication in vivo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 VLGLYNTLNPEASASPCCVPQDLEPLTILYYVGRTPKVEQLSNMVVKSCKCS 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   83.9%; Score 532; DB 11; Length 390; 79.5%; Pred. No. 9.6e-46; Live 13; Mismatches 10; Indels
                                                                                                                          HIV; AIDS; SIV; vaccine; AZT; CD4; cytokines; growth
                                                                                              Hybrid transforming growth factor TGF-betal/beta2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human TGF-Beta2 precursor; cancer; tumorcide; ss
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8..21
/label=Signal peptide
                                                                                                                                                                                                                                                                                                                                                                Brankovan V, Lioubin M, Purchio A;
                                                                                                                                                                      Location/Qualifiers 379..390
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      AAR05666 standard; protein; 390 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Fig 3; 20pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR05749 standard; protein; 390
                                                                                                                                                                                                                                                                         89EP-0115719.
                                                                                                                                                                                                                                                                                                      88US-0236698
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                                                                14-AUG-1990 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 79.5
Matches 89; Conservative
                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1990-068723/10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        390 AA;
                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAQ03511
                                                                                                                                                                                                                                                                         25-AUG-1989;
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                                                                                                                                                                                                                                            07-MAR-1990
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                                                                                                                                            factors; ds
                                                                                                                                                                                                               EP356935-A.
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                                    AAR05666;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
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Peptide
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RESULT

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Gaps 9

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Indels

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Hybrid transforming growth factor beta-1/TGF-beta-2 precursor - used to produce biologically active, mature TGF-beta-2
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                                                                   TGF-betal; TGF-betal; transforming growth factor; protein; cell differentiation; cell proliferation; CHO; Chinese hamster; ovary; COS; monkey kidney; animal; mammal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This hybrid sequence is expressed in a host cell, preferably a COS or CHO cell, so th host cell produces active TGF-beta2. The produced TGF-beta2 protein can be used to regulate cellular differentiation and proliferation.
                                    Simian-human hybrid TGF-beta1/TGF-beta2 precursor protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 VLGLYNTLNPEASASPCCVPQDLEPLTILYYVGRTPKVEQLSNMVVKSCKCS
                                                                                                                                                                                                                             /note= "simian TGF-betal precursor"
279..390
/note= "human TGF-beta2 precursor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 507; DB 16;
Pred. No. 3.1e-43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      80.0%; Scor.
76.8%; Pred. No. ...
12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chimeric simian TGF-beta1/beta2 gene product.
                                                                                                                                                                                               "signal peptide"
                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ą
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR05492 standard; protein; 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 4; Fig.1b; 52pp; English.
                                                                                                                                                                                                                                                                                                                                                               89EP-0104223
                                                                                                                                                                                                                                                                                                                                                                                             89US-0446020.
88US-0285140.
      (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Madisen L, Purchio AF,
                                                                                                                                                                                                 /note=
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                                                                                                                                                                                                                                                                                                                                                                                                                                             (ONCO ) ONCOGEN LP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   389 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; AAT04115
                                                                                                                                     Homo sapiens
      26-MAR-1996
                                                                                                                                                                                                                                                                                                                                                               14-DEC-1989;
                                                                                                                                                                                                                                                                                                                                                                                              05-DEC-1989;
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                                                                                                                                                                                  Peptide
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                                                                                                                                                                                                                                                  Protein
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Matches
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                                                                                                                                                                     Key
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          · 1 ALDTNYCFRNLEENCCVRPLYIDFRQDLGWKWVHEPKGYYANFCSGPCPYLRSADTTHST 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Compsn. comprising new chimeric TGF-B (TGF-beta 1-beta 2) -
inhibits proliferation of vascular endothelial cells, useful for
treating cancer and to promote wound healing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Purchio AF:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Fig 1; 45pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                           (BRIM ) BRISTOL-MYERS SQUIBB CO
                                                                                                                                                                'label= V17L
                                  label= S10N
                                                                  'label= T11V
                                                                                                 /label= E12Q
                                                                                                                                  label= K13D
                                                                                                                                                                                               'label= Q19P
                                                                                                                                                                                                                              'label= R25K
                                                                                                                                                                                                                                                              /label= K26R
/label= S9R
Misc-difference 288
                                                                                                                                                                                                                                                                                                                                                                                           91US-0669171
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1992-348938/42.
N-PSDB; AAQ29177.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              390 AA;
                                                 Misc-difference
                                                                               Misc-difference
                                                                                                                                                                                                            Misc-difference
                                                                                                                Misc-difference
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Compsn. co

Sequence

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13-MAR-1992; 14-MAR-1991;

WO9216228-A. 01-0CT-1992 ö

Gaps

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14; Indels

Transforming growth factor; TGF-beta; cancer; CHO; ds.

AAR79921 standard; Protein; 389 AA

RESULT 70 AAR79921 AAR79921;

Circopithecus aethiops

Length 389;

Purchio AF,

EP374044-A.

efficiency.

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This sequence is that of mature human transforming growth factor-beta 1 (TGF-beta 1) polypeptide. It differs from human and porcine TGF-beta subtype 3 sequences at positions 9-11,13,19,40,45,52,57,57,58,60,58,68,71,75,82,87,and 95. In addition porcine TGF-beta 3 has an AA substitution at posn. 96. The N-terminal AA sequence of bovine TGF-beta 2 differs from that of human TGF-beta 1 at posns.4,5,9-13,and 19.

The nucleic acid sequence encoding the second subtype of TGF-beta (TGF-beta 3) is useful as a probe or trop produce TGF-beta 3 for both normal and neoplastic cell growth inhibition.
                                                Nucleotide sequence encoding transforming growth factor beta-3 used as a probe, or to produce TGF beta 3, for inhibiting growth of certain normal and neoplastic cells, eg A549.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The TGF-beta may be used to derive cartilage inducing factors (CIFs) useful for inhibition of acute/chronic inflammation, treatment of red blood cell dysfunction associated with polycythemia, thrombocytosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 ALDITNYCFRNLEENCCVRPLYIDFRQDLGWKWVHEPKGYYANFCSGPCPYLRSADTTHST 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Treating inflammation assosiated with transplants, etc. - using cartilage inducing factor polypeptide homodimer cpd.
                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 VLGLYNTLNPEASASPCCVPQDLEPLTILYYVGRTPKVEQLSNMVVKSCKCS 112
                                                                                                                                                                                                                                                                                                                                                                                           Length 112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cartilages inducing factor; CIF;
                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                       78.9%; Score 500; DB 11; 76.8%; Pred. No. 3.9e-43; iive 11; Mismatches 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              thrombocytosis; slpenomegaly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Armstrong R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Platelet-derived human TGF-beta monomer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAR08142 standard; protein; 112 AA.
                                                                                                                      Disclosure; Fig. 3; 61pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Fig 1; 14pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       88US-0263635
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Transforming growth factor;
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                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ellingsworth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (CLGE ) COLLAGEN CORP
              WPI; 1990-007474/01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1990-368150/49.
                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
Matches 86; Conserv
                                                                                                                                                                                                                                                                                                                                     112 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                polycythemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27-OCT-1988;
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                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR08142;
                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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qq
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 ALDINYCFRNLEENCCVRPLYIDFRQDLGWKWVHEPKGYYANFCSGPÇPYLRSADTTHST 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Transforming growth factor beta-3 (TGF beta 3); tumour cells; growth inhibition.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chimeric gene has TGF activity and may be more desirable than its parents TGF-beta1 and TGF-beta2. CHO cells expressing the product from a plasmid vector (p5beta/dhfr) are 2.5 times more bioactive than normal. The product is useful in treatment of cancer and wound
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 VLGLYNTLNPEASASPCCVPQDLEPLTILYYVGRTPKVEQLSNMVVKSCKCS 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            79.3%; Score 503; DB 11; Length 390; 75.9%; Pred. No. 7.9e-43; ive 14; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                  New chimeric transforming growth factor - with TGF-beta biological activity and increased secretion
         Key Location/Qualifiers
Misc-difference 287..298
/note="TGF-beta2 derived sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence of mature human TGF-beta 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAR04076 standard; protein; 112 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 2; Fig 1; 18pp; English.
                                                                                                                                                                                                                          (ONCO-) ONCOGEN LTD PARTNER
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                                                                                                                                                      89EP-0403463
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                                                                                                                                                                                                                                                               Madisen L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                WPI; 1990-187401/25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     See also EP-373994.
                                                                                                                                                                                                                                                                                                                 N-PSDB; AAQ04908
                                                                                                                                                      13-DEC-1989;
                                                                                                                                                                                         15-DEC-1988;
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Query Match Best Local S: Matches 85,

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RESULT 72 AAR04076

Sequence

WO8912101-A 14-DEC-1989

Dernyck RM,

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Gaps

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01-APR-1993;
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                                                                                                                                                             Gaps
                                                                                                                                                                                                                          1 ALDINYCFRNLEENCCVRPLYIDFRQDLGWKWVHEPKGYYANFCSGPCPYLRSADTTHST 60
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                                                                                                                                                                                                                                                                                           61 VLGLYNTLNPEASASPCCVPQDLEPLILLYYVGRTPKVEQLSNMVVKSCKCS 112
                                                                                                                                                                                                                                                                                                                    78.9%; Score 500; DB 11; Length 112; 76.8%; Pred. No. 3.9e-43; ive 11; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New platelet-derived growth regulating peptide-alpha - used treatment of eczema, stimulation of bone growth and as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Platelet derived growth inhibitor alpha; TGF-beta; trypsin; pepsin; cell proliferation; eczema; immunosuppressant; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pressant for immune diseases.
also AAR22135,6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR22134 standard; peptide; 112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    90JP-0238944.
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                                                                                                                                                         Conservative
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                                                                                                                                  Best Local Similarity
Matches 86; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (NAKA/) NAKAMURA T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 112 AA;
                                         112 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              immunosuppressant
  or splenomegaly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PDGI subunit a.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nakamura T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EP475719-A.
                                              Sequence
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SXS
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The mature form of TGF-beta is comprised of two identical chains, each of 112 amino acids. Since TGF-beta is a regulator of scar prodn. after a penetrating injury to the brain or spinal cord, which scar prodn. can preclude neuronal recovery, TGF-beta antagonists have potential use as adjuncts to those therapies designed to promote regeneration and reconnection of damaged neural pathways.
9
                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 ALDTNYCFRNLEENCCVRPLYIDFRQDLGWKWVHEPKGYYANFCSGPCPYLRSADTTHST 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 ALDINYCFRNLEENCCVRPLYIDFRQDLGWKWVHEPKGYYANFCSGPCPYLRSADTIHST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Inhibiting or enhancing scar formation in the CNS - by infusion of transforming growth factor-beta antagonists, e.g. anti-(TGF-beta)-antibodies, or TGF-beta itself, respectively
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
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                                                                                                            61 VLGLYNTLNPEASASPCCVPQDLEPLTILYYVGRTPKVEQLSNMVVKSCKCS 112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TGF; transforming growth factor; scar formation; CNS; central nervous system; infusion; antagonist; brain; spinal cord; regeneration; decorin; Arg-Gly-Asp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (WHIT-) WHITTIER INST DIABETES & ENDOCRINOLOGY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAR42311 standard; peptide; 112 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 5; 32pp; English.
                                                                                                                                                                                                                                                                                                              AAR43263 standard; protein; 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              93WO-US03068
                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1993-336598/42.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
Les 86; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Baird A, Logan A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAR42311;
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Gaps

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Indels

Length 112;

78.9%; Score 500; DB 13; ilarity 76.8%; Pred. No. 3.9e-43; Conservative 11; Mismatches 15;

Ouery Match Best Local Similarity Matches 86; Conserv

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Non-soluble, monomeric transforming growth factor TGF-beta 1 (AARQ2773) was recovered from E. coli LC 137 (DSM 5658) transformants carrying plasmid ppLMu-TGF-beta 1, which includes the coding sequence (AAT17235) for TGF-beta 1. A biologically active, dimeric form of TGF-beta 1 was obtd. by refolding this monomer in detergentiree buffer contg. DMSO and/or DMF. Dimers of TGF-beta 2 (AAR92774) and TGF-beta 3 (AAR92772), and hybrid dimers (see also AAR92775), were also produced.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 ALDINYCFRNLEENCCVRPLYIDFRQDLGWKWVHEPKGYYANFCSGPCPYLRSADTTHST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Prodn. of dimeric, biologically active transforming growth factor beta - by refolding denatured monomer in buffer contg. mild detergent and specific organic solvents to improve yields
                                                                                                                       Prodi. of dimeric biologically active transforming growth factor by refolding denatured monomer in detergent-free folding buffer contg. specific organic solvent to improve yield
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 VLGLYNTLNPEASASPCCVPQDLEPLTILYYVGRTPKVEQLSNMVVKSCKCS 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Transforming growth factor beta; TGF; regulator; method; proliferation; differentiation; wound healing; solvent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           78.9%; Score 500; DB 17; 76.8%; Pred. No. 3.9e-43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human transforming growth factor beta 1.
                                                                                                                                                                                                Example 1B; Page 29-30; 54pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR91956 standard; Protein; 112 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 1; Page 33; 59pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               86; Conservative
(CIBA ) CIBA GEIGY AG.
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                                                                    WPI; 1996-117000/12.
N-PSDB; AAT17235.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                     112 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO9603432-A1
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                                  Cerletti N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cerletti N;
                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 recombinant cells, and thus produced is stable in the presence of 50 microg/ml mathotreaxte. TGF-beta may be produced in large amounts via recombinant means and has uses such a wound healing, treatment of fractures, inflammation, autoimmune disease or tumours.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 ALDTNYCFRNLEENCCVRPLYIDFRQDLGWKWVHEPKGYYANFCSGPCPYLRSADTTHST 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Prodn. of recombinant cell for high expression of polypeptide such as human TGF-beta - for treatment of e.g. wounds, fractures, inflammation, auto-immune diseases or tumours
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human transforming growth factor (TGF) -beta can be produced in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       78.9%; Score 500; DB 14; Length 112; llarity 76.8%; Pred. No. 3.9e-43; Conservative 11; Mismatches 15; Indels (
                                                                                   Transforming growth factor beta; stable; treatment; wounds; fractures; inflammation; autoimmune disease; tumours.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Transforming growth factor type beta; TGF-beta 1; protein renaturation; protein folding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 15; 18pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAR92773 standard; Protein; 112 AA.
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                                                                                                                                          sapiens (recombinant).
                                               Recombinant human TGF-beta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17-JUL-1996 (first entry)
                                                                                                                                                                                                                                                                                                                             (EART ) EARTH SEIYAKU KK.
                                                                                                                                                                                                                                                                                                                                                               WPI; 1993-347572/44.
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Best Local Similarity
Matches 86; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human TGF-beta
                                                                                                                                                                             JP05252956-A
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AAR92773 RESULT

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Gaps 9

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15;

Length 112; Indels

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Growth factor (TGF) beta-1, TGF beta-2 and TGF beta-3 which are used to growth factor (TGF) beta-1, TGF beta-2 and TGF beta-3 which are used to produce TGF beta-1ike proteins in dimeric form. The TGF beta-1ike proteins produced are hybrids of 2 different types of TGF beta-6.

TGF beta-1-3, TGF beta-2-3, etc, or bone morphogenic proteins e.g. BMP-2. The TGF beta hybrids were made using a new process of producing dimeric, biologically active TGF beta-1ike proteins. The new process involves treating denatured TGF beta monomers with folding buffer contg. a mild detergent (CHAPS, CHAPSO or digitonin) and at least one of the solvents DMSC (dimethyl sulphone) and DMF (dimethyl formamide). The detergent allows folding of the monomer such that, after dimerisation, the TGF beta-like protein retains biological activity and remains in soluble form. The method allows relatively high yields of biologically active TGF beta-like proteins in their native dimeric form. TGF-beta like proteins are multifunctional regulators of cellular activity and a typical use is to stimulate wound healing.
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                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                  1 ALDINYCFRNLEENCCVRPLYIDFRQDLGWKWVHEPKGYYANFCSGPCPYLRSADITHSI 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Prepn. of transforming growth factor-beta fusion protein - useful to reduce surgery recovery time and to prepare artificial skin \,
                                                                                                                                                                                                                                                                                                                                                                                                  ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Transforming growth factor-beta fusion protein; wound healing; artificial skin; surgery recovery time.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 112;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGF-betal active fragment of a TGF-beta fusion protein.
                                                                                                                                                                                                                                                                                                                        78.9%; Score 500; DB 17; 76.8%; Pred. No. 3.9e-43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ï
                                                                                                                                                                                                                                                                                                                                                      11; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 12; Page 45-46; 59pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     96WO-US08973
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHEUNG D T. HALL F L. NIMNI M E.
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                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 86; Conserv
                                                                                                                                                                                                                                                                             AA;
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                                                                                                                                                                                                                                                                            112
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A novel transforming growth factor-beta (TGF-beta) fusion protein comprises a purification tag and a TGF active fragment. The present sequence represents a specifically claimed TGF-betal active fragment. Additionally, the fusion protein may comprise proteinase-sensitive linker sites and binding domain so the protein sequence may contain some or all of the following elements: purification tag:proteinase some or all of the following elements: purification tag:proteinase site:TGF-beta promotes wound healing, and the fusion protein can be used to reduce surgery recovery time and in the preparation of artificial skin. The inclusion of a purification tag facilitates purification of the fusion protein. The proteinase site is included to permit cleavage and release of the purification tag after purification if desired. The extracellular matrix binding site facilitates delivery of the fusion protein to the desired site of action. Delivery of the TGF-beta to the site to be treated reduces the amount of TGF-beta required to be administered to be effective and reduces the concentration of circulating TGF-beta
                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                      1 ALDTNYCFRNLEENCCVRPLYIDFRQDLGWKWVHEPKGYYANFCSGPCPYLRSADTTHST 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA encoding transforming growth factor-beta precursor sequence useful for analysis to perform manipulations to increase yield of recombinant production of the protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 VLGLYNTLNPEASASPCCVPQDLEPLTILYYVGRTPKVEQLSNMVVKSCKCS 112
                                                                                                                                                                                                                                                                                                                                                                  78.9%; Score 500; DB 18; Length 112; 76.8%; Pred. No. 3.9e-43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human transforming growth factor-beta 1 N-terminal sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                      15;
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85US-0715142.
89US-0389929.
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                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
les 86; Conserv
                                                                                                                                                                                                                                                                                                                 112 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13-MAR-1987;
22-MAR-1985;
04-AUG-1989;
04-MAR-1992;
05-NOV-1993;
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                                                                                                                                                                                                                                                                                                                   Sequence
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Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 80
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This is the amino acid sequence of human transforming growth factor beta-1 (TGF-beta 1, see also AAW78785). The sequence shows homology to human TGF-beta 3 (see AAW78782), porcine TGF-beta 3 (see AAW78784) and bovine TGF-beta 2 (see AAW78784) N·terminal sequences. The invention relates to the recombinant production of TGF-beta. DNA encoding TGF-beta has been isolated and cloned into vectors which are replicated in bacteria and expressed in eukaryotic cells. TGF-beta recovered from transformed cells can be used in known
                                                                                                                                                                                                                                                                                              1 ALDINYCFRNLEENCCVRPLYIDFRQDLGWKWVHEPKGYYANFCSGPCPYLRSADTTHST 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Growth factor; human; dimer; cysteine knot; cellular inclusion body;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Preparing active growth factor dimers from inclusion bodies in high
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                                                                                                                                                                                                                                                                                                                                                              61 VLGLYNTLNPEASASPCCVPQDLEPLTILYYVGRTPKVEQLSNMVVKSCKCS 112
                                                                                                                                                                                                              Length 112;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Weich
                                                                                                                                                                                                                                                 15;
                                                                                                                                                                                                            78.9%; Score 500; DB 19; 76.8%; Pred. No. 3.9e-43; iive 11; Mismatches 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human growth factor protein fragment TGF-Betal.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      97DE-1048734
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                               therapeutic applications.
                                                                                                                                                                                                                             Best Local Similarity 76.8
Matches 86; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1999-278785/24
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Length 112;

Score 500; DB 20; Pred. No. 3.9e-43;

78.9%; 76.8%;

Query Match Best Local Similarity

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence represents the mature form of transforming growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
              ALDINYCFRNLEENCCVRPLYIDFRQDLGWKWVHEPKGYYANFCSGPCPYLRSADITHST 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 ALDINYCFRNLEENCCVRPLYIDFRQDLGWKWVHEPKGYYANFCSGPCPYLRSADTIHST
                                                                                                                                                                                                                                                                                                             S-sulphonated TGF-beta-like protein; wound treatment; cancer; bone repair; tissue repair; bone marrow protective agent; cardioprotection; anti-inflammatory; immunosuppressive;
                                                           VLGLYNTLNPEASASPCCVPQDLEPLTILYYVGRTPKVEQLSNMVVKSCKCS 112
                                                                          Growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 112;
                                                                                                                                                                                                                                                                                               Transforming growth factor-beta-1; TGF-beta-like protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Schmitz A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Producing biologically active dimeric Transforming Grov
Factor-beta - by refolding new monomeric Transforming (
Factor-beta, useful for treatment of wounds and cancer
                                                                                                                                                                                                                                                                The mature form of transforming growth factor-beta-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      78.9%; Score 500; DB 20; 76.8%; Pred. No. 3.9e-43; Live 11; Mismatches 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Meyhack B,
                                                                                                                                                                       AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 1; Page 28; 32pp; English.
                                                                                                                                                                    AAW97091 standard; Protein; 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     90EP-0810922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  89GB-0027546
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1999-083520/08.
N-PSDB; AAX15245.
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86; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          112 AA;
                                                                                                                                                                                                                                                                                                                                                            bed sore.
                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    36-DEC-1989;
                                                                                                                                                                                                                                 28-APR-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                        EP891985-A1
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Best Local S
Matches 86
                                                                                                                                                                                                   AAW97091;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
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AAY92010 standard; Protein; 112 AA.

84

AAY92010

AAY92010;

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active
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                                                                                                                                                                                             Proteinase site; bone morphogenetic fusion protein; bone binding site; bone morphogenetic protein; transforming growth factor beta; active fragment; wound healing; bone growth; purification tag.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New bone morphogenetic fusion proteins - comprising a purification tag and a bone morphogenetic active fragment, used for enhancing wound healing or bone growth
VLGLYNTLNPEASASPCCVPQDLEPLTILYYVGRTPKVEQLSNMVVKSCKCS 112
                 Transforming growth factor beta active fragment.
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                                                                                      AAW84207 standard; Protein; 112
                                                                                                                                                                                                                                                                                                                             98WO-US11189
                                                                                                                                                                                                                                                                                                                                                     97US-0868452
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     or bone growth.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1999-059875/05.
                                                                                                                                                                                                                                                                                                                                                                                          HAN B.
NIMNI M E.
SHORS E C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            112 AA;
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                                                                                                                                                                                                                                                Homo sapiens
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                                                                                                                                                                                                                                                                                                                            02-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                     03-JUN-1997;
                                                                                                                                          25-MAR-1999
                                                                                                                                                                                                                                                                                                  10-DEC-1998.
                                                                                                                 AAW84207;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hall FL,
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(SHOR/) S
(WULL/) N
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(HANB/)
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Mutants comprise at least one electrostatic charge altering mutation in a beta hairpin loop, resulting in increased bloactivity.

Mutant cystine knot growth factor (CKGF) proteins comprising one or more mutant subunits and having novel properties or improved pharmacological properties, compared to wild type CKGFs, are claimed. The CKGF superfamily comprises at least four families of growth factors: the glycoprotein hormones, the platelet-derived growth factor (PDGF) family, the neurotrophins and the transforming growth factor beta family; the families are known to be structurally similar (especially comprising the cystine knot topology) and it was shown that mutations at certain positions in the CKGF hairpin loops of family members and other members of the CKGF superfamily could significantly alter the biological mutant transforming growth factor family proteins or analogues are useful
                                                                                                                                                                                                           /note= "optionally mutated to increase electrostatic interaction between beta hairpin structure and a receptor"
                                                                                                                                                                                                                                                                                                                                           /note= "optionally mutated to increase electrostatic interaction between beta hairpin structure and a receptor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "optionally mutated to increase electrostatic interaction between beta hairpin structure and a receptor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                more
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mutant cystine knot growth factor proteins comprising one or ant subunits, useful for treating or preventing diseases e.g.
                                                                                                                                                                                                                                                                                                   or more
                                                                                              human transforming growth factor beta 1 monomer; CKGF; mutant; cystine knot growth factor; hairpin loop; infertility.
                                                                                                                                                                                                                                                                                                /note= "mutant optionally comprises one substitutions in these residues"
                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "mutant optionally comprises one
   substitutions in these residues"
                                                                 Human transforming growth factor beta 1 monomer.
                                                                                                                                                                                                                                                                                                                                                                                              82..102
/label= beta_hairpin_loop_3
                                                                                                                                                                                                                                                                                beta_hairpin_loop_1
                                                                                                                                                                                Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothyroidism and thyroid cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (UYMA-) UNIV MARYLAND BALTIMORE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Szkudlinski MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98WO-US19772.
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                                 (first entry)
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/label= h
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                                                                                                                                                                                                                                                                                                                              41..81
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                                                                                                                                                                                                                                                                                                                              Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Weintraub BD,
                                                                                                                                                Homo sapiens
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                                 19-JUL-2000
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Gaps

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Length 112; 15; Indels

DB 20;

78.9%; Score 500; DB 20; 76.8%; Pred. No. 3.9e-43; Live 11; Mismatches 15

Conservative

86;

Best Loca Matches

Similarity

Query Match Local

1 ALDTNYCFRNLEENCCVRPLYIDFRQDLGWKWVHEPKGYYANFCSGPCPYLRSADTTHST 60

> g Qγ

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61 VLGLYNTLNPEASASPCCVPQDLEPLTILYYVGRTPKVEQLSNMVVKSCKCS 112 

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for treatment of ovulatory dysfunction, luteal phase defect, unexplained infertility, time-limited conception and in assisted reproduction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention describes the a method for screening potential inhibitors of the expression of the Pax4 gene by contacting the potential inhibitor with pancreatic beta cells and measuring the expression of the gene in these cells is new. Substances identified by the screening method potentiate the expression of the Pax4 gene in pancreatic beta cells and accelerate the expression of the Pax4 gene in those cells. The method can be used in the treatment of disorders in which the exhaustion of pancreatic beta cells is involved, such as diabetes. The present sequence represents the human transforming growth factor protein which is used in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; transforming growth factor; Pax4 gene; expression; potentiator; insulin; pancreatic beta cell; diabetes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Screening potential Pax4 gene potentiators, used in treatment of, e.g.
                                                                                                                          Gaps
                                                                                                                                                       1 ALDINYCFRNLEENCCVRPLYIDFRQDLGWKWVHEPKGYYANFCSGPCPYLRSADTTHST 60
                                                                                                                                                                       ;
0
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                                                                                          Length 112;
                                                                                                                          Indels
                                                                                            78.9%; Score 500; DB 21; 76.8%; Pred: No. 3.9e-43;
                                                                                                                                                                                                                                                                                                                                                                                                                       Human transforming growth factor SEQ ID NO:2.
                                                                                                                          11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 29; 38pp; Japanese.
                                                                                                                                                                                                                                                                                                                          AAY67950 standard; protein; 112 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (YAMA ) YAMANOUCHI PHARM CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98JP-0167976.
                                                                                                                          Conservative
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                                                                                                         Local Similarity
tes 86; Conserv
                                              112 AA;
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Matches
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providing attachment of a hearin binding peptide (HBP), a peptide comprising a binding domain which binds heparin with high affinity, heparin or heparin-like polymer, and a protein growth factor or peptide fragment which has a domain that binds heparin with low affinity, included in the invention is a vascular graft comprising the matrix, which is capable of supporting cell adhesion. The matrix is used for peptides in a controlled manner suitable for wound healing. The matrix can be used in an article for treating dermal wounds, and in an implantable sterilized composition capable of supporting cell adhesion. The present sequence represents a growth factor protein. The present sequence represents a growth factor protein. The protein is used in an example illustrating that non-heparin-based drug delivery
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matrix for controlled release of growth factor for wound healing, has
                                                                                                                                                                                                                                                                                                      Heparin binding; vascular graft; matrix; cell adhesion; growth factor; wound healing; dermal wound; wound healing; TGF-beta 1.
Indels · 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 ALDITNYCFRNLEENCCVRPLYIDFRQDLGWKWVHEPKGYYANFCSGPCPYLRSADTTHST 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This invention relates to a matrix comprising a substrate capable of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   substrate that attaches heparin binding peptide, protein growth f
that bind heparin with low affinity, and heparin or heparin-like
                                                                   61 VLGLYNTLNPEASASPCCVPQDLEPLTILYYVGRTPKVEQLSNMVVKSCKCS 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 112;
                                               61 VLGLYNTLNPEASASPCCVPQDLEPLTILYYVGRTPKVEQLSNMVVKSCKCS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               systems based on their low affinity for heparin.
                                                                                                                                                                  AAB35937 standard; protein; 112 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (ETHZ-) ETH ZURICH & UNIV ZURICH.
                                                                                                                                                                                                                                                                    TGF-beta 1 amino acid sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99WO-IB00800.
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Best Local Similarity 76.8
Matches 86; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hubbell JA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-024627/03.
                                                                                                                                                                                                                                                                                                                                                                                         WO200064481-A1.
                                                                                                                                                                                                                                                                                                                                                       Unidentified.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22-APR-1999;
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Gaps

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Indels

Length 112;

1 ALDINYCFRNLEENCCVRPLYIDFRQDLGWKWVHEPKGYYANFCSGPCPYLRSADTTHST 60

78.9%; Score 500; DB 21; ilarity 76.8%; Pred. No. 3.9e-43; Conservative 11; Mismatches 15;

Query Match Best Local Similarity

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           RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New substantially purified growth differentiation factor-8 polypeptide, useful for treating muscle wasting disease, obesity, muscular dystrophy, neuromuscular disorder, acquired immunodeficiency syndrome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          organ systems, particularly cells in muscle or adipose tissues and in gene therapy for the treatment of cell proliferative or immunological diseases mediated by GDF-8. In addition, GDF-8 is also useful for treating muscle wastling disease, neuromuscular disorder, spinal cord injury, traumatic injury, congestive obstructive pulmonary disease (COPD), AIDS or cachexia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gene therapy, growth differentiation factor-8; GDF-8; AIDS; cachexia; neurodegenerative disease; amyotrophic lateral sclerosis; obesity; muscular dystrophy; musculodegenerative disease; tissue repair; muscle wasting disease; neuromuscular disorder; spinal cord injury;
61 vlalynghnpgasaapccvpgaleplpivyyvgrkpkveglsnmivrsckcs 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             traumatic injury; congestive obstructive pulmonary disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (UYJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
                                                                                                                                                                                        AA.
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                                                                                                                                                                         AAB73204 standard; Protein; 115
                                                                                                                                                                                                                                                                                                                                                                                                   TGF-betal C-terminal sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17-AUG-2000; 2000WO-US22884.
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                                                                                                                                                                                                                                                                                                                               (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unidentified.
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                                                                                                                                                                                                                                                        AAB73204;
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The present sequence represents a novel transforming growth factor-beta (TGF-beta) fusion protein comprises a purification tag (shown in AAW01825) and a TGF active fragment (shown in AAW0173). Additionally, the fusion protein may comprise proteinase-sensitive linker sites and binding domain so the protein sequence may contain some or all of the fusion protein may comprise proteinase site; ECM binding site: FGF-beta. TGF-beta promotes wound healing, and the fusion protein can be used to reduce surgery recovery time and in the preparation of artificial skin. The inclusion of a purification tag facilitates purification of the fusion protein. The proteinase site is included to permit cleavage and release of the purification tag after purification if desired. The extracellular matrix binding site (facilitates delivery of the fusion protein to the desired site of action belivery of the TGF-beta to the site to be treated reduces the amount of the protein ministered to be defective and reduces the amount of the protein ministered to be effective and reduces the amount of the protein ministered to be effective and reduces the amount of the protein ministered to be effective and reduces the amount of the desired actions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     concentration of circulating TGF-beta which may result in undesirable
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                                                                                                                                         Transforming growth factor-beta fusion protein; wound healing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       78.9%; Score 500; DB 18; Length 11
76.8%; Pred. No. 4.1e-43;
.ive 11; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                   7..118
/label= TGF-betal_active_fragment
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                                                                                                                                                                                                                                                                      /label= Purification_tag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tuan T,
                                                                                                                                                         artificial skin; surgery recovery time
                                                                                                                                                                                                                                               Location/Qualifiers
AAW08176 standard; Peptide; 118 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page -; 59pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nimni ME,
                                                                                                       TGF-beta fusion protein 22:30.
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                                                                     (first entry)
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les 86; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hall FL,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TUAN T.
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                                                                                                                                                                                               Homo sapiens
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1 ALDINYCFRNLEENCCVRPLYIDFRQDLGWKWVHEPKGYYANFCSGPCPYLRSADTTHST 60

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Gaps

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Indels

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78.9%; Score 500; DB 76.8%; Pred. No. 4e-43 ive 11; Mismatches

Best Local Similarity 76.8 Matches 86; Conservative

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Query Match

DB 22; Length 115;

1 ALDTNYCFRNLEENCCVRPLYIDFRQDLGWKWVHEPKGYYANFCSGPCPYLRSADTTHST 60 

61 VLGLYNTLNPEASASPCCVPQDLEPLTILYYVGRTPKVEQLSNMVVKSCKCS 112 

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7 aldtnycfssteknccvrqlyidfrkdlgwkwihepkgyhanfclgpcpyiwsldtgysk 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Prepn. of transforming growth factor-beta fusion protein – useful to reduce surgery recovery time and to prepare artificial skin \,
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                                          11..122
/label= TGF-betal_active_fragment
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                                                                                                                                                                                                                                                                                                                                                                                                  /label= Purification_tag
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/label= Proteinase_site
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                                                                                                                                                  AAW08181 standard; Peptide; 122 AA.
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                                                                                                                                                                                                                                              PGF-beta fusion protein 22:13:30.
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HALL F L.
NIMNI M E.
TUAN T.
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(NIMN/)
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A novel transforming growth factor-beta (TGF-beta) fusion protein comprises a purification tag and a TGF active fragment. Additionally, the fusion protein may comprise proteinase-sensitive linker sites and binding domain so the protein sequence may contain some or all of the following elements: purification tag;proteinase site:ECM binding site:proteinase site:TGF-beta. The present sequence represents a fusion protein made up from a purification tag (AAM18225), a proteinase site
                                                                                                                                                                       Gaps
                                                                                                                                                                                                               1 ALDINYCFRNLEENCCVRPLYIDFRQDLGWKWVHEPKGYYANFCSGPCPYLRSADTTHST 60
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N.B. The present sequence is does not appear in the specification, but is derived from the sequences mentioned above.
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                                                                                                                                                                                                                                                                                                                        61 VLGLYNTLNPEASASPCCVPQDLEPLTILYYVGRTPKVEQLSNMVVKSCKCS 112
                                                                                                                               Length 122;
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/label= TGF-betal_active_fragment
                                                                                                                             ; DB 18;
4.2e-43;
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                                                                                                                                                                     11; Mismatches
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                                                                                                                             78.9%; Score 500; 76.8%; Pred. No. 4
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                                                                                                                                                                       86; Conservative
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                                                                                                                                                 Similarity
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(NIMN/) NIMNI M E.
(TUAN/) TUAN T.
                                                                122 AA;
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Would healing, and the fusion protein can be used to reduce surgery wound healing, and the fusion protein can be used to reduce surgery recovery time and in the preparation of artificial skin. The inclusion of a purification tag facilitates purification of the fusion protein. The proteinase site is included to permit cleavage and release of the purification tag after purification if desired. The extracellular matrix binding site facilitates delivery of the fusion protein to the desired site of action. Delivery of the TGF-beta to the site to be treated reduces the amount of TGF-beta required to be administered to be effective and reduces the concentration of circulating TGF-beta which may result in undesirable effects.

N.B. The present sequence is does not appear in the specification, but is derived from the sequences mentioned above.
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/label= Extracellular_matrix_binding_site
17..128
/label= TGF-betal_active_fragment
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/label= Purification_tag
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/label- Proteinase_site
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Best Local Similarity 76.8
Matches 86; Conservative
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(HALL/) HALL F L.
(NIMN/) NIMNI M E.
(TUAN/) TUAN T.
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                                                                                                                                                               124 AA;
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Synthetic.
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comprises a purification tag and a TGF active fragment. Additionally, the fusion protein may comprise proteinase sensitive linker sites and binding domain so the protein sequence may contain some or all of the following elements: purification tag; proteinase site:ECM binding site: protein made up from a purification tag (AAM18225), a proteinase site:TGF-beta. The present sequence represents a fusion protein made up from a purification tag (AAM18225), a proteinase site (AAW08159), an extracellular matrix binding site (AAW08171) and a TGF active fragment (AAW08173). TGF-beta promotes wound healing, and the fusion protein can be used to reduce surgery recovery time and in the preparation of artifical skin. The inclusion of a purification tag facilitates purification of the fusion protein. The proteinase site is included to permit cleavage and release of the purification tag after purification if desired. The extracellular matrix binding site facilitates delivery of the fusion protein to the desired site of action. Delivery of the fusion protein to be treated reduces the amount of TGF-beta to the site to be treated reduces the amount of TGF-beta required to be administered to be effective.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and reduces the concentration of circulating TGF-beta which may result in undesirable effects.
  of transforming growth factor-beta fusion protein - useful to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N.B. The present sequence is does not appear in the specification, but is derived from the sequences mentioned above.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 ALDINYCFRNLEENCCVRPLYIDFRODLGWKWVHEPKGYYANFCSGPCPYLRSADITHST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               growth factor-beta fusion protein; wound healing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 VLGLYNTLNPEASASPCCVPQDLEPLTILYYVGRTPKVEQLSNMVVKSCKCS 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 128;
                        surgery recovery time and to prepare artificial skin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Extracellular_matrix_binding_site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 500; DB 18;
Pred. No. 4.5e-43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /label- Purification_tag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label- Proteinase_site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       artificial skin; surgery recovery time.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGF-beta fusion protein 22:15:18:30.
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                                                              Disclosure; Page -; 59pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        78.9%;
76.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13..18
/label= E
19..130
/label= T
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Best Local Similarity
Matches 86; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  128 AA;
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Synthetic.
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                          reduce
Prepn.
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11..19 /label= Extracellular\_matrix\_binding\_site

/label= Purification\_tag 7..10 /label= Proteinase\_site

Location/Qualifiers

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Key
Region
                                              Region
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                                                                                                                                                                                                                                  comprises a purification tag and a TGF active fragment. Additionally, the fusion protein may comprise proteinase-sensitive linker sites and binding domain so the protein sequence may contain some or all of the full of proteinase site: ECM binding site: proteinase site: ECM binding site: proteinase site: TGF-ber. The present sequence represents a fusion protein made up from a purification tag (AAMU8225), a proteinase site: (AAW08173), an extracellular matrix binding site (AAW08171) and a TGF cusion protein can be used to reduce surgery recovery time and in the preparation of artificial skin. The inclusion of a purification from protein. The proteinase site is included to permit cleavage and release of the purification tag after purification if desired. The extracellular matrix binding site facilitates delivery of the fusion protein to the desired site of action. Delivery of the TGF-beta to the site to be treated reduces the amount of TGF-beta equired to be administered to be effective and reduces the concentration of circulating TGF-beta which may
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                                                                                                                                                                   Prepn. of transforming growth factor-beta fusion protein - useful to reduce surgery recovery time and to prepare artificial skin \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 ALDINYCFRNLEENCCVRPLYIDFRQDLGWKWVHEPKGYYANFCSGPCPYLRSADTTHST 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N.B. The present sequence is does not appear in the specification, but is derived from the sequences mentioned above.
                                                                                                                                                                                                                         novel transforming growth factor-beta (TGF-beta) fusion protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 130;
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Query Match

78.9%; Score 500; DB 18;
Best Local Similarity 76.8%; Pred. No. 4.6e-43;
Matches 86; Conservative 11; Mismatches 15;
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                                                                                                                          3
                                                                                                                         Tuan T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IGF-beta fusion protein 22:13:20:30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW08182 standard; Peptide; 131 AA.
                                                                                                                                                                                                    Disclosure; Page -; 59pp; English
                                                                                                                       Nimni ME,
                                                                                                                                                                                                                                                                                                                                                                                                                                    in undesirable effects.
           96WO-US08973.
                                 95US-0470837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26-AUG-1997 (first entry)
                                                                                                                       Hall FL,
                                                     CHEUNG D T. HALL F L. NIMNI M E.
                                                                                                                                              WPI; 1997-043065/04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              130 AA;
                                                                                       TUAN T.
                                                                                                    (WULL/) WU L.
           05-JUN-1996;
                                 06-JUN-1995;
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Synthetic.
                                                                                                                       DT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW08182;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                      CHEU/)
                                                                   (HALL/)
(NIMN/)
                                                                                                                      Cheung
                                                                                       TUAN/
                                                                                                                                                                                                                                                                                                                                                                                                                                    result
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comprises a purification tag and a TGF active fragment. Additionally, the fusion protein may comprise proteinase sensitive linker sites and biding domain so the protein sequence may contain some or all of the binding domain so the protein tag. Proteinase site:ECM binding site: proteinase site:ECF-beta. The present sequence represents a fusion protein made up from a purification tag:proteinase site:ECM binding site: protein made up from a purification tag (AAMN8125), a proteinase site (AAW08169), an extracellular matrix binding site (AAW08169), an extracellular matrix binding site (AAW08172) and a TGF active fragment (AAW08173). TGF-beta promotes wound healing, and the preparation of artificial skin. The inclusion of a purification tag is included to permit cleavage and release of the purification tag after purification if desired. The extracellular matrix binding site facilitates delivery of TGF-beta fusion protein to the desired site of action. Delivery of the TGF-beta to the site to be treated reduces the reduces the cancent the concentration of circulating TGF-beta which may result in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20 aldtnycfssteknccvrqlyidfrkdlgwkwihepkgyhanfclgpcpyiwsldtgysk 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N.B. The present sequence is does not appear in the specification, but is derived from the sequences mentioned above.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Prepn. of transforming growth factor-beta fusion protein - u reduce surgery recovery time and to prepare artificial skin
20..131
/label= TGF-betal_active_fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             78.9%; Score 500; DB 18; 76.8%; Pred. No. 4.6e-43;
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11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tuan T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page -; 59pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cheung DT, Hall FL, Nimni ME,
                                                                                                                                                                                                                                                                           95US-0470837.
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Matches 86; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                undesirable effects.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1997-043065/04
                                                                                                                                                                                                                                                                                                                                                             HALL F L.
NIMNI M E.
TUAN T.
                                                                                                                                                                                                                                                                                                                                       CHEUNG D T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 131 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              (WULL/) WU L.
                                                                                    WO9639430-A1
                                                                                                                                                                                                               05-JUN-1996;
                                                                                                                                                                                                                                                                           06-JUN-1995;
                                                                                                                                                   12-DEC-1996.
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                                                                                                                                                                                                                                                                                                                                                                   (HALL/)
(NIMN/)
                                                                                                                                                                                                                                                                                                                                    (CHEU/)
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A novel transforming growth factor-beta (TGF-beta) fusion protein comprises a purification tag and a TGF active fragment. Additionally, the fusion protein may comprise proteinase-sensitive linker sites and binding domain so the protein sequence may contain some or all of the following elements: purification tag:proteinase site:ECM binding site: Following elements: purification tag:proteinase site:ECM binding site: proteinase site: TGF-beta. The present sequence represents a fusion protein made up from a purification tag (AAMU8125), a proteinase site (AAW08169) and a TGF active fragment (AAW08173).

TGF-beta promotes wound healing, and the fusion protein can be used to reduce surgery recovery time and in the preparation of artificial skin. The proteinses site is included to permit cleavage and release of the purification tag after purification if desired. The extracellular matrix binding site facilitates delivery of the fusion protein. The proteinses site is included to permit cleavage and release of the purification tag after purification if desired. The extracellular matrix binding site facilitates delivery of the fusion protein to the desired site of action. Delivery of the TGF-beta to the cattered reduces the amount of TGF-beta required to be administered to be effective and reduces the concentration of circulating the present sequence is does not appear in the specification, which the present sequence is does not appear in the specification,
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                                                                                                                                                     Transforming growth factor-beta fusion protein; wound healing; artificial skin; surgery recovery time.
                                                                                                                                                                                                                                                                                                                                                              /label= Extracellular_matrix_binding_site
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                                                                                                                                                                                                                                                                                                                                                                                                                 21..132
/label= TGF-betal_active_fragment
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                                                                                                                                                                                                                                                                                                                                                                              17..20
/label= Proteinase_site
21..132
                                                                                                                                                                                                                                                                                                                           /label= Proteinase_site
                                                                                                                    TGF-beta fusion protein 22:13:18:13:30.
                                                                                                                                                                                                                                                           Location/Qualifiers
                 AAW08189 standard; Peptide; 132 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nimni ME,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       96WO-US08973
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                                                                                    (first entry)
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(HALL/) HALL F L.
(NIMN/) NIMNI M E.
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Synthetic.
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                                                                                    26-AUG-1997
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                                                   AAW08189
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AAW08189
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132 AA;

Sequence

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A novel transforming growth factor-beta (TGF-beta) fusion protein comprises a purification tag and a TGF active fragment. Additionally, the fusion protein may comprise proteinase-sensitive linker sites and binding domain so the protein sequence may contain some or all of the following elements: purification tag:proteinase site:ECM binding site: proteinase site:TGF-beta. The present sequence represents a fusion protein made up from a purification tag (AAM18225), a proteinase site (AAW08170), an extracellular matrix binding site (AAW08172) and a TGF active fragment (AAW08173). TGF-beta promotes wound healing, and the
                                                                   Gaps
                                                    1 ALDINYCFRNLEENCCVRPLYIDFRQDLGWKWVHEPKGYYANFCSGPCPYLRSADTIHST 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Prepn. of transforming growth factor-beta fusion protein – useful to reduce surgery recovery time and to prepare artificial skin \,
                            ö
                                                                                                                                                                                                                                                                                                         Transforming growth factor-beta fusion protein; wound healing;
                                                                                                        61 VLGLYNTLNPEASASPCCVPQDLEPLTILYYVGRTPKVEQLSNMVVKSCKCS 112
                                                                                                                       Length 132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    13..21
/label= Extracellular_matrix_binding_site
22..13
/label= TGF-betal_active_fragment
                            15; Indels
    DB 18;
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  Score 500; DB 18;
Pred. No. 4.6e-43;
                            11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                             /label= Purification_tag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tuan T,
                                                                                                                                                                                                                                                                                                                                                                                                                               7..12
/label= Proteinase_site
                                                                                                                                                                                                                                                                                                                      artificial skin; surgery recovery time
                                                                                                                                                                                                                                                                               TGF-beta fusion protein 22:15:20:30.
                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                 AAW08178 standard; Peptide; 133 AA.
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78.9%;
76.8%;
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                           86; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cheung DT, Hall FL,
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HALL F L.
NIMNI M E.
TUAN T.
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                Best Local Similarity
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Synthetic.
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fusion protein can be used to reduce surgery recovery time and in the preparation of artificial skin. The inclusion of a purification tag facilitates purification of the fusion protein. The proteinase site is included to permit cleavage and release of the purification tag after purification if desired. The extracellular matrix binding site facilitates delivery of the fusion protein to the desired site of amount of TGF-beta required to be administered to be effective and reduces the concentration of circulating TGF-beta which may result in undesirable effects.
                                                                                                                                                             Gaps
                                                                                                                                                                            1 ALDINYCFRNLEENCCVRPLYIDFRQDLGWKWVHEPKGYYANFCSGPCPYLRSADTTHST 60
                                                                                                                                                                                      B. The present sequence is does not appear in the specification,
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                                                                                                                                                                                                                      61 VLGLYNTLNPEASASPCCVPQDLEPLTILYYVGRTPKVEQLSNMVVKSCKCS 112
                                                                                                                                         Length 133;
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                                                                                               but is derived from the sequences mentioned above.
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Jabel- Proteinase_site
23..134
/label- TGF-betal_active_fragment
                                                                                                                                         78.9%; Score 500; DB 18; 76.8%; Pred. No. 4.7e-43;
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/label= F
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/label= F
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HALL F L.
NIMNI M E.
TUAN T.
                                                                                                                                                 Best Local Similarity
Matches 86; Conserv
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comprises a purification tag and a TGF active fragment. Additionally, the fusion protein may comprise proteinase-sensitive linker sites and binding domain so the protein sequence may contain some or all of the following elements: purification tag:proteinase site:ECM binding site: proteinase site:TGF-beta. The present sequence represents a fusion protein made up from a purification tag: (AAM08125), a proteinase site (AAM08169) and a TGF active fragment (AAM0817), an extracellular matrix binding site (AAM0817), another proteinase site (AAM08169) and a TGF active fragment (AAM0817).

TGF-beta promotes wound healing, and the fusion protein can be used to reduce surgery recovery time and in the preparation of artificial skin. The inclusion of a purification tag facilitates purification of the customer the proteinase site is included to permit cleavage and release of the purification tag after purification if desired. The extracellular matrix binding site facilitates delivery of the fusion protein to the desired site of action. Delivery of the TGF-beta to the site to be treated reduces the amount of TGF-beta required to be administered to be effective and reduces the concentration of circulating and the property of the TGF-beta required to be administered to be effective and reduces the concentration of circulating and the property of the top top the tage of the property of the tage of tag
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Prepn. of transforming growth factor-beta fusion protein - useful to reduce surgery recovery time and to prepare artificial skin \,
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                                                                                                                                                                                                                   A novel transforming growth factor-beta (TGF-beta) fusion protein
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/label= Extracellular_matrix_binding_site
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/label= TGF-betal_active_fragment
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/label= Proteinase_site
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/label= Proteinase_site
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                                                                                                                                Disclosure; Page -; 59pp; English.
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tgfb3p.rag

11..19 /label= Extracellular\_matrix\_binding\_site

/label= Purification\_tag Proteinase\_site

/label=

Location/Qualifiers

Homo sapiens.

Synthetic.

Key Region Region Region Region Region

20..23 Jabel- Proteinase\_site 24..135 /label- TGF-betal\_active\_fragment

96WO-US08973. 95US-0470837.

05-JUN-1996; 06-JUN-1995;

12-DEC-1996.

WO9639430-A1

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Anovel transforming growth factor-beta (TGF-beta) fusion protein comprises a purification tag and a TGF active fragment. Additionally, the fusion protein may comprise proteinase-sensitive linker sites and binding domain so the protein sequence may contain some or all of the binding domain so the protein sequence may contain some or all of the collowing elements: purification tag.proteinase site:ECM binding site: Collowing elements: purification tag.proteinase site a fusion protein made up from a purification tag (AAM08125), a proteinase site (AAW08169), an extracellular matrix binding site (AAW08170) and a TGF active fragment (AAW08173).

CTGF-beta promotes wound healing, and the fusion protein can be used to reduce surgery recovery time and in the preparation of artificial skin.

CTGF-beta promotes wound healing, and the fusion protein of the collision of the proteinses site is included to permit cleavage and release of the purification tag after purification if desired. The extracellular matrix binding site facilitates delivery of the fusion protein to the desired site of action. Delivery of the TGF-beta to the site to be treated reduces the amount of TGF-beta required to be administered to be effective and reduces the concentration of circulating concentration may result in undesirable effects.

N.B. The present sequences mentioned above.
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Best Local Similarity 76.8%; Pred. No. 4.7e-4
Matches 86; Conservative 11; Mismatches
                                                                                                                                                                                                                                                                      Tuan T,
                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page -; 59pp; English.
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                                                                           96WO-US08973.
                                                                                                               95US-0470837.
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                                                                                                                                                  CHEUNG D T.
HALL F L.
NIMNI M E.
                                                                                                                                                                                                                                                                                                     WPI; 1997-043065/04
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                                                                                                                                                                                                          TUAN T.
                                                                                                                                                                                                          (TUAN/) TUAN
(WULL/) WU L.
WO9639430-A1
                                                                                                               06-JUN-1995;
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Prepn. of transforming growth factor-beta fusion protein – useful to reduce surgery recovery time and to prepare artificial skin  $\,$ 

Disclosure; Page -; 59pp; English.

Wu L;

Tuan T,

Nimni ME,

Hall FL,

Cheung DT,

(UIMN/) NIMNI M E. (TUAN/) TUAN T. (WULL/) WU L. (CHEU/) CHEUNG D T. (HALL/) HALL F L.

WPI; 1997-043065/04.

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Anovel transforming growth factor-beta (TGF-beta) fusion protein

Comprises a purification tag and a TGF active fragment. Additionally,
the fusion protein may comprise proteinsae-sensitive linker sites and
binding domain so the protein sequence may contain some or all of the
binding domain so the protein sequence may contain some or all of the
Collowing elements: purification tag:proteinase site:ECM binding site:
Collowing elements: purification tag:proteinase site fusion

Collowing elements: purification tag (AAM/8215), a proteinase site
CC (AAW/8169), an extracellular matrix binding site (AAW/8172), another
CC (AAW/8169), an extracellular matrix binding site (AAW/8173).
CTGF-beta promotes wound healing, and the fusion protein can be used to
creduce surgery recovery time and in the preparation of artificial skin.
CC TGF-beta promotes wound healing, and the fusion protein can be used to
creduce surgery recovery time and in the preparation of a purification tag facilitates purification of the fusion
CC TGF-beta promotes alterial active to permit cleavage and
crelease of the purification tag after purification if desired. The
crelease of the purification and reduces the required to be
concentrated to be effective and reduces the concentration of circulating
CTGF-beta which may result in undesirable effects.

N.B. The present sequence is does not appear in the specification,
collowing the protein to the sequences mentioned above.
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Best Local Similarity 76.89
Matches 86; Conservative
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growth factor-beta fusion protein; wound healing;

TGF-beta fusion protein 22:13:20:13:30. Transforming growth factor-beta fusion artificial skin; surgery recovery time.

(first entry)

26-AUG-1997

AAW08183;

AAW08183 standard; Peptide; 135 AA

AAW08183

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Cheung DT,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A novel transforming growth factor-beta (TGF-beta) fusion protein

comprises a purification tag and a TGF active fragment. Additionally,
the fusion protein may comprise proteinase sensitive linker sites and
binding domain so the protein sequence may contain some or all of the
collowing elements: purification tag:proteinase site:ECM binding site:
Collowing elements: purification tag:proteinase site:ECM binding site:
Collowing elements: purification tag:proteinase site fusion
contains site: GARW08170) and a TGF active fragment (AAW08171), another
contains site (AAW08170), and a TGF active fragment (AAW08173).

TGF-beta promotes wound healing, and the fusion protein can be used to
reduce surgery recovery time and in the preparation of artificial skin.
TGF-beta promotes wound healing, and the fusion protein can be used to
reduce surgery recovery time and in the preparation of artificial skin.
TGF-beta promotes matrification tag after purification if desired. The
fusion protein The proteinase site is included to permit cleavage and
release of the purification tag after purification if desired. The
content matrix binding site facilitates delivery of the fusion
protein to the desired site of action. Delivery of the TGF-beta to the
site to be treated reduces the amount of TGF-beta required to be
contential to be effective and reduces the concentration of circulating
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                                                                                                                                                                                                                           Transforming growth factor-beta fusion protein; wound healing;
13..18
/label= Extracellular_matrix_binding_site
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Jabbl- Proteinase_site
25..136
/label- TGF-betal_active_fragment
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/label= Proteinase_site
                                                                                                                                                                                           TGF-beta fusion protein 22:15:18:15:30.
                                                                                                                                                                                                                                            artificial skin; surgery recovery time
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                                                                                             AAW08186 standard; Peptide; 136
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HALL F L.
NIMNI M E.
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Synthetic.
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A novel transforming growth factor-beta (TGF-beta) fusion protein comprises a purification tag and a TGF active fragment. Additionally,
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                                                                                                                                                                                                                                                              TGF-beta which may result in undesirable effects.
N.B. The present sequence is does not appear in the specification,
but is derived from the sequences mentioned above.
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                                                                                                                                                                                                                                                                                                                             VLGLYNTLNPEASASPCCVPQDLEPLTILYYVGRTPKVEQLSNMVVKSCKCS 112
                                                                                                                                                                                                                                                                                                                                                   Length 136;
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/label= Extracellular_matrix_binding_site
26..15
26..137
26..137
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                                                                                                                                                78.9%; Score 500; DB 18; 76.8%; Pred. No. 4.8e-43; iive 11; Mismatches 15;
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(HALL/) HALL F L.
(NIMN/) NIMNI M E.
(TUAN/) TUAN T.
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hes 86; Conserv
                                                                                     136 AA;
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the fusion protein may comprise proteinase-sensitive linker sites and binding domain so the protein sequence may contain some or all of the following elements: purification tag; proteinase site: ECM binding site: proteinase site: TGF-beta. The present sequence represents a fusion protein made up from a purification tag (AAWN8125), a proteinase site (AAWN8170), an extracellular matrix binding site (AAWN8173), another proteinase site (AAWN8170), an extracellular matrix binding site (AAWN8173), another proteinase site (AAWN8173) and the fusion protein can be used to reduce surgery recovery time and in the preparation of artificial skin. The inclusion of a purification tag facilitates purification of the tusion protein. The proteinase site is included to permit cleavage and extracellular matrix binding site facilitates delivery of the fusion protein to the desired site of action. Delivery of the TGF-beta to the site to be treated reduces the amount of TGF-beta required to be continued and in undestrable effects.

N.B. The present sequence is does not appear in the specification, but is derived from the sequences mentioned above. 137 AA; Sequence \$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$

Ouery Match 78.9%; Score 500; DB 18; Length 137; Best Local Similarity 76.8%; Pred. No. 4.8e-43; Matches 86; Conservative 11; Mismatches 15; Indels 0; Gaps

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1 ALDTHYCFRNLEENCCVRPLYIDFRQDLGWKWVHEPKGYYANFCSGPCPYLRSADTTHST 60

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Search completed: October 30, 2001, 08:51:22 Job time: 151 sec

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AF15598 Rattus norvegicus AF153013 Rattus norvegicus X57413 Mouse mRNA for trans AJ13218 Rattus norvegicus X57413 Mouse mRNA for trans AJ13218 Rattus norvegicus X576187 Xenopus laevis TGF-b X51817 Xenopus laevis TGF-b X51817 Xenopus laevis TGF-b X51817 Mouse transforming G X52498 Rat mRNA for transfor AJ009862 Mus musculus mRNA AJ009862 Mus musculus mRNA AF8277 H.sapiens TGF-beta l AA18277 H.sapiens TGF-beta l AA18277 H.sapiens TGF-beta l AA18277 H.sapiens TGF-beta l AA18277 H.sapiens TGF-beta l AA18275 TGF-betal coding regi A48563 Sequence l from Paten AA1856 Sequence l from Paten M38449 Human transforming gr I I05514 Sequence 1 from Paten M36271 Bovine transforming X76916 O.aries mRNA for tra IL34956 Canine transforming M1658 Simian fransforming Simian BC001125 Homo Sapiens, Simi
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A06669 Synthetic mRNA for p
X02812 Human mRNA for trans
M23703 Sus scrofa transform
X99438 E.caballus mRNA for
E00973 cDNA encoding human
1 A23756 TGF beta2(44445)beta1
1 L36038 Ovis aries transformi
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M19154 Human transforming g
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gb_part:108275

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gb_part:108375

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gb_part:108180

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A18281 H.sapiens TGF-beta 2 per
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A48553 Sequence 5 from Patent W
A48567 Sequence 1 from Patent W
A8036688 Sequence 33 from patent W
AR036688 Sequence 33 from patent U
556555 Sequence 3 from patent U
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A4856 Sequence 3 from Patent W
A803687 Sequence 31 from patent
15685 Sequence 2 from patent
A05306 Complete nucleotide sequent
A11707 mature H.sapiens G-TsF g
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J03585 African green monkey BG
A05308 Nucleotide sequence
A11709 H.sapiens G-TgF gene pd
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                                                                                                                                             About: Results were produced by the GenCore software, version 4.5, Copyright (c) 1993-2000 Compugen Ltd.
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Ratio: 5.652
Percent Similarity: 100.000
                                                                        CIBA-GEIGY AG
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    .339
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Cerletti,N., McMaster,G.K., Cox,D., Schmitz,A. and Meyhack,B. Process for the production of biologically active protein (e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25-JAN-1995
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    .339
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                                       Patent: EP 0433225-A 6 19-JUN-1991
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                                                                   Location/Qualifiers
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NOVEL PROCESS FOR THE PRODUCTION OF BIOLOGICALLY ACTIVE DIMERIC
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 339)
McMaster.G.K., Cox.D., Cerletti, N. and Kuhla, J.
Novel hybrid transforming growth factors
Patent: EP 0542679-A 3 19-MAY-1993;
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Other publication AU 3109595 960222
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A48553
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SGPCPYLRSADTTHSTVLGLYNTLNPEASASPCCVPQDLEPLILIYYVGRTPRVEQLS
                                conflict with the conceptual
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         51 GCGCCCCTCTACATTGACTTCCGACAGGATCTGGGCTGGAAGTGGGTCC 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
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Gaps: 0
Percent Identity: 100.000
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Mittl, P., Gruetter, M. and Arvinte, T.
TRANSPORMING GROWTH FACTOR BETA CRYSTALS
Patent: WO 9705166-A 1 13-FEB-1997;
CIBA GEIGY AG (CH)
Location/Qualifiers
1. 339
 /db_xref="taxon:32644"
1. .336
/note="Protein sequence is in
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/db_xref="taxon:32644"
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Sequence 1 from Patent W09705166.
A59779
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                                                translation"
                                                                                                                                                          NMVVKSCKCS"
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Percent Similarity: 100.000
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Quality:
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TGFB3P x A48567
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                                                                                                                     /translation="AldTNYCFRNLEENCCVRPLYIDFRQDLGWKWVHEPKGYYANFC
SGPCPYLRSADTTHSTVLGLYNTLNPEASASPCCVPQDLEPLTILYYVGRTPKVEQLS
                              /note="Protein sequence is in conflict with the conceptual
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 (bases 1 to 339)
Cerletti,N.
NEW PROCESS FOR THE PRODUCTION OF BIOLOGICALLY ACTIVE PROTEIN
PRACESS FOR THE PRODUCTION OF BIOLOGICALLY ACTIVE PROTEIN
PATENT: WO 9603433-A 5 08-FEB-1996;
CIBA GEIGY AG (CH)
Other publication AU 3109695 960222.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    07-MAR-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             151 CTCCGCAGTGCAGACACAACCCACAGCACGGTGCTGGGGACTGTACAACAC 200
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                                                                                                                                                                                                                                                 Length:
                                                           /codon_start=1
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Sequence 5 from Patent W09603433.
A48567.1 GI:2302337
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/db_xref="taxon:32644"
                                                                                                                                                                  86 g
                                             translation
                                                                                                                                                     NMVVKSCKCS"
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                                                                                                                                                                                                                                                              Ratio: 5.652
Percent Similarity: 100.000
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LOCUS A48567
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unclassified.
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TGFB3P x A48553
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06-MAR-1998

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<1. .339
/codon_start=1
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SGPCPYLRSADTHSTVLGLYNTLNPEASASPCCVPQDLEPLTILYYVGRTPKVEQLS</pre>
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1 (bases 1 to 339)
Hall,F.L., Nimni,M.E., Tuan,T., Wu,L. and Cheung,D.T.
Artificial skin prepared from coclagen matrix containing transforming growth factor. beta. having a collagen binding site Patent: US 5800811-A 33 01-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29-SEP-1999
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                                                                                                                                                                       Length: 112
Gaps: 0
Percent Identity: 100.000
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AR036688
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104 c 86 q
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                                                                                         NMVVKSCKCS"
a 104 c
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                                                                                                                                                                               Ratio: 5.652
Percent Similarity: 100.000
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LOCUS AR036688
                                                                                                                                                                       Quality:
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TGFB3P x A59779
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Unclassified.

1 (bases 1 to 339)

Cerletti,N., McMaster,G.Kent, Cox,D., Schmitz,A. and Meyhack,B. Process for refolding recombinantly produced TGF. beta.-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-0CT-1997
                                                                                                                                                                                                                                                                                                          17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
                                                                                                                                                                                                                                     34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
                                                                                                                         1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17
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                                                                                                                                                                                                                                                                                                                                                                 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG
                              Percent Identity: 100.000
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Gaps: 0
Percent Identity: 100.000
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                                                                                                to: 339
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       156856 339 bp DNA
Sequence 3 from patent US 5650494
156856
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104 c 86'o
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              Ratio: 5.652
Percent Similarity: 100.000
                                                                                               to: AR036688
633.00
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Percent Similarity: 100.000
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TGFB3P x I56856
                                                     alignment_block
                                                                                               Align seg 1/1
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1052 CTGTCCAACATGGTGGTGAAGTCGTGTAAGTGCAGC 1087
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      pCMV-SPORT6'
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         /note="Vector:
                                                   /codon_start=2
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                         .1090
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Ratio: 5.652
Percent Similarity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tissue Procurement: Gilbert Smith, Ph.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Sequencing Group at the Stanford Human Genome

Center, Stanford University School of Medicine, Stanford, CA 94305

Web site: http://www-shgc.stanford.edu

Contact: (Dickson, Mark) mcd@paxil.stanford.edu

Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Clone distribution: MGC clone distribution information can be found through the I.M. AGC E. Consortium/Link at: http://image.llnl.gov Series: IRAK Plate: 8 Row f Column: 13.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BC005513 2164 bp mRNA ROD 03-APR-2001
Mus musculus, Similar to transforming growth factor, beta 3, clone
IMAGE:3492763, mRNA, partial cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Musili (bases 1 to 2164)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue_type="Mammary tumor metastatized to lung. Tumor arose spontaneously from a senescent normal mammary (clonal) outgrowth infected with the virus MMTV." /clone_lib="NCI_CGAP_Lu29" /lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (27-MAR-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                         84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
                                                                                                                                                                                                                                                                                                                                                                                                                                  101 ATGAACCTAAGGGCTACTATGCCAACTTCTGCTCAGGCCCTTGCCCATAC 150
                                                                                                                                         20
                                                                                                                                                                                                                                 67
                                                                                                                                                                                                                                                                                                                         84
1 GCTTTGGACACCAATTACTGCTTCCGCAACTTGGAGGAGAACTGCTGTGT
                                                                                                                                  34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr
                                                                                                                                                                                                                          51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh
                                                                                                                                                                                                                                                                                                                  67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG
                                                                                                                                                                                                                                                                                                                                                              201 TCTGAACCCTGAAGCATCTGCCTCGCCTTGCTGCGTGCCCCAGGACCTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          101 LeuSerAsnMetValValLysSerCysLysCysSer 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:10090"
/clone="IMAGE:3492763"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BC005513
BC005513.1 GI:13529607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 216
Strausberg,R.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_name: gb_rol:BC005513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq_documentation_block:
LOCUS BC005513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   house mouse.
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JOURNAL
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SOURCE
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WLARRESNIGLEISTHCPCHTFQPNGJILENVHEVWEIKFKGVDNEDDHGRCDLGRLK
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DLGWKWWHEPRGYYANESGSCPFYLRAADTHSTVLGLKNTLNPEASASPCCVPQDLE
PLTILYYVGRTPRYJEQLSNMVYKSCKCS"
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Human placental and umbilical cord (cell line A673), cDNA to mRNA, from library lambda-gt10.

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases I to 2529)

1 (bases I to 2529)

I chases, P., Hansen, P., Iwata, K.K., Pieler, C. and Foulkes, J.G. Identification of another member of the transforming growth factor type beta gene family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (TGF-beta3) mRNA, complete
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   901
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Identity: 100.000
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Human transforming growth factor-beta 3
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growth

9

Source

FEATURES

gene

JOURNAL

COMMENT

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                                                                                                                                                                                                                                                                                                                                            Direct Submission
Submitted (23-MAR-1989) Chen E.Y., Genentech Inc., 460 Pt. San Branch Blvd., San Francisco, CA 94080, USA
2 (bases 1 to 2574)
Derynck,R., Lindquist,P.B., Lee,A., Wen,D., Tamm,J., Graycar,J.L., Rhee,L., Mason,A.J., Miller,D.A., Coffey,R.J., Moses,H.L. and Chen,E.Y.
                                                                                                                                                                                          Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2574)
         Human mRNA for transforming growth factor-beta 3 (TGF-beta 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A new type of transforming growth factor-beta, TGF-beta 3
EMBO J. 7 (12), 3737-3743 (1988)
                                                                                               growth factor; transforming growth factor; transforming
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="placenta, ovary glioblastoma"
/cell_line="A172 glioblastoma"
254. 1492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      <J03241> for alternative sequence of TGF-beta
Location/Qualifiers
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Gaps: 0
Percent Identity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
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                                  X14149
X14149.1 GI:37095
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Percent Similarity: 100.000
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                                                                                                                                 factor-beta 3.
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   DEFINITION
ACCESSION
VERSION
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JOURNAL
MEDLINE
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                                                                                                                                                                                                                                                                                      REFERENCE
                                                                                                                                                                                                                                                                                                                AUTHORS
                                                                                                                                                                                                                                                                                                                                                                               JOURNAL
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                                                                                               KEYWORDS
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                                                                                                                                                           SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KEIHKFDMIOGLAEHNELAVCPKGITSKVFRFNVSSVEKNRTNLFRAEFRVLRYPNPS
SKRUSQRIELEQILAPDEHIAKQRYIGGKNLPTRGTAEWLSPDYDTYPRYREWLIRRESN
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EPKGYYANFCSGPCPYLRSADTHSTVLGLYNTLNPEASASPCCVPQDLEPLIILYYV
                                                         Draft entry and computer-readable sequence [1] kindly submitted by C.Pieler 12-SEPT-1988 The authors have found that this transforming growth factor contains multiple growth inhibitory elements.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="MKMHLQRALVVLALLNFATVSLSLSTCTTLDFGHIKKKRVEAIR
GOILSKLRLTSPPEPTVMTHVPYQVLALYNSTRELLEEMHGEREEGCTQENTESEYYA
Natl. Acad. Sci. U.S.A. 85 (13), 4715-4719 (1988)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1213 GCGCCCCTCTACATTGACTTCCGACAGGATCTGGGCTGGAAGTGGGTCC 1262
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                                                                                                                                                                                                                                                                                                                                                                                                                               /note="transforming growth factor-beta3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh
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Gaps: 0
Percent Identity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /codon_start=1
                                                                                                                                                                                                                                                                                                                                         /gene="TGFB3"
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Ratio: 5.652
Percent Similarity: 100.000
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LOCUS HSTGFB3M
Proc. Nat
88263019
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BASE COUNT ORIGIN

12-SEP-1993

PRI

mRNA

2574 bp

1313 2

21

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1705 ccreaacccaeaeecercreccreecarecrececcaeeaccree 1754
                                                 1555 ACGCCCCTTTATATTGACTTCCGGCAGGATCTAGGCTGGAAATGGGTCC 1604
                                                                                      1755 AGCCCCTGACCATCTTGTACTATGTGGGCAGAACCCCCAAGGTGGAGCAG 1804
                                                                                                                                                                                                                                                                                                                                         84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
                                                                                                                                                                                                                                                           rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and its uses
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1 (bases 1 to 1899)

Derynck, R.M. A. and Goeddel, D.V.

Nucleic acid encoding TGF-.beta. and
Patent: US 4886747-A 11 12-DEC-1989)
Genentech, Inc.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           103320 1899 bp ss-DNA
Sequence 11 from Patent US 4886747.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          507
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1. .1899
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425 c 452 q
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GI:270714
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Ratio: 5.625
Percent Similarity: 100.000
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TGFB3P x I03320
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KGYYANFCSGPCPYLRSADTHSTVLGLYNTLNPEASASPCCVPQDLEPLTILYYVGR
TPRVVELSNWVVKSCKCS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Complementary DNA cloning of the murine transforming growth factor-beta-3 (TGF-beta-3) precursor and the comparative expression of TGF-beta-3 and TGF-beta-1 messenger RNA in murine embryos and adult
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 2879)
Miller, D.A., Lee, A., Matsui, Y., Chen, E.Y., Moses, H.L. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            611. 1843
/note="transforming growth factor beta-3 (TGF beta-3)
precursor (start site 611 could be 368 or 477)"
                                                                                                                                                                                                                                                                                                               MUSTGEB3 2879 bp mRNA ROD 27-APR-1993 mouse transforming growth factor beta-3 mRNA, complete cds.
1404 AGCCCCTGACCATCCTGTACTATGTTGGGAGGACCCCCAAAGTGGAGCAG 1453
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811 c 724 g 671 t
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Gaps: 0
Percent Identity: 100.000
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M32745.1 GI:201949
transforming growth factor.
Mouse cell line AKR-2B, cDNA to mRNA.
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90190650
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1. .2879
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Percent Similarity: 100.000
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source

mRNA

CDS

MEDLINE

FEATURES

JOURNAL

BASE COUNT ORIGIN

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

AUTHORS

TITLE

REFERENCE

67

21-MAY-1993

PAT

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alignment_block:
TGFB3P x RRU03491
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                                                           Align seg 1/1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cloning and expression of glucocorticoid-induced genes in fetal rat lung fibroblasts. Transforming growth factor-beta 3 J. Biol. Chem. 270 (6), 2722-2728 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /translation="wkwhloralvulallnlatvslslstgttldfghikkkrvbair
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HLILMMIPPHRLDSPGQGGQRKKRALDTNYCFRNLEENCCVRPLYIDFRQDLGWKWVH
EPKGYYANFCSGPCPYLRSSDTHSTVLGLYNTLNPEASASPCCVPQDLEPLTILYYV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 (bases 1 to 2633)
Wang,J., Kuliszewski,M., Yee,W., Sedlackova,L., Xu,J., Tseu,I. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
Submitted (16-NOV-1993) M. Post, The Hospital for Sick Children,
Paediatrics & Research Institute, 555 University Avenue, Toronto,
Ontario MSG 1X8, Canada
                                                                                                                                                                                                                                                                                                                              RRU03491 2633 bp mRNA ROD 06-JUN-1995 Rattus norvegicus Wistar transforming growth factor beta-3 mRNA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:10116"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="transforming growth factor beta-3"
/protein_id="AAA67915.1"
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                                                                                              84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
                                        ATGCCCAGGACCTGG
                                                                                                                   rLeuAsnProGluAlaSerAlaSerProCysCyfValkroGlnAspLeuG
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Gaps: 0
Percent Identity: 99.107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue_type="lung"
/dev_stage="day 20 fetus"
399. 1637
                                    TCTGAACCCTGAAGCATCTGCCTCGCCTTGCTG
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Ratio: 5.625
Percent Similarity: 100.000
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/protein_dd="AAA49089.1"
//protein_dd="AAA49089.1"
//db_xraf="G1:212759"
//db_xraf="G1:2
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Chicken transforming growth factor beta (TGF-beta-3) mRNA, complete
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1 (bases 1 to 2187)
Jakowlew,S.B., Dillard,P.J., Kondaiah,P., Sporn,M.B. and Roberts,A.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="transforming growth factor beta precursor"
                                                                                                                                                                     1299 GCCCTGGACACCAATTACTGCTTCCGCAACTTGGAGGAGAACTGCTGTGT 1348
                                                                                                                                                                                                                                                                                                                                                                                 1349 GCGCCCCCTCTACATTGACTTCCGGCAGGATCTAGGCTGGAAATGGGTCC 1398
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                                                                                                        1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa
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transforming growth factor-beta.
Chicken embryo chondrocyte, cDNA to mRNA.
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/db_xref="taxon:9031"
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89096966
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1. .2187
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Derynck,R., Lindquist,P.B., Lee,A., Wen,D., Tamm,J., Graycar,J.L., Rhee,L., Mason,A.J., Miller,D.A., Coffey,R.J., Moses,H.L. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Euteleostomi;
Sus.
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/note="transforming growth factor beta signal peptide
                                                                                            growth factor beta signal peptide
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia: Eutheria; Cetartiodactyla; Suina; Suidae;
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Percent Identity: 99.107
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Direct Submission
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Percent Similarity: 100.000
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GYYANFCSGSPCPYLRSADTTHSSVLGLYNTLNPEASASPCCVPQDLEPLTILYYVGRT
ARVVEQLSNWVKSCKS"

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                                   See <X14149> and <J03241> for human TGF-beta 3 mRNA sequence
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                                                                                                                                                                              /note="TGF-beta 3 (AA 1-409)"
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Sequence 2 from Patent EP 0267463.
105432
105432.1 GI:590974
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268. .1497
                                                                                                                                                                                                 /codon_start=1
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89091120
                                                                                   /organism="Sus scrofa"
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                                                       Location/Qualifiers
1. .2585
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                                 1 (bases 1 to 498)
Iwata,K.K., Gold,L.I. and Stephenson,J.R.
Tissue-derived tumor growth inhibitors, methods of preparation and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-MAY-1993
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Derynck, R.M.A. and Goeddel, D.V.
Nucleic acid encoding TGF-.beta. and its uses
Patent: US 4886747-A 10 12-DEC-1989;
Genetech, Inc.;
South San Francisco, CA
Location/Qualifiers

ce 1. .1981
/organism="unknown"
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                                                                                  Patent: EP 0267463-A2 2 18-MAY-1988;
Location/Qualifiers
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Seguence 10 from Patent US 4886747.
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ORIGIN
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           ORGANISM
                                               AUTHORS
TITLE
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TITLE
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                                                                                  JOURNAL
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SOURCE
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SOURCE
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (Mammalla; Portebrata; Primates; Catarrhini; Hominidae; Homo. McMaster, G.K., Cox, D., Cerletti, N. and Kuhla, J. Novel hybrid transforming growth factors Patent: Ep 0542679-A 5 19-MAY-1993; CIBA-GEIGY AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25-JAN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1159 GCCCTGGACACCAACTACTCCTTCCGCAATTTCCAGGAGAAACTGCTGTT 1208
                                                                                                                                                                                                                                                            1259 AIGAACCTAAGGCTACTATGCCAACTTCTGCTCAGGCCCTTGCCGTAC 1308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
                                                                                                                                                                                  1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17
                                                                                                                                                                                                                                                                                                                                                                                                                          LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
Length: 112
Gaps: 0
Percent Identity: 95.536
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Locus A23755 336 bp mRNA
DEFUNITION TGF-betal(44/45)beta3 hybrid coding region.
ACCESSION A23755
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Gaps: 0
Percent Identity: 92.857
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LeuSerAsnMetValValLysSerCysLysCysSer 112
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a 109 c 86 g 66
                                                                                                                                          Align seg 1/1 to: I03319 from: 1 to: 1981
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
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5.459
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="C-TERMINAL 68 AMINO ACIDS OF HUMAN TGF-BETA3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cerletti, N.
NEW PROCESS FOR THE PRODUCTION OF BIOLOGICALLY ACTIVE PROTEIN
PATENT: WO 9603433-A 7 08-FEB-1996;
CIBA GETGY AG (CH)
Other publication AU 3109695 960222.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                  84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17
                                                                                                                                                                                        17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH
                                                                                                                                                                                                                                                                                                                                                                                             51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh
                                                                                                                                                                                                                                                                                                                                                                                                                  67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG
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Gaps: 0
Percent Identity: 92.857
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LOCUS A48569 336 bp DNA
DEFINITION Sequence 7 from Patent W09603433.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="unidentified"
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unclassified.
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Percent Similarity:
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                                                                          alignment_block:
TGFB3P x A48555
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VERSION
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AUTHORS
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JOURNAL
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109 c 86 t 66 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="n-TERMINAL 44 AMINO ACIDS OF HUMAN TGF-BETA1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            07-MAR-1997
                                                                                                                                                                                                                                         151 CTCCGCAGTGCAGACACAACCCACAGCAGCGGGGACTGTACAACAC 200
                                                                                                                                                                                                                                                                                                                                                                                             84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
                                                                                            1 GCCTGGACACCAACTATTGCTTCAGCTCCACGGAGAACTACTGCTGCTT 50
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                                                                                                                                               17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
                                                                      1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CIBA GEIGY AG (CH)
Other publication AU 3109595 960222.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Patent: WO 9603432-A 7 08-FEB-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 7 from Patent WO9603432.
A48555
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1. .132
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Cerletti, N.
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                                  Align seg 1/1 to: A23755
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LOCUS A48555
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TGFB3P x A23755
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DEFINITION

ACCESSION VERSION

ORGANISM

KEYWORDS SOURCE

AUTHORS TITLE

JOURNAL

REFERENCE

Source

COMMENT FEATURES

COUNT

07-MAR-1997

200

84

67

34

250

Tue

alignment\_block: TGFB3P x A48569

alignment\_scores

ORIGIN

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to: 336
to: A23757 from: 1
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Cerletti, N.
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unidentified
unclassified.
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LOCUS A48557
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Align seg 1/1
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VERSION
KEYWORDS
SOURCE
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 336)
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                                                                                                                                           1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17
                                                                                                                                                        McMaster, G.K., Cox, D., Cerletti, N. and Kuhla, J.
Novel hybrid transforming growth factors
Patent: EP 0542679-A 7 19-MAY-1993;
CIBA-GEIGX AG
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Gaps: 0
Percent Identity: 91.071
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                                  Length:
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94 c 84 q 77
                                                                                                                    to: 336
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5.373
98.214
                                595.00
5.459
97.321
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Ratio:
Percent Similarity:
                                  Quality:
                                                        Percent Similarity:
                                               Ratio:
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151

21

201

67

human.

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

alignment\_scores:

source

FEATURES

BASE COUNT

TITLE JOURNAL

REFERENCE AUTHORS alignment\_block: TGFB3P x A23757

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    .336
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translation"

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                                                                                                                                                                                                                                                                                                                                                                                                                        07-MAR-1997
                                         151 CTCCGCAGTGCAGACACCACAGCACGGTGCTGGGACTGTACAACAC 200
                                                                                                           201 TCTGAACCCTGAAGCATCTGCCTCGCCTTGCTGCGTGCCCAGGACCTGG 250
                                                                                                                                                                           84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
                                                                                                                                                                                                 51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh
                                                                                      67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CIBA GEIGY AG (CH)
Other publication AU 3109595 960222.
Location/Qualifiers
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/organism="unidentified"
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1. 132
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Sequence 9 from Patent WO9603432.
A48557
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alignment_block:
TGFB3P x A23759
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/note="Protein sequence is in conflict with the conceptual
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| ...132
/product="N-TERMINAL 44 AMINO ACIDS OF HUMAN TGF-BETA2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="C-TERMINAL 68 AMINO ACIDS OF HUMAN TGF-BETA3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 (bases 1 to 336)
Cerletti.N.
NEW PROCESS FOR THE PRODUCTION OF BIOLOGICALLY ACTIVE PROTEIN
PREMEDTE: WO 9600433-A 9 08-FEB-1996;
CIBA GEIGY AG (CH)
Other publication AU 3109695 960222.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              07-MAR-1997
                                                                                                                                                                                                                                 84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
                                                                                                                                                                                                                                                                                                                                                                                                                             17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
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                                                                                                                 1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17
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   Gaps: 0
Percent Identity: 91.071
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Sequence 9 from Patent W09603433.
A48571.1 GI:2302341
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5.373
98.214
                                                                                      Align seg 1/1 to: A48557
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unidentified
unclassified.
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LOCUS A48571
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Ratio:
Percent Similarity:
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TGFB3P x_A48557
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
I (bases 1 to 336)
McMaster,G.K., Cox.D., Cerletti,N. and Kuhla,J.
Novel hybrid transforming growth factors
Patent: EP 0542679-A 9 19-MAY-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                     67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG
              Length: 112
Gaps: 0
Percent Identity: 91.071
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TGF-beta3(44/45)beta2 hybrid coding region.
A23759
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Percent Identity: 88.393
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87 c 71 q 90
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LOCUS A23759
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TGFB3P x A48571
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Align seg 1/1

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="N-TERMINAL 44 AMINO ACIDS OF HUMAN TGF-BETA3"
1. .336
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87 c 71 g 90 t
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                                                                                                                                                                                                                          51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh
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    Percent Identity: 88.393
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Sequence 11 from Patent WO9603433.
A48573

    .336
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1. .132
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Cerletti, N.
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    Percent Similarity:
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                                alignment_block:
TGFB3P x A48559
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87 c 71 g 90 t
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                                                                                   luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
                                                                                                                                                                251 AACCTCTAACCATTCTCTACTACATTGGCAAAACACCCCAAGATTGAACAG 300
                           34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
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Gaps:
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    ,336
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    /db_xref="taxon:32644"
    ,132

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Sequence 11 from Patent A48559 GI:2302329
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Cerletti, N.
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to: A23759
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LOCUS A48559
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LOCUS DEFINITION

84

51

ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE

JOURNAL

source

FEATURES

COMMENT

BASE COUNT

ORIGIN

07-MAR-1997

17 50 67

84

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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 336)
McMaster, G.K., Cox, D., Cerletti, N. and Kuhla, J.
Movel hybrid transforming growth factors
Patent: EP 0542679-A 8 19-MAY-1993;
CIBA-GEIGY AG
                                                                                                                       84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
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Percent Identity: 83.929
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LOCUS A23758 336 bp mRNA
DEFINITION TGF-beta3(44/45)beta1 hybrid coding region.
ACCESSION A23758
VERSION A23758.1 GI:825592
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109 c 98 q 66
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Percent Similarity:
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Emmaniais; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 336)
McMaster, G.K., Cox, D., Cerletti, N. and Kuhla, J.
Novel hybrid transforming growth factors
Patent: EP 0542679-A 4 19-MAY-1993;
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                                                                                                                                                  17 largProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
                                                                                                                                                                                                                                                                         34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr
                                                                                                                                                                                                                                                                                                                                                                                                  67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A23754 TGF-betal(44/45)beta2 hybrid coding region. A23754 GI:825588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length: 112
Gaps: 0
Percent Identity: 81.250
                                              Percent Identity: 88.393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             301 CTTTCTAATATGATTGTAAAGTCTTGCAAATGCAGC 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           101 LeuSerAsnMetValValLysSerCysLysCysSer 112
               Length:
                               Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/db_xref="taxon:9606"
92 c 72 q 83
                                                                                                                     to: 336
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                                                                                                                    Align seg 1/1 to: A48573 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       to: A23754 from: 1
            577.00
5.393
95.536
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5.183
92.857
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seq_name: gb_pat1:A23754
              Quality:
Ratio:
Percent Similarity:
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alignment_scores:
                                                                         alignment_block:
TGFB3P x A48573
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TGFB3P x A23754
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25-JAN-1995

51 GCGCCCCCTCTACATTGACTTCCGACAGGATCTGGGCTGGAAGTGGGTCC 100 17 largproLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34 34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50 Align seg 1/1 to: A23758 from: 1 to: 336

to: 336

Align seg 1/1

source

FEATURES

BASE COUNT

ORIGIN

DEFINITION

ACCESSION VERSION

ORGANISM

KEYWORDS SOURCE

REFERENCE AUTHORS

JOURNAL

TITLE

Length:

99

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 319)
McMaster,G.K., Cox,D., Cerletti,N. and Kuhla,J.
Patent: EP 0542679-A 2 19-MAY-1993;
CIBA-GEIGY AG
 201 CATAAATCCAGAAGCATCTGCTTCTCCTTGCTGCGTGTCCCAAGATTTAG 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17
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                                                                                                                       67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG
                                                           51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr
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Gaps: 0
Percent Identity: 79.464
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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LOCUS A23752 339 bp n
ACCESSION A23752
ACCESSION A23752
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TGFB3P x A23752
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /protein_id="cad1386.1"
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AGACPYLWSSDTQHSRVLSLYNTINPEASASPCCVSQDLEPLTILYYIGKTPKIEQLS
NMIVKSCKCS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1. 339
/note="Protein sequence is in conflict with the conceptual
                                                                                                                                                                                                                                                                                                                                                                                                                    synthetic construct
artificial sequence.
1 (bases 1 to usp.)
Cerletti,N., McMaster,G.K., Cox,D., Schmitz,A. and Meyhack,B.
Process for the production of biologically active protein (e.g.
                                                                                                                                                                                                                                                                                                                                 17-MAY-1994
                                                                                                                                                             101 ATGAACCTAAGGGCTACTATGCCAACTTCTGCCTCGGGCCCTGCCCTAC 150
                                                         1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17
                                         51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh
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Percent Identity: 79.464
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H.sapiens TGF-beta 2 peptide seq ID No:2.
A18279
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/organism="synthetic construct"
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LOCUS A18279
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Ratio:
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source

FEATURES

CDS

DEFINITION

ACCESSION VERSION KEYWORDS

ORGANISM

SOURCE

AUTHORS REFERENCE

TITLE

JOURNAL

alignment\_scores

BASE COUNT ORIGIN

alignment\_block: TGFB3P x A18279

25-JAN-1995

07-MAR-1997

DEFINITION ACCESSION VERSION KEYWORDS

ORGANISM

SOURCE

REFERENCE AUTHORS TITLE

JOURNAL

source

FEATURES COMMENT

tqfb3p.rge

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Protein sequence is in conflict with the conceptual
                                                                                                                                                                                                                                                                                                                                                                                       1 (bases 1 to 339)
Cerletti,N.
NEW PROCESS FOR THE PRODUCTION OF BIOLOGICALLY ACTIVE PROTEIN
PALENT: WO 960733-A 3 08-FEB-1996;
CIBA GEIGY AG (CH)
Other publication AU 3109695 960222.
     84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
                                                                         1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
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Percent Identity: 79.464
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                                                                                                                                                                                                                                     A48565 339 bp DNA
Sequence 3 from Patent WO9603433.
A48565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="unidentified'
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:32644"
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Percent Similarity:
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TGFB3P x A48565
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ORIGIN
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TITLE
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KEYWORDS
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NMIVKSCKCS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Protein sequence is in conflict with the conceptual
                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 339)
Cerletti,N.
NOVEL PROCESS FOR THE PRODUCTION OF BIOLOGICALLY ACTIVE DIMERIC
                                                                                                                                                                                                                               07-MAR-1997
201 CATAAATCCAGAAGCATCTGCTTCTCCTTGCTGCGGTGTCCCAAGATTTAG 250
                                84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
                                                  1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
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5.095 Gaps: 0
93.750 Percent Identity: 79.464
                                                                                                 Patent: WO 9603432-A 3 08-FEB-1996;
CIBA GEIGY AG (CH)
Other publication AU 3109595 960222.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="unidentified"
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1. .336
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Sequence 3 from Patent WO9603432.
A48551
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                                                                                                                                                                                                                                                                                                                unidentified.
unidentified
                                                                                                                                                                                                         seq_documentation_block:
LOCUS A48551
                                                                                                                                                                         seq_name: gb_pat1:A48551
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alignment\_scores:

BASE COUNT

alignment\_block: TGFB3P x A48551

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/organism="unknown"
77 c 70 q
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                                       Sequence 2 from patent US 156855
                             339 bp
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synthetic construct
artificial sequence.
1 (bases 1 to 342)
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                                                                   I56855.1 GI:2477268
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5.095
93.750
                                                                                                                    Unclassified.
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LOCUS A05306
                 seq_name: gb_pat1:A05306
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                                                                                                                                                                                                                                                                                                     Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                          Percent Similarity:
                                                                                                           Unknown.
                                                                                              Unknown
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TGFB3P x I56855
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                                                                                             SOURCE
                                                                                                                                                                                                                                                   Unknown.
Unknown.
Unclassified.
I (bases 1 to 339)
1 Alli.F.L., Nimni,M.E., Tuan,T., Wu,L. and Cheung,D.T.
Halli.F.L., Nimni,M.E., Tuan,T., wa,L. and cheung,D.T.
Artificial skin prepared from coclagen matrix containing
transforming growth factor-.beta. having a collagen binding site
Patent: US 5800811-A 31 01-SEP-1998;
Location/Qualifiers
                                                                                                                                                                                  29-SEP-1999
                                   101 ACGAACCCAAAGGGTACAATGCCAACTTCTGTGCTGGAGCATGCCCGTAT 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
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                                                                                                                                                                                   PAT
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Percent Identity: 79.464
                                                                                       Length:
                                                                                                                                                                                              5800811.
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                                                                                                                                                                       Sequence 31 from patent US :
                                                                                                                                                                                                                    AR036687.1 GI:5954543
                                                                                                                                                                                                                                                                                                                                                                                                                                                      535.00
5.095
93.750
                                                                                                                                          seq_name: gb_pat1:AR036687
                                                                                                                                                                  seq_documentation_block:
LOCUS AR036687
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Ratio:
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                                                                                                                                                                                                                                             Unknown.
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TGFB3P x AR036687
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                                                                                                                                                                                           DEFINITION
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ORGANISM

REFERENCE AUTHORS

TITLE

JOURNAL FEATURES

ACCESSION VERSION KEYWORDS BASE COUNT

ORIGIN

Cerletti, N., McMaster, G.Kent, Cox, D., Schmitz, A. and Meyhack, B. Process for refolding recombinantly produced TGF. beta.-like proteins
Patent: US 5650494-A 2 22-JUL-1997;
Location/Qualifiers
1. 339 07-0CT-1997 07-MAY-1993 101 CATABARTCCAGAAGCATCTGCTTGCTTGCTGCGTGTCCCAAGATTAG 250 51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67 67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84 1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17 17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34 Complete nucleotide sequence of mature human G-TsF PAT Percent Identity: 79.464 Length: Gaps: 94 5650494 Align seg 1/1 to: I56855 from: 1 to: 339

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TGFB3P x A11707
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                                                                                                                                                                                                                                            BASE COUNT
ORIGIN
      TITLE
JOURNAL
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AUTHORS
TITLE
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KEYWORDS
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                                                                                                                          FEATURES
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Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 342)
De Martin,R., Fontana,A., Hofer,E., Hofer-Warbinek,R. and Wrann,M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-NOV-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length: 112
Gaps: 0
Percent Identity: 79.464
                                                                                            construct'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           101 LeuSerAsnMetValValLysSerCysLysCysSer 112
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WO 8803807-A 10 02-JUN-1988;
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                                                                            /organism="synthetic cd/db_xref="taxon:32630"
1. .342
                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           71 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mature H.sapiens G-TsF gene.
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                                                                                                                                                                            /gene="G-TsF"
                                                                                                                                                                                                                                   /gene="G-TsF"
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Ratio: 5.095
Percent Similarity: 93.750
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LOCUS A11707
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Patent:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           86
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TGFB3P x A05306
                                                             source
JOURNAL
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ORIGIN
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KEYWORDS
SOURCE
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                           FEATURES
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
1 (bases 1 to 1427)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          רוסיים אמא אמא 16-JUL-1996
Sus scrofa transforming growth factor beta 2 mRNA, 3' end.
L08375
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transforming growth factor beta 2.
Sus scrofa (strain crossbreed) male adult Lung cDNA to mRNA.
Sus scrofa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              in immune cells
Unpublished (1993)
On Jul 16, 1996 this sequence version replaced gi:164688
Location/Qualifiers
Production and use of a novel T-cell suppressor factor
Patent: EP 0.268561-A 6 25-MAY-1988;
SANDOZ AS: SANDOZ-PATENT-GMBH; SANDOZ-ERFINDUNGEN
Verwaltungsgesellschaft m.b.H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               104 ACGAACCCAAAGGGTACAATGCCAACTTCTGTGCTGGAGCATGCCCGTAT 153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17
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                                                                                                                                                                                                                                                                                    112
                                                                                                                                                                                                                                                                                                                          Percent Identity: 79.464
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                                                                                                                            /organism="Homo sapiens"
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78 c 71 q 95
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/organism="Sus scrofa"
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/db_xref="taxon:9823"
                                                                                      Location/Qualifiers
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5.095
93.750
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LOCUS
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CDS

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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae,
                                 Cercopithecinae; Cercopithecus. 1 (bases 1 to 1585)
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                                                                                                                                                                                                                                                                                                                           200. .1444
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TGFB3P x AGMGIBSC1
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                                                       REFERENCE
                                                                         AUTHORS
                                                                                                                                                                MEDLINE
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                                                                                                                                                                                                                   FEATURES
                                                                                                         TITLE
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                                                                                                                                                                           TPHLILMLIPSYGLESQOSNPRKKRANDARYCFRNVQDNCCLRPLYIDFKRDLGWKWI HEPKGYNANCAGACPYLWSDYGNRRKKRANDARYCFRNVQDNCCLRPLYIDFKRDLGWKWI IGKTPKIEQLSNMIVKSCKCSKTKLAAFARLYHSHSNLGSET"

904. 1302
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LOCUS AGMGIBSCI 1585 bp mRNA PRI 27-APR-1993
DEFINITION Affican green monkey BSC-1 cell growth inhibitor, complete cds.
ACCESSION J03585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         J03585.1 G1:176495
BSC-1 cell growth inhibitor; cartilage-inducing factor B; polyergin; transforming growth factor-beta 2.
African green monkey kidney epithelium, cDNA to mRNA.
Cercopithecus aethiops
                                                                                                                       /product="transforming growth factor beta 2"
/protein_id="AAB03850.1"
/db_xref="GI:164689"
                                                                                                                                                                                                                                                                                                                                         /product="transforming growth factor beta 2" 395 c 336 g 307 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17 largProLeuTyrIleAspPheArgClnAspLeuGlyTrpLysTrpValH 34 :||||||||||||||||||:::|| 954 GCGTCCACTTTACATGATTCAAGAGGGATCTTGGGTGGAAATGGATAC 1003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1004 ATGAGCCTAAAAGGTACAATGCCAACTTCTGTGCCGGGGCGTGCCCGTAC 1053
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 /cell_type="alveolar macrophage cells"
/dev_stage="adult"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percent Identity: 79.464
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              from: 1 to: 1427
                                                   type="Lung"
                                                                                          /note="precursor"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Align seg 1/1 to: PIGTGFB2A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5.095
93.750
                                                       /tissue_
                                                                                                                                                                                                                                                                                                                                                                                                                                                    535.00
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                                                                                                                                                                                                                                                                                                                            mat_peptide
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BASE COUNT

ORGANISM

SOURCE

VERSION KEYWORDS

1054

21

84

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VPEQRIELYOILKSKOLTSPTORY TOSKVYKTRAEGEWLLSFDYTDAHEWLHHEDRIL
GFKISLHCPCCTFVPSNNY IIPNKSEELEARFAGIDGTSTYTSGDQKTIKSTRKNSG
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                                                                                                                  88124824
Draft entry and computer-readable sequence for [1] kindly provided
                        Holley,R.W. Anino acid sequence of the BSC-1 cell growth inhibitor (polyergin) deduced from the nucleotide sequence of the CDNA Proc. Natl. Acad. Sci. U.S.A. 85, 79-82 (1988)
Hanks, S., Armour, R., Baldwin, J.H., Maldonado, F., Spiess, J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh
                                                                                                                                                                                                                              /organism="Cercopithecus aethiops" /db_xref="taxon:9534" <1. .>1585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length: 112
Gaps: 0
Percent Identity: 79.464
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                to: 1585
                                                                                                                                                                                                                                                                                                                                                             /note="polyergin precursor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              397
                                                                                                                                                                                                                                                                                                                                                                                                  /protein_id="AAA35358.1"
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10-DEC-1993

PAT

sig\_peptide

source

FEATURES

AUTHORS JOURNAL

REFERENCE

112

DEFINITION ACCESSION

SOURCE ORGANISM

VERSION KEYWORDS

```
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1695)
De Martin, R., Fontana, A., Hofer, E., Hofer-Warbinek, R. and Wrann, M. Production and use of a novel T-cell suppressor factor
Patent: EP 0268561-A 8 25-MAY-1988;
SANDOZ AG; SANDOZ-PATENT-GMBH; SANDOZ-ERFINDUNGEN
                                                                                                1338 AACCTCTAACCATTCTCTACTACATTGGCAAAACACCCAAGATTGAACAG 1387
                                         1288 CATAAATCCAGAAGCATCTGCTTCTCCTTGCTGCGTGTCCCAAGATTTAG 1337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1188 ACGAACCCAAAGGGTACAATGCCAACTTCTGTGCTGGAGCATGCCCGTAT 1237
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                                                                            84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr
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Percent Identity: 79.464
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                                                                                                                                                         101 LeuSerAsnMetValValLysSerCysLysCysSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
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386 c 354 g 433
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                                                                                                                                                                                                                                                                                                                  precursor.
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1. .1695
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5.095
93.750
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                                                                                                                                                                                                                                  seq_name: gb_pat1:A11709
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Ratio:
Percent Similarity:
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TGFB3P x A11709
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ORIGIN
                                                                                                                                                                                                                                                                                                               DEFINITION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                  ACCESSION
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                       SOURCE
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                                                                                                                                                                                                                                                                                                                                                                    182. .1087
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182. .1426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="glioblastoma-derived T-cell suppressor factor"
386 c 354 g 432 t
                                                                                                  07-MAY-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          precursor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH
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                                                                                                  PAT
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Gaps: 0
Percent Identity: 79.464
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182. .1087
                                                                                                Nucleotide sequence for the human G-TsF A05308
1406 CTTTCTAATATGATTGTAAAGTCTTGCAAATGCAGC 1441
                                                                                                                                                                                                                                                                                           WO 8803807-A 12 02-JUN-1988,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Align seg 1/1 to: A05308 from: 1 to: 1695
                                                                                                                                                                                                                                                                                                             Location/Qualifiers
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1088. .1423
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/gene="G-TsF"
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/gene="G-TsF"
                                                                                                                                                                                          synthetic construct.
synthetic construct
artificial sequence.
1 (bases 1 to 1695)
                                                                                              1695 bp
                                                                                                                                                     A05308.1 GI:345051
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5.095
93.750
                                                                            seq_documentation_block:
                                       seq_name: gb_pat1:A05308
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Ratio:
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1137

20

67

17

alignment\_scores:

alignment\_block: TGFB3P x A05308

mat\_peptide

gene

BASE COUNT

ORIGIN

DEFINITION

ACCESSION

KEYWORDS

SOURCE

ORGANISM

AUTHORS TITLE JOURNAL

REFERENCE AUTHORS

REFERENCE

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Unclassified.

1 (bases 1 to 2569)
Purchio,A.F., Madisen,L. and Webb,N.
Cloning and expression of transforming growth factor beta 2
Patent: EP 0376785-A2 3 04-JUL-1990;
                                                   1338 AACCTCTAACCATTCTCTACTACATTGGCAAAACACCCCAAGATTGAACAG 1387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1457 GCTTTGGATGCGGCCTATTGCTTTAGAAATGTGCAGGATAATTGCTGCCT 1506
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                                                                                                                                                                                  51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh
                                                                                                          34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr
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Gaps: 0
Percent Identity: 79.464
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Sequence 3 from Patent EP 0376785
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="unknown"
599 c 512 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Align seg 1/1 to: I08281 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 r08281.1 GI:589009
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5.095
93.750
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JOURNAL
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VPEORIELYOILKSKDLTSPTQRYIDSKVVKTRAEGEWLSFDVTDAVHEWLHHKDRNL
SKTSI-HCFOCCTFVPSNNYIIPUNKSEELEARFROIDOTSTYTSGDQWTIKSTRKKNSG
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                                                                                                                    HSGTSF 1695 bp mRNA PRI 27-MAR-1995 Human mRNA for glioblastoma-derived T-cell suppressor factor G-TsF (transforming growth factor-beta2, TGF-beta2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hofer, E. Complementary DNA for human glioblastoma-derived T cell suppressor factor, a novel member of the transforming growth factor-beta gene
                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1695)
                                                                                                                                                                                                                                                                                                                                                            Direct Submission
Submitted (02-NOV-1987) Hofer, E., Sandoz AG, Department for
Biotechnology, Preclinical Research, Bullding 386/328, Sandoz AG,
CH-4002 Basel
                                                                                                                                                                                                                                                                                                                                                                                                                                          2 (bases 1 to 1695)
de Martin,R., Haendler,B., Hofer-Warbinek,R., Gaugitsch,H.,
Wrann,M., Schlusener,H., Seifert,J.M., Bodmer,S., Fontana,A. and
                                                                                                                                                                              Y00083
Y00083.1 GI:31959
T-cell suppressor factor; transforming growth factor-beta2
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/db_xref="glioblastoma 308"
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/clone="lambda SUP25, lambda SUP40, lambda SUP42"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1088 GCTTTGGATGCGGCCTATTGCTTTAGAAATGTGCAGGATAATTGCTGCCT 1137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          site"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1087. .1088
/note="put. protease cleavage
1088. .1423
/product="put. mature G-Tsf"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps:
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88111555
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="G-Tsf precursor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /codon_start=1
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93.750
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                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                  seg_documentation_block:
                                                           seq_name: gb_pr9:HSGTSF
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FEATURES

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ORIGIN BASE

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Direct Submission
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Webb,N.R., Madisen,L., Rose,T.M. and Purchio,A.F.
Structural and sequence analysis of TGF-beta 2 cDNA clones predicts
two different precursor proteins produced by alternative mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /procein_ii="AAA50404.1"
/db_xref="GI:339550"
/translation="MHYCVLSAFLILHLVTVALSLSTCSTLDMD@FMRKRIEAIRGQI
LSKLKITSPEDY PEPEFVPEVYSIY NSTRDLLQEKASRRAAACERERSDEEYYAKE
VYKIDMAPPFPSETVCPVYTPPSGSVGSLCSRQSQULGGYLDAIPPFFYRPYFRIVRF
DVSAMEKNASNLVKAEFRVFRLQNPKARVPEQRIELYQILKSKDLTSPTQRYIDSKVV
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AYCFRNVQDNCCLRPLYIDFKRDLGWKWIHEPKGYNANFCAGACPYLWSSDTQHSRVL
SLYNTINPEASASPCCVSQDLEPLTILYYIGKTPKIEQLSNMIVKSCKCS"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KTRAEGEWLSFDVTDAVHEWLHHKDRNLGFKISLHCPCCTFVPSNNYIIPNKSEELEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue_type="tamoxifen-treated prostatic adenocarcinoma"
/map="19q13.1-q13"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              468, 527
/note="transforming growth factor-beta-2 signal peptide"
                                                                                                                                                                                                                                                                                                                    seq_documentation_block:
LOCUS HUMTGFB2A 2570 bp mRNA PRI 11-OCT-1994
DEFINITION Human transforming growth factor-beta-2 mRNA, complete cds.
ACCESSION M19154 M22045 M22046
VERSION M19154.1 GI:339540
KEYWORDS alternative splicing; transforming growth factor.
SOURCE Homo sapiens tamoxifen-treated prostatic adenocarcinoma CDNA 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Madisen, L., Webb, N.R., Rose, T.M., Marquardt, H., Ikeda, T., Twardzik, D., Seyedin, S. and Purchio, A.F.
Transforming growth factor-beta 2: cDNA cloning and sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="transforming growth factor-beta-2 precursor"
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/protein_id="AAA50405.1"
/db_xref="GI:557563"
84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
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/note="alternatively spliced precursor"
                                                                                                                                                                                  /organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_line="PC-3"
/clone=" lambda-PC21"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="TGB-beta-2 mRNA"
468. .1796
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DNA 7 (7), 493-497 (1988)
89090808
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88166349
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                                                                                                                                                                                                                                                                            seq_name: gb_pr10:HUMTGFB2A
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DNA 7 (1)
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TITLE

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VYKIDMPPFFPSEAIPPTFYRPYFRIVRFDVSAMEKNASNLVKAEFRVFRLQNPKARV PEQRIELYGULKSKDLYSPYRPZYRTRDVSTABGEGLIKSKDVPDAVHENLGPRLGNLGSRLVSFDGLIKSKDVSTRSDGLIKSKDRIGSTRISHGROUT IFRISHGROUT IPPRSEELARFAGIDGTTYTSGDGKTIKSTRKNSGK TPHLLLMLLPSYRLESQQTNRRKRALDAAYCFRNVQDNCCLRRLYIDFKRDGWKGT HEPKGYNANFCAGAGCPYLWSSDTQHSRVLSLYNTINPEASASPCCVSQDLEPLTILYY IGRTPRIEDGLSNMIVKSCKCS"

//note="transforming growth factor-beta-2"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_documentation_block:
LOCUS AF135598 1255 bp mRNA ROD 11-APR-1999
DEFINITION Rattus norvegicus transforming growth factor beta 2 precursor,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 (bases 1 to 1255)
Plisov,S.Y., Ivanov,S.V., Plisova,T.M., Lerman,M. and
Perantoni,A.O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 (bases 1 to 1255)
Plisov,S.Y., Ivanov,S.V., Plisova,T.M., Lerman,M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1458 GCTTTGGATGCGGCCTATTGCTTTAGAAATGTGCAGATAATTGCTGCCT 1507
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                                                                                                                                                                                                                                                                                        Gaps:
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                                                                                                                                                             772 a 598 c 513 g
Chromosome 19q13.1-q13.
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AF135598
AF135598.1 GI:4580714
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5.095
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tgfb3p.rge

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51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
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/gene="TGF-beta2"
                                                                                                                                                                                                                                                                                                                  /strain="Wistar"
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659 c 583
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TGFB3P x AF153013
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     ORGANISM
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                                                                                      AUTHORS
TITLE
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                                                                                                                                                                                                                      /translation="MHYCVLRTFLLLHLVPVALSLSTCSTLDMDOFMRKRIEAIRGOI
LSKLKLTSPPEDYPEPDEVPPEVISIYNSTRDLLQEKASRRAAACERERSDEEYYAKE
VYKIDMPSHFPSENAIPPTFYRPYFRIVRFDVSTMEKNASNLVKAEFRVFRLQNPKAR
Submitted (18-MAR-1999) Laboratory of Comparative Carcinogenesis, National Cancer Institute, FCRDC, Bldg.538, Room 206, Frederick, MD
                                                                                                                                                                                                                                                                           VAEORIELYQILKSKDLTSPTQRYIDSKVVKTRAEGEWLSFDVTDAVHEWLHKDRNL
KRYISLHCFOCTFIPSNNYITRNKSQEEARRFAGIOFTSTKASGOWTIKSTRKKSSG
KFPHLDEIMILDSY BLESQOSSRRKRALDAAYCFRNVODNCCLRPLYIDFRDLGWKW
IHEPKGYNANFCAGACPYLWSSDTQHTKVLSLYNTINDEASASPCCVSQDLEPLTILI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product-"transforming growth factor beta 2 precursor"
/protein_id-"AAD24484.1"
/db_xref="GI:4580715"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1108 CATAAACCCCGAAGCTTCTGCTTCCCCTTGCTGTGTGTCCCAGGATCTGG 1157
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Gaps: 0
Percent Identity: 78.571
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                                                   Location/Qualifiers
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                                                                                                                                     'note="TGF-beta2"
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                                 21702, USA
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Ratio:
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TGFB3P x AF135598
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (18-MAY-1999) Anatomy & Structural Biology, University of Otago, Dunedin PO Box 913, New Zealand
To (bases 1 to 2796)
Koishi,K., Dalzell,K.G. and McLennan,I.S.
The expression and structure of TGF-beta2 transcripts in rat
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20461836
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Gaps: 0
Percent Identity: 78.571
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Koishi,K., Dalzell,K.G.B. and McLennan,I.S.
Direct Submission

    2796
    /organism="Rattus norvegicus"

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604 g

684 c

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824 a
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Koishi,K., Dalzell,K.G.B. and McLennan,I.S.

Direct Submission

Submitted (18-MAY-1999) Anatomy & Structural Biology, University of Otago, Dunedin PO Box 913, New Zealand
On Jun 3, 1999 this sequence version replaced gi:4929795.

Location/Qualifiers
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DVSTMEKNASNLVKAEFRVFRLQNPKARVAEQRIELYQILKSKDLTSPTQRIDSKVV
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                                                                                                                                                                                                                                                                                                                       seq_documentation_block:
LOCUS AF153012 2880 bp mRNA ROD 24-JUL-2000
DEFINITION Rattus norvegicus TGF-beta 2 long form precursor (TGF-beta2) mRNA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Koishi,K., Dalzell,K.G. and McLennan,I.S.
The expression and structure of TGF-beta2 transcripts in rat
Biochim. Biophys. Acta 1492 (2-3), 311-319 (2000) 20461836
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AF153012
AF153012.2 GI:4980482
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Rattus norvegicus
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TITLE
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MEDLINE
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 4267)
Miller, D.A., Lee, A., Pelton, R.W., Chen, E.Y., Moses, H.L. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14-JUN-1991
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X57413.1 G1:54772
cell proliferation; transforming growth factor-beta2.house mouse.
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                                                                                                                                                               1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17
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Length: 112
Gaps: 0
Percent Identity: 78.571
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93.750
530.00
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   Quality:
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      Transforming growth factor-beta2 mediates mesenchymal-epithelial interactions of testicular somatic cells Endocrinology 141 (10), 3679-3686 (2000)
                                                                                                     Konrad L.
Direct Submission
Submitted (02-FEB-1999) Konrad L., Anatomy and Cell Biology,
Philipps University, Robert-Koch-Str. 6, 35033 Marburg, GERMANY
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                  /sex="male"
                                                                                        (bases 1 to 1274)
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
  factor-beta2 precurser"
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                                                                                                                                                                                                                                                                            /product="transforming growth factor-beta2" 4260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2374 AACCACTGACCATTCTCTATTACATTGGAAATACGCCCAAGATCGAACAG 2423
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Konrad,L., Albrecht,M., Renneberg,H. and Aumuller,G.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
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LOCUS
RN0132718 1274 bp mRNA
BERINITION Rattus norvegicus mRNA for TGF-beta2 protein.
ACCESSION AJ132718 GI:4753895
KEYWORDS tgf-beta2 gene; TGF-beta2 protein.
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1022 ATGAACCCAAGGGGTACAATGCTAACTTCTGTGCTGGGGCATGCCCTTAT 1071
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                                                                                                                                                                                                                                                                                                              34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr
                                                                                                                                                                                                                                                                                                                                                                  LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh
                                                                                                                                                                                                                                                                                                                                                                                                                        67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG
                                                                              112
                                                                                                        Percent Identity: 78.571
                                                                              Length:
YIGNTPKIEQLSNMIVKSCKCS"
            303 g
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5.029
93.750
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DEFINITION

ACCESSION VERSION ORGANISM

SOURCE

AUTHORS TITLE

REFERENCE

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HEPKGYNANFCAGACPYLWSSDTQHSRVLSLYNTINPEASASPCCVSQDLDSLTILYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        136. 1317 /note-"Protein sequence is in conflict with the conceptual
                                                                      XLTGFB2 2724 bp mRNA VRT 08-NOV-1993
Xenopus laevis TGF-beta2 mRNA for transforming growth factor-beta2.
X51817
                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (07-FEB-1990) Rebbert M.L., Laboratory of Molecular Genetics, National Institute of Child, Health and Human Development, Bldg G fm 324, Bethesda MD 20892, U S A sequence revised by [3]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (08-NOV-1993) Rebbert M.L., Laboratory of Molecular Genetics, National Institute of Child, Health and Human Development, Bldg 6 Rm 324, Bethesda MD 20892, U S A On Nov 9, 1993 this sequence version replaced 91:65136. Data kindly reviewed (16-AUG-1990) by Rebbert .M.L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rebbert, M.L., Bhatia-Dey, N. and Dawid, I.B.
The sequence of TGF-beta 2 from Xenopus laevis
Nucleic Acids Res. 18 (8), 2185 (1990)
                                                                                                                                                           X51817.1 G1:414789
growth factor; transforming growth factor.
African clawed frog.
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Rebbert, M.L.
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Rebbert, M.L.
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Mulheron, G.W., Mulheron, J.G., Danielpour, D. and Schomberg, D.W. Porcine granulosa cells do not express transforming growth factor-beta 2 (TGF-beta 2) messenger ribonucleic acid: molecular basis for their inability to produce TGF-beta activity comparable
                                                                                                             SSTGFB2 477 bp mRNA MAM 30-JUN-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="Transforming Growth Factor-beta 2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
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                                                                                                                                                                                                       X70142.1 GI:312949
TGF-beta 2; transforming growth factor-beta2.
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<1. .>477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      to that of rat granulosa cells
Endocrinology 131 (6), 2609-2614 (1992)
1222 CTTTCCAACATGATCGTCAAGTCTTGTAAATGCAGC 1257
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Align seg 1/1 to: SSTGFB2 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        . .477
124 c
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                                                                                                                  _documentation_block:
                                                                    seq_name: gb_om:SSTGFB2
                                                                                                                                                                                                                                                          pig.
Sus scrofa
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source

FEATURES

JOURNAL MEDLINE mRNA

BASE CC ORIGIN

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to: 108275 from: 1
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Quality: 503.00
                                                                                                                                                                                                                                                                                                                                                          seq_name: gb_rol:MUSTGFRNA
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LOCUS MUSTGFRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                           M13177
                     Align seg 1/1
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KEYWORDS
SOURCE
ORGANISM
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ORIGIN
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 1561)
Purchlo,A.F. and Madisen,L.
TGF - beta 1 / beta 2 : a novel chimeric transforming growth factor-beta
                                                                                                                                                                                     29
                                                                                                                                                                                                                    17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
                                                                                                                                                                         1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17
                                                                                                                                                                                                                                                                                                                                                      rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
                                                                                                                                                                                                                                                                34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr
                                                                                                                                                                                                                                                                                                           LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh
                                                                         Length: 112
Gaps: 0
Percent Identity: 76.786
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps: 0
Percent Identity: 75.893
                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="mature TGF-beta2"
866 a 527 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Patent: EP 0374044-A2 3 20-JUN-1990;
Location/Qualifiers
                                                                                                                                                     to: 2724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 3 from Patent EP 0374044
108275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism-"unknown"
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                                                                      516.00
5.010
91.964
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89.286
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Ratio:
                                                                         Quality:
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Percent Similarity:
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                                                             alignment_scores
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TGFB3P x 108275
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                  BASE COUNT
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FEATURES

ORIGIN

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KSSVEQHVELYQYSNISWRYLGSNRLITPTDTPFWLSTRYNY LIFT FLANKLINGEN FESAHCSCDSRDNKLHVGINGTRGTRGTRF FSAHCSCDSRDNKLHVEINGISPRRRGDLGTIHDMNRPFLLLMATPLERAQHLHSSRH RRALDTNYCESSTERNCVRQLYIDFRRDLGWRWIHBERGYHANFCLGPCPYIWSLDT RYSKVLALYNQHNPGASSPCCVPQALEPLPIVYYVGRKPRVEQLSNMIVRSCKCS" 540 c 540 c 599 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /translation="MPPSGLRLLPLPLPWLVUTPGRPAAGLSTCKTIDMELVKRK
RIEAIRGQILSKLRLASPPSQGEVPPGPLPEAVLALINSTRDRVAGESADPEPEPEAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YYAKEVTRVLMVDRNNAIYEKTKDISHSIYMFFNTSDIREAVPEPPLLSRAELRLQRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mouse monocytic cell, cDNA to mRNA.
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MUSTGERNA 1579 bp mRNA ROD 27-APR-1993
Mouse transforming growth factor beta mRNA (TGF-beta), complete
                                                                                                                                                                                                            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; 1 (bases 1 to 1579)
Derynck, R., Jarrett, J.A., Chen, E.Y. and Goeddel, D.V. The murine transforming growth factor-beta precursor 86168129
                                                   1096 GCCCTGGACACCAACTACTGCTTCAGAAATGTGCAGGATAATTGCTGCCT 1145
                                                                                                                                                        1146 ACGTCCGCTTTACATTGACTTCAAGAGGGACCTCGGCTGGAAGTGGATCC 1195
                                                                                                                                                                                                                                                                                                                                               LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17
                                                                                                       67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1396 CTGTCCAACATGATCGTGGCTCCGTCAAATGCAGC 1431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        101 LeuSerAsnMetValValLysSerCysLysCysSer 112
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/note="TGF-beta precursor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /protein_id="AAA40423.1"
/db_xref="GI:201953"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Mus musculus"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="TGF-beta mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /codon_start=1
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112

Length:

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KEYWORDS
SOURCE
ORGANISM
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DEFINITION
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VERSION
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TITLE
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                                                                                                                                                                                                                                ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (01-MAR-1990) Su Wen Q., National Cancer Institute NIH, Bldg 41 Room C629, Laboratory of Chemoprevention, NCI Bethesda MD 20892, U S A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Métazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RNTGFB1 1585 bp mRNA ROCD 23-MAR-1995
Rat mRNA for transforming growth factor-beta 1.
X52498 48.852498 GI:57341
growth factor; TGF-beta 1; transforming growth factor-beta 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                beta-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 (bases 1 to 1585)
Qian,S.W., Kondaiah,P., Roberts,A.B. and Sporn,M.B.
CDNA cloning by PCR of rat transforming growth factor
Nucleic Acids Res. 18 (10), 3059 (1990)
                                                                                                                                                                                        84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
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                                                                                                                              1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa
                                                                                                                                                                                                                                                             34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr
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                                                                                                                                                                                                                                                                                                                                                                                        67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG
 Gaps: 0
Percent Identity: 77.679
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="heart"
413. .481
/product="signal peptide (AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="prepro-TGF-beta 1 (AA
/codon_start=1
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                                                                                                to: 1579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /strain="Sprague Dawley"
/db_xref="taxon:10116"
/dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /protein_id="CAA36741.1"
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1. .1585
                                                                                              Align seg 1/1 to: MUSTGFRNA from: 1
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1 (bases 1 to 1585)
Su Wen, Q.
Direct Submission
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5.133
87.500
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             Percent Similarity:
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                                              alignment_block:
TGFB3P x MUSTGFRNA
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TITLE
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TITLE
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KSTVEQHVELYQKYSNNSWRYLGNRLLTPTDTPEWLSFDVTGVVRQWLNQGDGIQGFR
FRAHCSCOSTEKNCYLHVEINGISPKRKGDLGTTHDMNRPFLLLMATPLERAQHLHSISRH
FRALDTUYCSSSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDT
QYSKVLALYNQHNPGASASPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS"
482. .1582
/db_xref="G1:57342"
/db_xref="Swiss-ProT:P17246"
/db_xref="Swiss-ProT:P17246"
/translation="MPPSGRLLPLLIPLPWILULTPGRPAAGLSTCKTIDMELVKRK
RIEAIRGOILSKLRHASPPSGGEVPFGPLPEAVLALVNSTRDRVAGESADPEPEPEAD
YYAKEVTRVLMVDRNNAIYDKTKDITHSIYMFFNTSDIREAVPEPPLLSRAELRLQRF
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Musot, L.
Poirot, L.
Direct Submission
Submitted (07-AUG-1998) Poirot L., Department of Immunology,
I.G.B.M.C., PB 163, 67404 Illkirch, FRANCE
2 (bases 1 to 2094)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MMU009862 2094 bp mRNA ROD 01-OCT
Mus musculus mRNA for transforming growth factor-beta 1.
AJ009862.1 GI:3688423
                                                                                                                                                                                                                                                  /product="mature TGF-beta 1 (AA 255 to 367)"
538 c 403 g 307 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
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                                                                                                                                                                                               /note="pro-TGF-beta 1 (AA 1 to 367)"
1247. .1582
                                                                                                                                                                                                                                                                                                                                                                         Length: 112
Gaps: 0
Percent Identity: 77.679
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5.133
87.500
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Percent Similarity:
                                                                                                                                                                                                                                                                       337
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                                                                                                                                                                                                                                                                                                                                                      alignment_scores:
                                                                                                                                                                                                                                 mat_peptide
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FEATURES
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                                                                                                                                                                                                                                                                                                                                                                              RIEATRGOIISKLRAASPPSGGEVPPGPLPBAVLALYNSTRORVAGESADPEEPEPEN
YYAKEVTRVLMVDRNNAIYEKTKDISHSIYMFPNTSDIREAVPEPPLLSRAELRLORL
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                                                                                                                                                                                                                                                                                                                                                                                                                                         FSAHCSCDSKDNKLHVEINGISPKRRGDLGTIHDMNRPFLLLMATPLERAQHLHSSRH
RRALDTNYCFSSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1952 AGCCACTGCCCATCGTCTACTACGTGGGTCGCAAGCCCAAGGTGGAGCAG 2001
Poirct, L., Benoist, C. and Mathis, D. Transforming growth factor-beta 1 sequence and expredifference between NOD/Lt and C57B1/6 mouse strains Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1802 ACGAGCCCAAGGCTACCATGCCAACTTCTGTCTGGGACCCTGCCCCTAT 1851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps: 0
Percent Identity: 77.679
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        to: 2094
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/gene="TGF beta 1"
                                                                            Location/Qualifiers
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87.500
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Ratio:
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                                                                                              source
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                                                                                                                                                                                                             gene
AUTHORS
                                                      JOURNAL
                                                                        FEATURES
                 TITLE
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LGPCPYIWSLDTQYSKVLALYNQHNPGASAAPCCVPQALEPLPIVYYVGRKPKVEQLS
                                                                                                                        Oryctolagus cuniculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                       2 (bases 1 to 339)
Taylor,T.K., James,E.R., McGonigle,S. and Yoho,E.R.
Direct Submission
Submitted (16-APR-1997) Ophthalmology, Med.Univ. S.C., 171 Ashley
Avenue, Charleston, SC 29464, USA
Location/Qualifiers
      ocaruuulaa aaga mRNA MAM 06-MAY-1997
Oryctolagus cuniculus transforming growth factor beta-1 mRNA,
partial cds.
                                                                                                                                                           1 (bases 1 to 339)
Taylor,T.K., James,E.R., McGonigle,S. and Yoho,E.R.
Rabbit transforming growth factor beta-1 active region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa
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Gaps: 0
Percent Identity: 76.786
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<1. .339
                                                                                                                                                                                                                                                                                                                                                                                                      /note="encodes active region"
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                                                                             AF000133.1 GI:2072531
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seq_documentation_block:
LOCUS OCAF000133
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TGFB3P x OCAF000133
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                                                                                                             rabbit
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                                                                                            KEYWORDS
SOURCE
ORGANISM
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                             DEFINITION
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AUTHORS
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          201 GCATAACCCGGGCGCCTCGGCGCGCGCGTGCTGCGTGCCGCAGGCGCTGG 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 GCCCTGGACACCAACTATTGCTTCAGCTCCACGGAGAAGAACTGCTGCGT 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG
                                                                                                                                                                                                                                   1 (bases 1 to 339)
McMaster, G.K., Cox, D., Cerletti, N. and Kuhla, J.
Novel hybrid transforming growth factors
Patent: EP 0542679-A 1 19-MAY-1993;
                                                                                                PAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length: 112
Gaps: 0
Percent Identity: 76.786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PAT
    101 LeuSerAsnMetValValLysSerCysLysCysSer 112
                                                                                                                                                                                                                                                                                                                                                                             59
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114 c 100 g 55
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LOCUS A48549 339 bp DNA
DEFINITION Sequence 1 from Patent W09603432.
ACCESSION A48549.1 GI:2302319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Align seg 1/1 to: A23751 from: 1 to: 339
                                                                                                                                                                                                                                                                                                                Location/Qualifiers
1. .339
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                                                                                   TGF-betal coding region.
                                                                                                                                           A23751.1 GI:825585
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                                                                            seq_name: gb_pat1:A23751
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TGFB3P x A23751
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                                                                                                           DEFINITION
                                                                                                                                                                                        ORGANISM
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VERSION
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AUTHORS
TITLE
                                                                                                                                                                                                                                                                                   JOURNAL
                                                                                                                                                        KEYWORDS
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LGPOPYIMSLDTQYSKVLALYNQHNPGASAAPCCVPQALEPLPIVYYVGRKPKVEQLS
                                                                                                                                                                                                                                                                                                                                                                           'note="Protein sequence is in conflict with the conceptual
                                                                                                                                                   synthetic construct.
synthetic construct
artificial sequence.
1 (bases 1 to 339)
Cerletti,N., McMaster,G.K., Cox,D., Schmitz,A. and Meyhack,B.
Process for the production of biologically active protein (e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Identity: 76.786
                                                                                                                                                                                                                                                                                                                        /organism="synthetic construct"
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                                                                              H. sapiens TGF-beta 1 gene seq ID No:1.
301 CTGTCCAACATGATCGTGCGCTCCTGCAAGTGCAGC 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 101 LeuSerAsnMetValValLysSerCysLysCysSer 112
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                                                                                                                                                                                                                                                                Patent: EP 0433225-A 1 19-JUN-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       to: 339
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                                                                           339 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NMIVRSCKCS"
                                                                                                                        A18277.1 GI:513237
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                                                           seq_documentation_block:
LOCUS A18277
                                seq_name: gb_pat1:A18277
                                                                                                                                                                                                                                                                                CIBA-GEIGY
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Ratio:
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Percent Similarity:

alignment\_block: TGFB3P x A18277

21

alignment\_scores:

99

BASE COUNT

TGE)

JOURNAL

AUTHORS TITLE

REFERENCE

DEFINITION

ACCESSION VERSION

ORGANISM

KEYWORDS SOURCE

ORGANISM

KEYWORDS

AUTHORS TITLE

REFERENCE

JOURNAL

source

FEATURES COMMENT

SASE COUNT

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/note="Protein sequence is in conflict with the conceptual
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Cerletti,N.
NEW PROCESS FOR THE PRODUCTION OF BIOLOGICALLY ACTIVE PROTEIN
PATENT: WO 9603433-A 1 08-FEB-1996;
CIBA GEIGY AG (CH)
Other publication AU 3199695 960222.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               51 GCGCAGCTGTACATTGACTTCCGCAAGGACCTCGGCTGGAAGTGGATCC 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       101 ACGAGCCCAAGGCTACCATGCCAACTTCTGCCTCGGGCCCTGCCCTAC 150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          151 ATTIGGAGCCTGGACACGCAGTACAGCAAGGTCCTGGCCCTGTACAACCA 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17 largProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length: 112
Gaps: 0
Percent Identity: 76.786
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     translation"
     GI:2302333
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                                                    unidentified.
unidentified
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LOCUS AR036686
  A48563.1
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TGFB3P x A48563
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                                                                                    ORGANISM
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VERSION
KEYWORDS
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                                                                                                                                                                                                   TITLE
                                                                                                                                                                                                                                                                                     COMMENT
                                                                                                                                                                                                                                                                                                                                                              /organism="unidentified"
/db_xref="taxon:32644"
1. 336
/note="Protein sequence is in conflict with the conceptual
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /translation="ALDTNYCESSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFC
LGPCPYIWSLDTQYSKVLALYNQHNPGASAAPCCVPQALEPLPIVYYVGRKPKVEQLS
                                                                                                                                                                NOVEL PROCESS FOR THE PRODUCTION OF BIOLOGICALLY ACTIVE DIMERIC
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                                                                                                                                                                                                                     Patent: WO 9603432-A 1 08-FEB-1996;
CIBA GEIGY AG (CH)
Other publication AU 3109595 960222.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /codon_start=1
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/protein_id="CAA03113.1"
/db_xref="GI:2302320"
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Sequence 1 from Patent WO9603433.
A48563
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                                                                              unclassified.
1 (bases 1 to 339)
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LOCUS A48563
                       unidentified
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TGFB3P x A48549
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34

21

29-SEP-1999

DEFINITION

ACCESSION

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KEYWORDS
SOURCE
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                                ORIGIN
                                         Unknown.
Unclassified.
Unclassified.
1 (bases 1 to 339)
Hall,F.L., Nimni,M.E., Tuan,T., Wu,L. and Cheung,D.T.
Artificial skin prepared from coclagen matrix containing transforming growth factor..beta. having a collagen binding site Patent: US 5800811-A 29 01-SEP-1998;
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1 (bases 1 to 339)
Cerletti,N., McMaster,G.Kent, Cox,D., Schmitz,A. and Meyhack,B. Process for refolding recombinantly produced TGF-.beta.-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
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Gaps: 0
Percent Identity: 76.786
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Location/Qualifiers
1, 339
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JS 5650494.
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113 c 100 g
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  GI:5954542
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 AR036686.1
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Ratio:
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TITLE
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TITLE
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                                                                       REFERENCE
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Homo sapiens
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Butheria; Primates; Catarrhini; Hominidae; Homo.
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Urushizaki,Y., Niitsu,Y., Terui,T., Koshida,Y., Mahara,K.,
Kohgo,Y., Urushizaki,I., Tarkahashi,Y. and Ito,H.
Kohgo,Y., Urushizaki,I., Tarkahashi,Y. and Ito,H.
Cloning and expression of the gene for human transforming growth factor-beta in Escherichia coli
Tumor Res. 22, 41-55 (1987)
Location/Qualifiers
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Human transforming growth factor-beta mRNA, complete cds, clone
PTGF-beta-trp114.
M38449 M55656
M38449.1 GI:339557
Hransforming growth factor-beta.
Human nasopharyngeal carcinoma cell line KB, cDNA to mRNA.
Homo sablens
                                                                                                                                                                                                                                                                                                                                                         201 GCATAACCCGGGCGCTCGGCGGCGCGCGTGCTGCGTGCCGCAGGCGCTGG 250
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue_type="nasopharyngeal carcinoma"
                                                                                                                                                                                                                                                                                  51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh
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                 59
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/db_xref="taxon:9606"
/cell_line="KB"
                                                                                                                                                                                                                                             Align seg 1/1 to: I56854 from: 1 to: 339
/organism="unknown"
114 c 100 q
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/codon_start=1
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LOCUS HUMTGFBA
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Ratio:
                                                                                                                                                 Percent Similarity:
                                                                                              alignment_scores:
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TGFB3P x I56854
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BASE COUNT ORIGIN

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561 GCATAACCCGGGCGCCTCGGCGCGCCCTGCTGCGTGCCGCAGGCGCTGG 610
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                                                                                                                                1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17
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Derynck, R.M.A. and Goeddel, D.V.
Nucleic acid encoding TGF-. Deta. and its uses
Patent: US 4886747-A 3 12-DEC-1989;
South San Francisco, CA
Location/Qualifiers
      Gaps: 0
Percent Identity: 76.786
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Gaps: 0
Percent Identity: 76.786
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Sequence 3 from Patent US 4886747.
103312.
103312.1 GI:270706
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284 c 231 g
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Unclassified.
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                                                  alignment_block:
TGFB3P x 105434
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VERSION
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TITLE
JOURNAL
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/product="transforming growth factor-beta"
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/db_xxef="dg1:339558"
/translation="ALDTNYCFSSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFC
LGPCPYIWSLDTQYSKVLALYNQHNPGASAAPCCVPQALEPLPIVYYVGRKPKVEQLS
NMIVRSCKCS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 (bases 1 to 699)
Iwata, K.K., Gold, L.I. and Stephenson, J.R.
Tissue-derived tumor growth inhibitors, methods of preparation and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  02-DEC-1994
                                                                                                                                                                                                                                                                                                                                                                                                 84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
                                                                                                                                                                                                                                                                                                                                                                                 17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa
                                                                                                                                                                         Length: 112
Gaps: 0
Percent Identity: 76.786
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Patent: EP 0267463-A2 4 18-MAY-1988;
Location/Qualifiers
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                                                                                                                                                                                                                                                                                      to: 650
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105434.
105434.1 GI:590975
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221 c 204 q
                                                                                            179 g
                                                                                                                                                                                                                                                                                    Align seg 1/1 to: HUMTGFBA from: 1
                                                                                                244 C
                                                                                                                                                                       500.00
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                                                                                                                                                                         Quality:
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Percent Similarity:
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PAT

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DEFINITION

ACCESSION

KEYWORDS

VERSION SOURCE

ORGANISM

AUTHORS

TITLE

REFERENCE

source

JOURNAL

BASE COUNT

ORIGIN

21

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/translation="MPPSGLRLLPLLLPLLMLLMLTPGRPVAGLSTCKTIDMELVKRK
GIEAIRGQILSKLRLASPPSQGDVPPGPLPEAILALYNSTRDRVAGESAETEPEPEAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YYAKEVTRVLMVEYGNKIYDKMKSSSHSIYMFINTSELREAVPEPVLLSRADVRLIKL
KLKVEQHVELYQKYSNNSWRYLSNRLLAPSDSPEMLSFDVTGVVRQWLTHREEIEGFR
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RRALDTNYCFSSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae; Caprinae; Ovis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QYSKVLALYNQHNPGASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 (bases 1 to 1173)
Woodall,C.J., McLaren,L.J. and Watt,N.J.
Sequence and chromosomal localisation of the gene encoding ovine
latent transforming growth factor-beta 1
Gene 150 (2), 371-373 (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (24-DEC-1993) C. Woodall, Univ. of Edinburgh, Dept. o
Veterinary Pathology, Sc. of Vet. Studies, Univ. of Edinburgh,
Edinburgh EH9 IQH, UK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /codon_start=1 /codon_start=1 /prodoc="transforming growth factor-beta 1" /protein_id="CAA5442.1" /db_xref="GI:496649"
                                                                                                                                                             84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
                                                                                                                                                                                                                                                    762 ATCTGGAGCCTGGATACACAGTACAGCAAGGTCCTGGCCCTGTACAACCA 811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OATGFB1 1173 bp mRNA 10.aries mRNA for transforming growth factor-beta I.
                                                                                                                                     17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyfrpLysTrpValH 34
                                                                                                                                                                                                                                                                                                                     LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
                                                  1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa
                                                                       812 GCACAACCGGGGGGCTTCGGCGGCGCGCTGCTGCTCAGGCGCTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1sGluProLysGlyTyrAlaAsnPheCysSerGlyProCysProTyr
                                                                                                                                                                                                                                                                                                                                                                                                          rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG
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/organism="Ovis aries"
      to:
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      to: BOVIGFB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seq_documentation_block:
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    Align seg 1/1
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SOURCE
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/db_xref="GI:163748"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IYDKMKSSSHSIYMFFNTSELREAVPEPVLLSRADVRLLRLKLKVEGHVELYQKYSNN
SWRLLSNRLLARSDSPEWLSFBYTGVYRQWLTRREBIEGFREAHCSODSRDNTLQVD
INGFSSGRRGDLATIFGMNRFPLLLMATPLERAQHJHSSRHRRALDTRYCFSSTERNC
CVRQLXIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALINQHNPGAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      transforming growth factor-beta 1.
Bovine fibropapilloma, cDNA to mRNA, (library of Okayama and Berg).
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Van Obberghen-Schilling, E., Kondaiah, P., Ludwig, R.L., Sporn, M.B. and Baker, C.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Complementary deoxyribonucleic acid cloning of bovine transforming
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bovine transforming growth factor-beta-1 (TGF beta-1) mRNA, 3'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27-APR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="transforming growth factor-beta-1 precursor"
                         luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
                                                                                                                                                                                                                                                                                                                                                                                        51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
                                                                                                                                                                                                                                                                       84
                                                                                     34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
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/note="transforming growth factor-beta-1"
301 م 193 t
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17 largProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH
                                                                                                                                                                                                                                                                    67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG
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Percent Identity: 76.786
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Mol. Endocrinol. 1, 693-698 (1987)
91042552
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TGFB3P x BOVTGFB
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SOURCE ORGANISM

REFERENCE AUTHORS

DEFINITION

101

84

ACCESSION VERSION

KEYWORDS

source

CDS

MEDLINE

FEATURES

JOURNAL

TITLE

BASE COUNT

ORIGIN

18-APR-1995

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VERSION
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                                                                                                                                                                                                                                                                                                                                        BASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.

1 (bases 1 to 1369)
Manning,A.M., Auchampach,J.A., Drong,R.F. and Slightom,J.L.
Cloning of a canine cDNA homologous to human transforming growth factor-beta 1 (TGFbetal)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOGTGFB1A 1369 bp mRNA 30-OCT-1994
Canine transforming growth factor-beta 1 (TGFB1) mRNA, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  homologue; transforming growth factor-beta 1.
Canis familiaris adult jugular vein endothelial cDNA to mRNA.
Canis familiaris
               /product="transforming growth factor-beta 1"
378 c 336 q 214 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
                                                                                                                                                                                                                                                                                      17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
                                                                                                                                                                                                                                                                                                                                                                                                        34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
                                                                                                                                                                                                                                                                      1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tissue_type="jugular vein endothelial"
                                                                                                                                     Gaps: 0
Percent Identity: 76.786
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                                                                                                                  Length:
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/cell_type="LPS-activated"
/dev_stage="adult"
                                                                                                                                                                                                                                       to: 1173
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/gene="TGFB1"
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L34956.1 GI:516071
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                                                                                                                                                                                                                                     Align seg 1/1 to: OATGFB1
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835.
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                                 245 a
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Ratio:
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TGFB3P x OATGFB1
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                                 BASE COUNT
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KLKAEQHVELYQKYSNDSWRYLSNRLLAPSDTPEWLSFDVTGVVRQWLSHGGEVEGFR
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1039. 1227
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                                                                                                                                                                                                                                                                                                                                                                                                          YYAKEVTRVLMVENTNKIYEKVKKSPHSIYMLFNTSELREAVPEPVLLSRAELRLLRL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="transforming growth factor-beta 1" 1231. 1369 /gene="TGFB1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        942 CCGGCAGCTCTACATTGACTTCCGCAAGGATCTGGGCTGGAAGTGGATCC 991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 84
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Gaps: 0
Percent Identity: 76.786
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    415
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               473 c
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LOCUS AGMTGFR
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tgfb3p.rge

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FEATURES
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YAAKEVTRYLAVETHRIYDKFKOSTHSIYMFFTSELREAVPEPVLLSRAEIRLLRI
KLKVEQHVELYQKYSNNSWYRLSNRLLAPSNSPEWLSFDYTGVYRQWLSRGEIEGFR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OYSKVLALYNQHNPGASAAPČCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS"
1096. 1431
1006e-"transforming growth factor-beta"
547 c 547 c
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; Cercopithecinae; Cercopithecinae; Cercopithecinae; Cercopithecinae; Cercopithecinae; Catarrhini; Catarrhini; Catarrhini; Carcopithecidae; Cercopithecinae; Cercopithecinae; Cercopithecidae; Catarrhini; Catarrhini; Cercopithecidae; Losses 1 to 1561)
Sharples, K., Plowman, G.D., Rose, T.M., Twardzik, D.R. and Purchio, A.F.
Cloning and Sequence analysis of simian transforming growth factor-beta cDNA
DNA 6, 239-244 (1987)
87246074
                                                                                                                                                                                                                                                                                    /note="transforming growth factor-beta precursor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1096 GCCCTGGACACCAACTACTGCTTCAGCTCCACGGAGAAGAACTGCTGCGT 1145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17
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Gaps: 0
Percent Identity: 76.786
                                                                                                                                                                                                                Location/Qualifiers
1. 1561
/organism="Cercopithecus aethiops"
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5.102
87.500
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TGFB3P x AGMTGFB
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seq\_name: gb\_om:SSTGFBR

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                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
                                                                                                                                                                                   1 (bases 1 to 1605)
Derynck, R. and Rhee, L. Squence of the porcine transforming growth factor-beta precursor Nucleic Acids Res. 15 (7), 3187 (1987)
                                     Porcine mRNA for transforming growth factor-beta (TFG) precursor.
Y00111
                   27-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
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404. 1576
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Gaps: 0
Percent Identity: 76.786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              647. 655
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1238. .1573
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572 c 437 g 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Align seg 1/1 to: SSTGFBR from: 1 to: 1605
                                                                                           transforming growth factor-beta
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                                                                                                                                                                                                                                                                                           Location/Qualifiers
                   1605 bp
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                                                                         Y00111.1 GI:2129
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5.102
87.500
documentation_block:
                                                                                                                                   Sus scrofa
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Ratio:
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                     SSTGFBR
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TGFB3P x SSTGFBR
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                                   DEFINITION
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VERSION
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                                                                                                                                                                                                             AUTHORS
TITLE
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SOURCE
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Clone distribution: MGC clone distribution information can be found
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LOCUS BC000125
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                          TGFB3P x GGTGFB1
        alignment_block:
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ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="SWISS-PROT:P07200"
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YYAKEVTRVLMVESGNOIYDKFKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLLRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KLKVEQHVELYQKYSNDSWGYLSNRLLAPSDSPEWLSFDVTGVVRQWLTRREAIEGFR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
Submitted (14-JUL-1988) Jakowlew S.B., National Institute of health, National Cancer Institute, Laboratory of Chemoprevention, Building 41, Room B902, Bethesda, Maryland 20892, USA 2 (bases 1 to 1750)
Zakowlew, S.B., Dillard, P.J., Sporn, M.B. and Roberts, A.B. Nucleotide sequence of chicken transforming growth factor-beta 1 (TGF-beta 1)
                                                                                                                                                                                                                                                                                                                                                                                                              Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The submitters believe that the chicken cDNA library was contaminated with porcine cDNA, and that the sequence is infact porcine TGF-beta-1. 27-MAR-1996. Location/Qualifiers
                                                                                                                                                                                                                                                                     27-MAR-1996
1438 GCACAACCCGGGGGGGGGGGGGGGCGTGCTGCGTGCCGCAGGCGCTGG 1487
                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Jakowlew, S.B.
                                       84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
                                                                                                                                                                                                                                                GGTGFB1 1750 bp mRNA MAM 2
Porcine mRNA for transforming growth factor-beta 1.
X12373
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                                                                                                                                          101 LeuSerAsnMetValValLysSerCysLysCysSer 112
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                                                                                                                                                                                                                                                                                                                                               transforming growth factor-beta 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /strain="white leghorn"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1. .1750
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/gene="TGF-beta 1"
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627 c
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                                                                                                                                                                                                       seg_name: gb_om:GGTGFB1
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BASE COUNT
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Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield, Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin, Letticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacqueline Schein, Duane Smallus, Michael Smith, Lorraine Spence, Jeff Stott, Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy, George Yang, Scott Zuyderduyn, Marco Marra.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens, Similar to transforming growth factor, beta 1, clone acondity, mRNA, complete cds.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1780)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
Submitted (03-007-2000) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Robert Strausberg, Ph.D.
Tal: (301) 496-1550
Email: Robert_Strausbergenih.gov
Tissue Procurement: AFCC
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
info@bcgsc.bc.ca
                                                                                                                                                                                                                                                                                                                                                                               1484 GCACAACCCGGGCGCGCTGCCGCGCGCGCGCGCGCGCTGC 1533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1284 GCCCTGGATACCAACTACTGCTTCAGCTCCACGGAGAAGAACTGCTGCGT 1333
                                                                                                                                                                                                                                                                        1334 GCGGCAGCTCTACATTGACTTCCGGAAGGACCTGGGCTGGAAGTGGATTC 1383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        84
                                                               1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG
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Align seg 1/1 to: GGTGFB1 from: 1 to: 1750
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Quality:
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TGFB3P x BC001180
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KIKVEQHVELYQKYSNNSWRYLSNRLLAPSDSPEWLSFDVTGVVRQWLSRGGEIEGFR
                                                                                                                                                                                                                                                                                                                                                                               LSAHCSCDSRDNTLQVDINGFTTGRRGDLATIHGMNRPFLLLMATPLERAQHLQSSRH
RRALDTNYCBSSTERNCVRQLXIDFREDLGWRWIHBERGYHANFCLGPCPYTWSLDT
QSSRVLALLYNGNNPRAFASPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS"
648 c 493 g 298 t
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Homo sapiens, Similar to transforming growth factor, beta 1, clone
MGC:2323, mRNA, complete cds.
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAL Plate: 6 Row: e Column: 11.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1281 GCCCTGGACACCAACTATTGCTTCAGCTCCACGGAGAAGAACTGCTGCGT 1330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   84 luProLeuThrIleLeuTyrTyrValGlyArqThrProLysValGluGln 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length: 112
Gaps: 0
Percent Identity: 76.786
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                                                                                                                                                                                        /note="Vector: pOTB7"
                                                                                                                                                                                                          447. .1619
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87.500
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                                       FEATURES
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BC001180.1 GI:12654682

ACCESSION

VERSION

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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAL Plate: 6 Row: e Column: 10.
Location/Qualifiers
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LSAHCSCDSRDNTLQVDINGFTTGRRGDLATTHGWNRPFLLLMATPLERAQHLQSSRH
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QYSSVVLALYNQHNGAPAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS"
648 c 298 t
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YYAKEVTRVLMVETHNEIYDKFKQSTHSIYMFFNTSELREAVPEPVLLSRAELRLLRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield, Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin, Letticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saedi, Jacqueline Schelin, Duane Smallus, Michael Smith, Lorraine Spence, Jeff Stott, George Yang, Scott Zuyderduyn, Marco Marra.
                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                        Submitted (11-DEC-2000) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length: 112
Gaps: 0
Percent Identity: 76.786
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//tissue_type="Eye, retinoblastoma"
/clone_lib="NIH_MGC_16"
/lab_host="DH10B-R"
                                                                                                                                                                                                                                                                                                                             NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Proourement: ATCC
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                                                           Mammalia; Eutheria; I
1 (bases 1 to 1780)
Strausberg,R.
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                                                                                                                                                                Direct Submission
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5.102
87.500
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Homo sapiens
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326
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                                                        alignment_scores
                                                                                                                        alignment_block:
TGFB3P x E03028
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ORIGIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutherlai; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1821)
Ohases it no 1821)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MIYAGAWA KIYOSHI, TAKAKU FUMIMARO
C12P21/00,C07K13/00,C12N5/10,C12N15/18//C12Q1/68,(C12P21/00,
C12R1:91),
(C12N15/18,C12R1:91);
Strandedness: Double;
topology: Linear;
                                                                                                                                                                                                                                                                                                                                                             29-SEP-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TARAKU,F. .
PRODUCTION OF HUMAN PRO-TGF-BETA1 BY GENETIC RECOMBINATION
PACENC: JP 1991180192-A 1 06-AUG-1991;
KIRIN BREWERY CO LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FI
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07-DEC-1989 JP 1989318243
OHASHI HIDEYA, ISHII YASUYUKI, MIYATA YOSHINORI, PI
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511. .1683

/product='human prepro TGF-betal' FT

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/note='human pro TGF-betal'

1345. .1680

/product='human TGF-betal'

1684. .1820.
84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
                                                                                                                                                             84
                                                                                                       51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
                                                    34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr
                                                                                                                                                           67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG
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                                                                                                                                                                                                                                                                                  101 LeuSerAsnMetValValLysSerCysLysCysSer 112
                                                                                                                                                                                                                                                                                                                                                            DNA encoding human prepro TGF-betal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              anti-sense: No;
*source: tissue_type=placenta;
*source: clone=pVCl9-TGF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1. .1821
/organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (human)
JP 1991180192-A/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical: No;
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JP 1991180192-A/1.
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Homo sapiens
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FT mat_pept
FT mat_pept
FT 3'UTR
                                                                                                                                                                                                                                                                                                                      seq_name: gb_pat2:E03028
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LOCUS E03028
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VERSION
KEYWORDS
SOURCE
ORGANISM
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DEFINITION
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JOURNAL
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YYAKEVTRVLMVETHNEIYDKFKQSTHSIYMFRITSELREAVPEPVLLSRAELRLLRL
KLYRQHVELGYVEYSNNSWRYLSNRLLAPSDSBEMLSPDYGVYRQWISGGETEGFR
LSAHCSCDSRDNTLQVOINGFTTGRRGDLATHGMRPFLLLMATPLERAQHLQSSRH
RRALDTNYCFSSTEKNCCVRQLYIDPRKDLGMWWIHEPKGYHANFCLGPCPYIMSLDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /translation="MPPSGLRLLPLLLPLLMLLVLTPGPPAAGLSTCKTIDMELVKRK
RIEAIRGQILSKLRLASPPSQGEVPPGPLPEAVLALYNSTRDRVAGESAEPEPEAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29-JUL-1993
                                                                                                                                                                                                                                                                                                                                                                   1445
                                                                                                                                                                                                                                                                                                                                                                                                  1546 GCATAACCCGGGCGCCTCGGCGCGCGCGTGCTGCGTGCCGCAGCCGCTGG 1595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           67
                                                                                                                                                                                                                                                                           1346 GCCCTGGACAACTATTGCTTCAGCTCCACGAGAAGAACTGCTGCGT
                                                                                                                                                                                                                                                                                                                             17 largProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH
                                                                                                                                                                                                                                                                                                                                                51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUCLEIC ACID ENCODING TGF- beta 3 AND ITS USE Patent: WO 8912101-A 4 14-DEC-1989; Location/Qualifiers
                                                                                       Length: 112
Gaps: 0
Percent Identity: 76.786
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/organism="synthetic construct"
/db_xref="taxon:32630"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /transl_table=11
/product="preTGF-beta1"
/protein_id="CAA00588.1"
/db_xref="GI:412941"
                                                                                                                                                                                                                       to: 1821
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synthetic construct
artificial sequence.
1 (bases 1 to 2537)
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87.500
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LOCUS
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                                                                                                                            Percent Similarity:
                                                                                           Quality:
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BASE COUNT
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QYSKVLALYNQHNPGASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS"
1 893 c 739 g 432 t
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Derynck, R., Jarrett, J.A., Chen, E.Y., Eaton, D.H., Bell, J.R., Assolan, R.K., Roberts, A.B., Sporn, M.B. and Goeddel, D.V. Human transforming growth factor-beta complementary DNA sequence and expression in normal and transformed cells Nature 316 (6030), 701-705 (1985)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27-MAR-1995
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                                                                                                                                                                                                                                                                                                                                 1676 GCCTGGACACCAACTATTGCTTCAGCTCCACGAGAACAGAACTGCTGCGT 1725
                                                                                                                                                                                                                                                                                                                                                                                                                   1726 GCGCCAGCTGTACATTGACTTCCGCAAGGACCTCGGCTGGAAGTGGATCC 1775
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1826 ATTIGGAGCCTGGACACGCAGTACAGCAGGTCCTGGCCCTGTACAACCA 1875
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
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                                                                                                                                                                                                                                                                                                                                                                                             17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="pot. hairpin loops-forming region"
                                                                                                                                                                                                                                                                                                              1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG
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X02812.1 GI:37092
Signal peptide; transforming growth factor-beta
                                                                                                                                                              Percent Identity: 76.786
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/note="TGF-beta precursor"
/codon_start=1
                                                                                                                                                                                                                                                                     to: 2537
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/db_xref="taxon:9606"
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                   473 a
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                                                                                                                      LKLKVEQHVELYQKYSNNSWRYLSNRLLAPSDSPEWLSFDVTGVVRQWLSRGGEIEGF
RRSAHGSCDSRDNTLQVDINGFTTGRRGDLATHGMRPFLLLMATPLERAOHLQSSR
HRRALDTNYCFSSTEKNCCVRQLYIDFRKDLGWKWIHBPKGYHANFCLGPCPYIWSLD
TQYSKVLALYNQHNFGASAAPCCVPQALEPLPIVYXVGRKPKVEQLSNMIVRSCKCS*
863. .910
                                                                                                                                                                                                                         /note="pot. core sequence of signal peptide (aa -272 to -257)"
                                                                                                                                                                                                                                                                                  /note="pot. altern. translation start site"
1035. .1043
/note="put. glycosylation site"
1247. .1255
/note="put. glycosylation site"
1370. .1378
/note="put. glycosylation site"
1679. .2014
/product="mature TGF-beta (aa 1-112)"
2018. .2096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1729 GCGCAGCTGTACATTGACTTCCGCAAGGACCTCGGCTGGAAGTGGATCC 1778
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2517. .2522
/note="put. polyadenylation signal"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length: 112
Gaps: 0
Percent Identity: 76.786
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/note="fpA7-box-like region"
2517. .2522
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/note="GC-rich region"
2097. .2103
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938 c 801 g 4
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LOCUS

ACCESSION VERSION

ORGANISM

REFERENCE AUTHORS

KEYWORDS

JOURNAL MEDLINE

TITLE

FEATURES

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.890 ATCTGGAGCCTAGACACTCAGTACAGCAAGGTCCTGGCTCTGTACAACCA 1939
                                                                                                                                                                                                                                                                                                                                                                                                X99438.1 GI:2598418
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Penha-Goncalves, M.N.
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LOCUS
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VERSION
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AUTHORS
TITLE
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AUTHORS
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MEDLINE
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SOURCE
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KLKVEGHYELYQKYSNDSWRYLSNRLLAPSDSPEWLSFDYTGVYRQYLTRREATEGFR
LSAHCSCDSKDWTLHVETINGFNGSREDLATTHGMNRPFLLAMTPLERAQHLHSSRH
RRALDTNYCFSSTERKOCVRQLYTDFRKDLGAWWIREPKGYHAMTCLGFCPYTWSLDY
QYSKVLALYNQHNPGASAAPCCVPQALEPLPTVYYVGRKPKVEQLSNMIVRSCKCS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /translation="MPPSGLRLLPLLLPLLVLTPGRPAAGLSTCKTIDMELVKRK
RIEAIRGQILSKLRLASPPSQGDVPPGPLPEAVLALYNSTRDRVAGESVEPEPEAD
                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                        PIGTGFB1A 3206 bp mRNA MAM 31-MAR-1995
Sus scrofa transforming growth factor beta-1 mRNA, complete cds.
M23703
                                                                                                                                                                                                                                                                                            cDNA cloning of porcine transforming growth factor-beta 1 mRNAs. Evidence for alternate splicing and polyadenylation By Biol. Chem. 263 (34), 18313-18317 (1988) 89054010 On Apr 1, 1995 this sequence version replaced gi:341017.
                                                                                                                                                                                                              Mammalia: Butheria; Cetartiodactyla; Suina; Suidae; Sus. 1 (bases 1 to 3206)
Kondaiah, P., Van Obberghen-Schilling, E., Ludwig, R.L., Dhar, R., Sporn, M.B. and Roberts, A.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="transforming growth factor-beta-1"
/protein_id="AAA64616.1"
/db_xref="GI:755045"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1840 ATGAACCCAAGGCTACCATGCCAATTTCTGCCTGGGGCCCTGTCCCTAC 1889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /strain="miniature swine"
/db_xref="texon:9823"
/cell_type="peripheral blood lymphocyte"
906. .3191
                                                                                                                M23703.1 GI:755044
transforming growth factor-beta-1.
Sus scrofa (strain miniature swine) cDNA to mRNA.
Sus scrofa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length: 112
Gaps: 0
Percent Identity: 76.786
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                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Sus scrofa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     906. .3191
/gene="TGF-beta-1"
906. .2078
/gene="TGF-beta-1"
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/gene="TGF-beta-1"
3206
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1041 c
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87.500
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seq_name: gb_om:PIGTGFB1A
                                      seq_documentation_block:
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Ratio:
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TGFB3P x PIGTGFB1A
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COUNT

BASE CC ORIGIN

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/db_xref-"SWISS-PROT:019011"
/translation="MPPSGLRLIPLLIPLUMLIVITPGRPAAGLSTCKTIDMELVKRK
/translation="MPPSGLRLIPLLIPENVLALVRSTRAQVAGESAETEPPERAD
YAKEVITRULMVEKIASPPSGGESPPFGPLENVLALVRSTRAQVAGESAETERLIRL
YYAKEVTRULMVEKIANSTKTVETGSHSIYMFPNTSELRAAVPDPMLLSRAELRLIRL
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LSAHCSCDSKDNTLRVGINGFSSSRRGDLATIDGMNRPFLLLMATPLERAQQLHSSRH
RRALDTNYCFSSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDT
QYSKVLALYNQHNPGASAAPCCVPQVLEPLPIVYYVGRKPKVEQLSNMIVRSCKCS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 1173)
Penha-Goncalves, M.N., Onions, D.E. and Nicolson, L.
Cloning and sequencing of equine transforming growth factor-beta 1
(TGF beta-1) CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
                                                                                                                                                                                                                                                                                                                                                                                    07-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
Submitted (18-JUL-1996) M.N. Penha-Goncalves, University of
Glasgow, Veterinary Pathology Department, Veterinary School,
Bearsden Road, Glasgow G61 10H Scotland, UK
                                                                                                                                                                                                                                                                                                                                                                            E.caballus mRNA for transforming growth factor beta 1.
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/protein_id="CAA67801.1"
/db_xref="GI:2598419"
84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="PBMC, ConA and LPS stimulated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGF-beta 1; transforming growth factor-beta 1.
                                                                                                                                                                                                                                    LeuSerAsnMetValValLysSerCysLysCysSer 112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Equus caballus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue_type="lymph node"
/tissue_type="spleen"
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98185507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref-"taxon:9796"
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1155. .1173
/gene="TGF-beta 1"
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/gene="TGF-beta 1"
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382 c 357
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Ratio
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TGFB3P x E00973
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 2527)

Riku,M.A.D.D. and Debitsudo,B.G.

NUCLEIC ACID CONED WITH TGP-BETA AND ITS USE
Patent: JP 1986219395-A 1 29-SEP-1986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PF 20-MAR-1986 JP 1986064661
PR 22-MAR-1985 US 85 715142
PI RIKU MAIKERU ANDORE DERINKU, DEBITSUDO BANNOOMAN GETSUDERU C12P21/00,C12N1/00,C12N15/00//C1201/68,(C12P21/00, PC C12R1:91),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Key
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                                                                                                                                                                                                                                                                                                                                                                         51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
                                                                                                                                                                                                                                                                                                                         67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
                                   Percent Identity: 76.786
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/product='pre TGF-beta'
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                            Gaps:
                                                                                                  to: 1173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EUU973 2527 bp RNA
CDNA encoding human TGF-beta.
E00973
                                                                                                Align seg 1/1 to: ECRGFB1 from: 1
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29-SEP-1986
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JP 1986219395-A/1.
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                       5.092
87.500
              499.00
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LOCUS E00973
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              Quality:
                     Ratio: Percent Similarity:
                                                                         TGFB3P x ECRGFB1
alignment_scores
                                                            alignment_block:
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SOURCE
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TITLE
JOURNAL
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 336)
McMaster,G.K., Cox,D., Cerletti,N. and Kuhla,J.
Novel hybrid transforming growth factors
Patent: EP 0542679-A 6 19-MAY-1993;
CIBA-GEIGY AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25-JAN-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                             1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17
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Gaps: 0
Percent Identity: 75.893
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1676. .2011
/product='TGF-beta'
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                                1. . 841
2015. . 2537
37. . 113
2015. . 2100
2514. . 2519.
                                                                                                                                        1. .2527 (
/organism="Homo sapiens"
/db_xref="taxon:9606"
1888 c 735 g 43
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                                                                   stem_loop 37. .113
stem_loop 2015. .2
polyA_site 2514. .2
Location/Qualifiers
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87.500
 mat_peptide
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                                  5'UTR
3'UTR
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Quality:
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TGFB3P x SHPGFBlW
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                                                              BASE COUNT
ORIGIN
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KEYWORDS
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Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
Bovidae, Caprinae, Ovis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sutton, R., Ward, W.G., Raphael, K.A. and Cam, G.R. Growth factor expression in skin during wool follicle development Unpublished (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ovis aries transforming growth factor-beta 1 mRNA, partial cds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11-SEP-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       L36038.1 GI:535759
transforming growth factor-beta 1.
Ovis aries (strain Merino) fetus dorsal skin cDNA to mRNA.
Ovis aries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /strain="Merino"
/db_xref="taxon:9940"
/dev_stage="fetus"
/tissue_type="dorsal skin"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="transforming growth factor-beta 1"
/protein_id="AAA31526.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           51 ACGICCACITIACALIGALITICAAGAGGGAICIAGGGIGGAAAIGGAIAC 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           84 luProLeuThrIleLeuTyrTyrValGlyArqThrProLysValGluGln 100
                                                                                                                                                                                                                                                                                                                                                                                                            101 ACGAACCCAAAGGGTACAATGCCAACTTCTGCCTCGGGCCCTGCCCTAC 150
                                                                                                                                                                                                                                                                                                                                                                            34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
                                                                                                                                                                                                                                                17
                                                                                                                                                                                                                                                                            1 GCTTTGGATGCGGCCTATTGCTTTAGAAATGTGCAGGATAATTGCTGCCT 50
                                                                                                                                                                                                                                                                                                              34
                                                                                                                                                                                                                                            1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa
                                                                                                                                                                                                                                                                                                            17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH
                                                                                              Length: 112
Gaps: 0
Percent Identity: 75.000
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                                                                                                                                                                                                              Align seg 1/1 to: A23756 from: 1 to: 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
1. 334
/organism="Ovis aries"
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99 c 97 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mRNA
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                                                                                            496.00
5.010
88.393
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                ø
                                                                                               Quality:
                                                                                                                            Percent Similarity:
                                                                                                              Ratio:
               71
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                                                                                alignment_scores:
                                                                                                                                                             alignment_block:
TGFB3P x A23756
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DEFINITION
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TITLE
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FEATURES
               BASE COUNT
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                               ORIGIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Euteleostomi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       beta 1
novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq_documentation_block:
LOCUS AF175709 1187 bp mRNA MAM 15-AUG-1999
DEFINITION Equus caballus transforming growth factor beta 1 (TGFb1) mRNA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mammalia; Butheria; Perissodactyla; Equidae; Equus.

1 (bases I to 187)

Nixon, A.J., Brower-Toland, B.T. and Sandell, L.J.

Molecular cloning of equine transforming growth factor beta reveals a divergent nucleotide structure that encodes a nove Unpublished
                                                                                                                                                                                                                                                                                                                                                                                    202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               102
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                                                                                                                                                                                                                                                                                                                 3 AspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysValArgPr 19
                                                                                                                                                                                                                                                                                                                                   36 roLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyrLeuArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              53 SerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnThrLeuAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     86 euThrileLeuTyrTyrValGlyArgThrProLysValGluGlnLeuSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          or process 1 to 1187)
Nixon, A.J., Brower-Toland, B.T. and Sandell, L.J. Direct Submission
Submitted (05-AUG.1999) Clinical Sciences, Corn O. Box 25, Ithaca, NY 14853, USA
Location/Qualifiers
                                                                                                                                                      Length: 110
Gaps: 0
Percent Identity: 76.364
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                                                                    64
                                                                                                                                                                                                                                                                               to: 334
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                                                                    106 c
                                                     IVRSCKCS
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87.273
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                                                                                                                                                        492.00
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93.269
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                                                                       97354301
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     AUTHORS
TITLE
                                                                       MEDLINE
REFERENCE
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JOURNAL
                                                                                                         AUTHORS
                                                       JOURNAL
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                                                                                                                                                                                                                                                                 CDS
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ORIGIN
                                                                                              /product="transforming growth factor beta 1"
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/product="transforming growth factor beta 1"
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/db_xref="61:5733114"
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YYAKEVTRVLWHYBERDEIYEYTSTGGBIYMFRENASELARAVPDMALLSRAELTELRL
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LSAHCPCDSKDNTLRVGINGFSSSRRGDLATIDGMNRPFLLLMATPLERAQOLHSSRH
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0YSKVLALYNOHHRDGAAAPCCYQULPLPLYVYVGRKPRVFQLISNMIVRSCRCS"
395 c 361 g 201 t
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Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Cyprininae; Cyprinus.
1 (bases 1 to 1083)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCU66874 1083 bp mRNA VRT 14-JUL-1997 Cyprinus carpio transforming growth factor-beta 2 mRNA, partial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GCTCTGGACACCAACTACTGTTCCAGCTCCACAGAGAAGAACTGCTGCGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr
                                                                                                                                                                                                                                                                                                                                                                 Length: 112
Gaps: 0
Percent Identity: 75.893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 101 LeuSerAsnMetValValLysSerCysLysCysSer 112
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                                                                                       /codon_start=1
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                                   /qene="TGFb1"
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U66874.1 GI:1519488
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5.062
86.607
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JS CCU66874
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Ratio:
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TGFB3P x AF175709
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SOURCE
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                                                   CDS
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2 (bases 1 to 1083) Sumathy, K., Desai, K.V. and Kondaiah, P. Direct Submission Submitted (14-AUG-1996) Center for Reproductive Biology and Molecular Endocrinology, Indian Institute of Science, Bangalore, Karnataka 560 012, India a fish, from 84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100 822 ACGCTCTCTCTACATCGACTTCAAGAAGGATCTGGGTTGGAAGTGGATCC 871 872 ACGAACCCAAGGGATATAACGCCAACTICIGIGCGGGAGCCIGICCGTAT 921 CDNA 34 84 1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17 17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG Sumathy, K., Desai, K.V. and Kondaiah, P. Isolation of transforming growth factor-beta2 Orprinus carpio by RR-PCR Gene 191 (1), 103-107 (1997) Length: 104 Gaps: 0 Percent Identity: 77.885 ROD CVSQDLEPLTILYYIGKTPKIEQLSNM"

310 c 281 g 210 t /organism="Cyprinus carpio" /db\_xref="taxon:7962" <1. .>1083 to: 1083 mRNA Location/Qualifiers Align seg 1/1 to: CCU66874 from: 1

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Submitted (18-SEP-1991) J.T. Yang, Harvard School of Dental Medicine, Laboratory of Molecular Carcinogenesis, Rm 122, 188Longwood Avenue, Boston, MA 02115, USA.

2 (bases 1 to 469)
Wong, D.T., Donoff, R.B., Yang, J., Song, B.Z., Matossian, K., Nagura, N., Elovic, A., McBride, J., Gallagher, G., Todd, R. et, al. Sequential expression of transforming growth factors alpha and beta lby eosinophils during cutaneous wound healing in the hamster 93304479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="transforming growth factor-beta 1"
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                                                                                                              Euteleostomi;
                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="transforming growth factor-beta 1"
450. .469
 M.auratus mRNA for transforming growth factor beta-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                /strain="LVG (Syr)"
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/cell_line="HCPC-1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length: 112
Gaps: 0
Percent Identity: 75.893
                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Mesocricetus auratus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PLPIVYVGRKPKVEQLSNMIVRSYKCS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           82
                                 X60296.1 GI:396177
transforming growth factor-beta-1.
golden hamster.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="primer JY-2"
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167 c 133 g
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/product="TGF-B1"
24. .416
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                                                                                          Mesocricetus auratus
                                                                                                                                                              (bases 1 to 469)
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86.607
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                                                                                                                                                Mesocricetus.
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                                                                                                                                                                                 Yang, J.T
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DEFINITION
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FEATURES
                                                                                                                                                           REFERENCE
AUTHORS
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TEARING TO THE TOTAL THE TOTA
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Guinea pig transforming growth factor-beta in peritoneal exudates after BCG vaccination
Unpublished
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Mammalia; Eutheria; Rodentia; Hystricognathi; Cavildae; Cavia.
1 (bases 1 to 1597)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Jeevan A., McMurray, D.N. and Yoshimura, T.
Direct Submission
Submitted (01-OCT-1999) Medical Microbiology & Immunology, Texas
A&M Univ. System Hith. Sci. Ctr., 407 Reynolds Medical Building,
College Station, TX 77843-1114, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AF191297 1597 bp mRNA ROD 16-OCT-1999 Cavia porcellus transforming growth factor-beta (TGF-beta) mRNA,
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/protein_id="AAF02780.1"
/db_xref="GI:6049851"
                                                                                                                                                                                                                                                                                                        84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
                                                                                                                                                                                                                               327
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   67
LeuargSeralaaspThrThrHisSerThrValLeuGlyLeuTyrAsnTh
                                                                                                                                                                                                67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG
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Gaps: 0
Percent Identity: 75.676
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299. .1471
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Cavia porcellus
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86.486
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LOCUS AF191297
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Percent Similarity:
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TGFB3P x AF191297
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TITLE
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Align seg 1/1
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Purchio, A.F., Gentry, L., Twardzik, D. and Brunner, A.M.
Cloning and expression of simian transforming growth factor-beta 1
Patent: EP 0373994.A1 2 20-JUN-1990;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      02-DEC-1994
                                           1286 TGGAGCCTGGACACACAGTACAGCAAGGTCCTGGCCCTGTACAACCAGCA 1335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1195 ACGAGCCCAAGGGTACCATGCCAACTTCTGCCTGGGGCCCTGTCCCTAC 1244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1095 GCCCTGGACACCAACTACTGCTTCAGCTCCACGGAAAGAACTGCTGCGT 1144
                            2 LeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysValAr 18
                                                                                                                                           35 luProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyrLeu 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17
                                                                                                                                                                                                   52 ArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnThrLe
                                                                                     gProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValHisG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr
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Gaps: 0
Percent Identity: 75.893
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 to: 1597
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 from: 1
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Sequence 2 from Patent EP
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I08268.1 GI:589017
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to: AF191297
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TGFB3P x IO8268
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ORIGIN
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FEATURES
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SOURCE
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/product="transforming growth factor-beta 2"
/protein_id="AAG02247.1"
/db_xref="G1:9965486"
/db_xref="G1:99654
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CPCCTFVPPRNNIIPRKSEELEARFAGIDGTSGHSSGHQETTKSTRKKNSGKTPHLLL
MLLESYRLESQGSNRFKRRALDAAYCFRNVODNCCLRPLYIDFKRDLGWKWIHEPRGY
NANFCAGACPYLWSDTQHTKVLSLYWIINPEASASPCCVSHDLEPLIILYIONTFK
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Ramesh,G., Kondalah,P. and Seshagiri,P.B.
Differential expression and selective localization of transforming
growth factor-beta isoforms in the hamster uterus during estrous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       golden hamster.
Mesocricetus auratus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
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Mesocricetus auratus transforming growth factor-beta 2 mRNA,
                                                                                                                                                                                                                                                1344
                                                                                 1245 ATTTGGAGCCTGGACACGCAGTACAGCACGTCCTGGCCCTGTACAACCA 1294
                                                                                                                                                                                                                                                                                                                                                                        84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
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                                                                                                                                                                                                         LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh
                                                                                                                                                                  rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG
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Percent Identity: 76.923
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/db_xref="taxon:10036"
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Ramesh,G., Kondaiah,P. and Seshagiri,P.B.
Direct Submission
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4.969
93.269
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LOCUS AY007214
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101 LeuSerAsnMetValValLysSerCysLysCysSer 112
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Purchio,A.P., Gentry,L. and Twardzik,D.
Cloning and expression of simian transforming growth factor-SS1
Patent: EP 0293785-AZ 2 07-DEC-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                  02-DEC-1994
                                                                                                                       84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
               17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
                                                                                                          34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
                                                                                                                                                                LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
                                                                                                                                                                                                                       rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
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 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17
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Sequence 2 from Patent EP 0293785.
106216
106216.1 GI:590649
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4.958
85.714
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1 (bases 1 to 1569)
Purchio, A.F., Gentry, L. and Twardzik, D.
Cloning and expression of simian transforming growth factor-SS1
Patent: EP 029785-42 3 07-DEC-1988;
Location/Qualifiers
                                                                                                                                                                                                                                         02-DEC-1994
                                                1154 GCGCCAGCTGTACATTGACTTCCGCAAGGACCTCGGCTGGAAGTGGATCC 1203
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Gaps: 0
Percent Identity: 75.000
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Sequence 3 from Patent EP 0293785.
106221
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564 c 442 g
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Ratio: 4.958
Allarity: 85.714
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ORIGIN
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05-AUG-1996

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On Apr 12, 1996 this sequence version replaced gi:212760.
The sequence overlaps with that reported by Derynck et al. in Nature 316:701-705(1985), X02812, and Derynck et al. in Nucl. Res.15:3187-3187(1987), Y001111, and Van Oberghen et al. in Mol. Endocrin. 1:693-698(1987).
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SIFYVRNSARRGGRPTLJHRAELRWLROKRAADSAGTEGRLELYGGYGNSSWRYLH
GRSVRATADDEWLSFDVTDAVUGWLSGSELLGVFKLSVHCPCEMGPGHAEBRISIEG
FEQQRGDMGSTAKHRRYPYVLAMALPAERANELHSARRRDLDTDYGFGPGTDEKNC
CVRPLYIDFRKDLQWKWIHEPKGYMANFCMGPCPYIWSADTQYTKVLALYNQHNPGAS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 (bases 1 to 1256)
Burt,D.W. and Jakowlew,S.B.
Correction: a new interpretation of a chicken transforming growth factor-beta 4 complementary DNA Mol. Endocrinol. 6 (6), 989-992 (1992)
                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.

1 (bases 1 to 1256)
Jakowlew, S. B., Dillard, P.J., Sporn, M.B. and Roberts, A.B.
Complementary deoxyribonucleic acid cloning of a messenger ribonucleic acid encoding transforming growth factor beta 4 from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="transforming growth factor beta 4 precursor"
/profess id="AABA6637 1"
                                                                                                                                                                                          LOCUS CHKTGFB4 1256 bp mRNA VRT 05-AUG-199
DEFINITION Chicken transforming growth factor beta 4 (TGF-beta 4) mRNA,
    151 CTGGGCCTGTACAACACCCTGAACCCTGAAGCCTCAGCCTCCCCTTGCTG 200
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                                                                                                                                                                                                                                                                               M31160.1 GI:1262437
M31160.1 GI:1262437
growth factor; transforming growth factor-beta 4.
Chicken cDNA to mRNA.
                                              Length: 113
Gaps: 1
Percent Identity: 71.681
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Mol. Endocrinol. 2 (12), 1186-1195 (1988)
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/tissue_type="chondrocyte"
<1. .1256

    1256
    /organism="Gallus gallus

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/db_xref="taxon:9031"
/dev_stage="embryo"
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/db_xref="GI:1262438"
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/protein_id="AAR73231.1"
/protein_id="AAR73231.1"
/db_xxef="G1:8132131"
/translation="EBNCCVRPLYIDFRQDLGWKWVHEPKGYYANFCSGPCPYLRSSD
/THSYYLGLYYTLANDRASASPPCCYPQDLEPLTILYYV"
84 c 57 g 51 t
                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoidea;
Cervidae; Odocoileinae; Capreolus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 (bases 1 to 244)
Wagener,A. and Fickel,J.
Wagener,A. and Fickel,J.
Direct Submission
Submitted (19-MAY-1999) Evolutionary Genetics, Institute for Zoo
Blology and Wildlife Research, Alfred-Kowalke-Str. 17, Berlin
D-10315, Germany
                                                                                                                                                                                                                                                                                                                                                                                                   1 (bases 1 to 244)
Wagener,A., Blottner,S., Goeritz,F. and Fickel,J.
Detection of growth factors in the testis of roe deer (Capreolus
                                                                                                                                          AF152592 244 bp mRNA MAM 28-MAR-2001
Capreolus capreolus transforming growth factor beta 3 (TGF-b3)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       51 GGGCTGGAAATGGGTCCATGAACCTAAGGGCTACTATGCCAACTTCTGCT 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 101 CAGGCCCATGCCCATACCTCCGCAGCTCAGACACAACCCACAGGACGGTG 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28 uGlyTrpLysTrpValHisGluProLysGlyTyrTyrAlaAsnPheCysS 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      erGlyProCysProTyrLeuArgSerAlaAspThrThrHisSerThrVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps: 0
Percent Identity: 98.765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Anim. Reprod. Sci. 64 (1-2), 65-75 (2000)

    244
    /organism="Capreolus capreolus"
/db_xref="taxon:9858"

Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               to: 244
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    <1. .>244
/gene="TGF-b3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="TGF-b3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /codon_start=1
                                                                                                                                                                                                                                   AF152592.1 GI:8132130
                                                                                                                                                                                                                                                                                                          Capreolus capreolus
                                                                                                                                                                                        mRNA, partial cds.
AF152592
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ratio: 5.716
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             463.00
                                                                                                               seq_documentation_block:
LOCUS AF152592
                                                                   seq_name: gb_om:AF152592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            capreolus)
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Ratio:
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52

BASE COUNT

ORIGIN

alignment\_scores

TGFB3P x AF152592

45

alignment\_block

20532861

JOURNAL MEDLINE PUBMED REFERENCE AUTHORS

AUTHORS TITLE

REFERENCE

source

FEATURES

gene

CDS

TITLE JOURNAL

roe

ORGANISM

KEYWORDS SOURCE

DEFINITION

ACCESSION

VERSION

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goat.
Capra hircus
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Percent Similarity:
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                                                                                                                                                                                                      Quality:
                                                                                                          905
                                                                                                                                                                                                                                                                                            TGFB3P x XELTGFB5
                                   polyA_signal
                                                                       polyA_signal
                                                                                                                                                                                 alignment_scores:
mat_peptide
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SOURCE
ORGANISM
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                                                                                                          BASE COUNT
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VERSION
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JOURNAL
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                                                                                                                             ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Xenopodinae; Xenopus.

1 (bases 1 to 278)

1 (bases 1 to 278)

Sporn,M.B. and Melton,D.A.
Identification of a novel transforming growth factor-beta (TGF-beta 5) mRNA in Xenopus laevis
90110090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WKYOENGTTHSRYLESKYITPVTDDEWMSFDVTKTVNEWLKRAEENEQFGLQPACKCP
PYQAKOLDIEGEPALKODLASLSSKBWYRYLANTSMPARENIDIVTSSRKKRGYGOEY
CFGNNGPNCCWKPLYITRKRLIGWKNIHEPKGYEANYCIGNCPYIWSDTQYSKVLSL
YNQNNPGASISPCCVPDVLEPLPIIYYVGRFAKVEQLSNMVYRGCNCS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /translation="mevimmllvllvlhlsslamslstckavdmeevrkrrieairgo
ilsklkldktpdvdsekmtvpseaiflynstlevirekatreeehvghdoniqdyyak
qvyrfesiteledhefkfkfnashvrenvgmnsllhhaelrmykkqtdknmdqrmelf
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Draft entry and computer-readable sequence for [1] kindly submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="transforming growth factor-beta (TGF-beta 5)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A.L. Laevis transforming growth factor-beta (TGF-beta 5) mRNA, complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           504. .566
//note="fransforming growth factor-beta 5 signal
504. .1652
                                                                                                                                                                                                                                                                                                                                                             933 TACATCTGGAGCGCCGACACGCAGTACACCAAGGTGCTGGCGCTGTACAA 982
                                                               99
                                                                                                                                                                                                                                                                                                                                         66 nThrLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspL 83
                                                2 LeuAspThrAsnTyrCysPhe.....ArgAsnLeuGluGluAsnCysCy 16
                                                                                                                                                                                                                                                                                                                                                                                                                  euGluProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGlu 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          transforming growth factor-beta.
X.laevis neurula, cDNA to mRNA, clone XC-beta-4.
Xenopus laevis
                                                                                                                                                                                                                                                                  TyrLeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1083 CAGCTCTCCAATATGGTGGTCCGTGCCTGCAAGTGCAGC 1121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100 GlnLeuSerAsnMetValValLysSerCysLysCysSer 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Xenopus laevis"
/db_xref="taxon:8355"
              to: 1256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /protein_id="AAA49968.1"
/db_xref="G1:214822"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P.Kondajah, 21-Nov-1989.
Location/Qualifiers
             from: 1
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              to: CHKTGFB4
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LOCUS XELTGFB5
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             Align seg 1/1
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                83
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TITLE

SOURCE

COMMENT

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoldea; Bovoidee; Caprinea; Capriae; Capra. 1 (273)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (10-JUN-2000) College of Animal Science and Veterinary Medicine, Northwest Science and Technology University, Yangling, Shaanxi 712100, China
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26-JUL-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1329 TATTGCTTTGGGAACAATGGGCCAAACTGCTGTGTGAAACCTCTTTACAT 1378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22
                      5
1314. .1649
Anote-Transforming growth factor-beta
7.0016. .125
Anote-Tputative.
2.737. .2742
Anote-Tputative.
3.755. .5742
Anote-Tputative.
5.55. .599 g 725 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        euTyrTyrValGlyArgThrProLysValGluGlnLeuSerAsnMetVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      39 yrTyrAlaAsnPheCysSerGlyProCysProTyrLeuArgSerAlaAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   56 ThrThrHisSerThrValLeuGlyLeuTyrAsnThrLeuAsnProGluAl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              72 aSerAlaSerProCysCysValProGlnAspLeuGluProLeuThrIleL
                                                                                                                                                                                                                                                                                                                                                                                               TyrCysPheArgAsnLeuGluGluAsnCysCysValArgProLeuTyrIl
                                                                                                                                                                                                                                      Gaps: 0
Percent Identity: 71.963
                                                                                                                                                                                                                        107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AF276986 273 bp mRNA MP
Capra hircus TGF beta 2 mRNA, partial cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Goat ovarian TGF beta 2 cDNA sequence
                                                                                                                                                                                                                                                                                                                                                             to: 2754
                                                                                                                                                                                                                                                                                                                                                           from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1629 GTAAGGTCTTGCAACTGCAGC 1649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     106 ValLysSerCysLysCysSer 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AF276986
AF276986.1 GI:9454282
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Wang, B. and Zhang, Y.
                                                                                                                                                                                                                                      4.933
                                                                                                                                                                                                                                                                                                                                                         Align seg 1/1 to: XELTGFB5
                                                                                                                                                                                                                     439.00
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CDS

ORIGIN

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protein_id="AAD45756.1"
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    .18
/note="phosphorylated by casein kinase II; phosphorylation

                                                                                                                                                                                                                                                                            13. .21
/note="phosphorylated by protein kinase C; phosphorylation
                                                                                                                                                                                                            IWSLHTQYSKVLALYNQHNPGASASPCCVPQALEPLPIVYYVGRKPKVEQLSNMFVR"
                                                                                                                                                                                                                                                                                                                                73. .99
/note="phosphorylated by tyrosine kinase; phosphorylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_documentation_block:
LOCUS
AF097509
DEFINITION Cavia porcellus interleukin TGF beta gene, partial cds.
ACCESSION AF097509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 151 CAGTACAGCAAGGTCCTTGCCCTCTACAACCAACAACCCGGGCGCGTTC 200
                                                                                                                                                                                                                                                                                                                                                                                 79. .126
/note="Region: TGF-beta family signature"
256. .267
/note="amidation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     201 GGGGTGCCGTGCTGCGTGCCGCAGGGGCGTGGAGCCGCTGCCCATCGTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7 CysPheArgAsnLeuGluGluAsnCysCysValArgProLeuTyrIleAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              57 ThrHisSerThrValLeuGlyLeuTyrAsnThrLeuAsnProGluAlaSe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                73 rAlaSerProCysCysValProGlnAspLeuGluProLeuThrIleLeuT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps: 0
Percent Identity: 74.000
                   /organism="Meriones unguiculatus"
                                                              /tissue_type="renal lymph node"
<1. .>302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                to: 302
                                   /db_xref="taxon:10047
                                                                                                                                                                                                                                                                                                                                                                                                                                                          6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                to: AF161218 from: 1
                                                                                                     /note="TGF-beta"
                                                                                                                     /codon_start=1
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83.000
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                                                                                                                                                                                                                                                                                                                   site"
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     source
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KEYWORDS
SOURCE
                                                                                     CDS
                                              <1. .>273
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SADTQHSRVLSLYNTINPEASASPCCVSQDLEPLTILYYIGNTPKIE"
63 g 70 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Gerbillinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
Submitted (21-JUN-1999) Microbiology and Parasitology, School of
Veterinary Medicine, South Stadium Drive, Baton Rouge, LA 70803,
USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 (bases 1 to 302)
Rao,U.R. and Klei,T.R.
CDNA Cloning of Gerbil Transforming Growth Factor-beta by
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 AGAAATGTGCAGGATAATTGCTGCCTACGCCCACTTTACATTGATTTCAA 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gGlnAspLeuGlyTrpLysTrpValHisGluProLysGlyTyrTyrAlaA 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            snPheCysSerGlyProCysProTyrLeuArgSerAlaAspThrThrHis 58
                                                                                                                                                                                                                                                                                                                                                                                                                     9 ArgAsnLeuGluGluAsnCysCysValArgProLeuTyrIleAspPheAr 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SerThrValLeuGlyLeuTyrAsnThrLeuAsnProGluAlaSerAlaSe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   rProCysCysValProGlnAspLeuGluProLeuThrIleLeuTyrTyrV
                                                                                                                                                                                                                                                            91
                                                                                                                                                                                                                                                                                Gaps: 0
Percent Identity: 79.121
                                /tissue_type="ovarian follicle"
<1. .>273
                                                                                                                                                                                                                                                              Length:
/organism="Capra hircus"
/db_xref="taxon:9925"
                                                                                                                                                                                                                                                                                                                                                                                       <u>ن</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                     from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        92 alGlyArgThrProLysValGlu 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AF161218
AF161218.1 GI:5616326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 (bases 1 to 302)
Rao, U.R. and Klei, T.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mongolian gerbil.
Meriones unguiculatus
                                                                                                                                                                                                                                                          435.00
5.118
93.407
                                                                                                                                                                                                                                                                                                                                                                                   to: AF276986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq_name: gb_rol:AF161218
                                                                                                                                                                                                                                                              Quality:
                                                                                                                                                                                                                                                                                              Percent Similarity:
                                                                                                                                                                                                                                                                                Ratio:
                                                                                                                                                                       73
                                                                                                                                                                                                                                                                                                                                                TGFB3P x AF276986
                                                                                                                                                                                                                                            alignment_scores
                                                                                                                                                                                                                                                                                                                                 aliqnment_block
                                                                                                                                                                                                                                                                                                                                                                                   Align seg 1/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                       BASE COUNT
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25

51 42 59

09-DEC-1998

AUTHORS TITLE JOURNAL REFERENCE

REFERENCE

ACCESSION

201

75

AUTHORS TITLE JOURNAL

FEATURES

73

50 23

100

```
/codon_start=2
/product="transforming growth factor-beta-2"
/protein_id="AAB05257.1"
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TQHSRYLSLYNTINPEASASPCCVSQDLEPLTLLYYMGKTPK"
                                                                                                                                                                                                Cervus elaphus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoidea;
Cervindae; Cervinae; Cervus.

1 (bases 1 to 259)
Francis,S.M. and Suttie,J.M.
Reverse-Transcriptase Polymerase Chain Reaction (RT-PCR) to measure the expression of growth factors and proto-oncogenes in the tip of Unpublished
                                                                          CEU62111 259 bp mRNA MAM 31-JUL-1996
Cervus elaphus transforming growth factor-beta-2 (TGF beta-2) mRNA,
partial cds.
                                                                                                                                                                                                                                                                                                                                                                         2 (bases 1 to 259)
Francis, S.M. and Suttie, J.M.
Francis, Submission
Submitted (26-JUN-1996) AgResearch, Invermay Agricultural Centre,
Puddle Alley, Mosgiel, New Zealand
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12 GluGluAsnCysCysValArgProLeuTyrIleAspPheArgGlnAspLe 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     78 sValProGlnAspLeuGluProLeuThrIleLeuTyrTyrValGlyArgT 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 CAGGATAATTGTTGCCTACGCCCACTTTACATTGATTGAATGAGGGATCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     erGlyProCysProTyrLeuArgSerAlaAspThrThrHisSerThrVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length: 86
Gaps: 0
Percent Identity: 79.070

    .259
    /organism="Cervus elaphus"
/db_xref="taxon:9860"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="growing antler"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="TGF beta-2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  58
g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="TGF beta-2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   from: 1
                                                                                                                                                       U62111.1 GI:1470104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               65 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              <1. .>259
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93.023
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                412.00
                                                                      seq_documentation_block:
                                         gb_om:CEU62111
      348 TCCAACATG 356
                                                                                                                                                                                          red deer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                alignment_scores:
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                                                                                      LOCUS
DEFINITION
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ORIGIN
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AUTHORS
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AUTHORS
                                         sed_name:
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KEYWORDS
SOURCE
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                                                                                                                                                                                                                                                                                                                                                          JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CDS
                                                                                                                                                                                                                                                                                                                                                                                                            TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                  /codon_start=3
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/product="interleukin TGF beta"
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                                                1 (bases 1 to 358)
Wicher, V., Scarozza, A.M., Ramsingh, A.I. and Wicher, K.
Cytokine gene expression in skin of susceptible guinea-pig infected
                                                                                                                                                                                      pig blood and
               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Hystricognathi, Caviidae, Cavia.
                                                                                                                                                                                                                                                                              Direct Submission
Submitted (05-OCT-1998) New York State Dept of Health, David
Axelrod Institute, Wadsworth Center for Laboratories & Research,
120 New Scotland Ave, Albany, NY 12208, USA
Location/Qualifiers
                                                                                                                                                                 Scarozza, A.M., Ramsingh, A.I., Wicher, V. and Wicher, K. Spontaneous cytokine gene expression in normal guinea
                                                                                                                                                                                                                                               3 (bases 1 to 358)
Scarozza, A.M., Ramsingh, A.I., Wicher, V. and Wicher, K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 LeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysValAr 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98 GCAGCTCTACATTGACTTCCGCAAGGACCTAGGATGGGAGTGGATCCACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length: 103
Gaps: 0
Percent Identity: 71.845
                                                                                                                                                                                                                                                                                                                                                                    1. .358
/organism="Cavia porcellus"
/db_xref="taxon:10141"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            to: 358
                                                                                                  with Treponema pallidum
Immunology 95 (2), 242-247 (1998)
                                                                                                                                                                                                                Cytokine 10 (11), 851-859 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         103 g
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                                                                                                                                                  (bases 1 to 358)
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83.495
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   Cavia porcellus
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                                                                                                                                                                                                                                   99144670
                                                                                                                                    99069279
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                                                                                                                                                                                                      tissues
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alignment_scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BASE COUNT
ORIGIN
ORGANISM
                                              REFERENCE
AUTHORS
TITLE
                                                                                                                                                                AUTHORS
TITLE
                                                                                                                                                                                                                                 MEDLINE
REFERENCE
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JOURNAL
                                                                                                               JOURNAL
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                                                                                                                                                                                                                                                                  AUTHORS
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68 t

61

tgfb3p.rge

DEFINITION

ACCESSION

VERSION

ORGANISM

KEYWORDS SOURCE

REFERENCE AUTHORS JOURNAL

TITLE

REFERENCE AUTHORS JOURNAL

TITLE

FEATURES

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52 ArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnThrLe 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         of 1228 b
unknown l
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Center Project Name: 0
Center clone name: RPCI-23_235H2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Web site: http://www.jgi.doe.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          oŧ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Center: Joint Genome Institute
Center Code: JGI
                                                                                                                                                                                                                                                                                                  HTG; HTGS_PHASE1; HTGS_DRAFT.
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gap of
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gap of
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gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                2 (bases 1 to 215287)
DOE Joint Genome Institute.
                                                                                                                                        85 roLeuThrIleLeuTyrTyrVal 92
                                                                                                                                                                                                                                                                                   AC079432.1 GI:9958044
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2450:
2550:
3734:
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5348:
6444:
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9299:
                                                                                                                                                                                                                                                                                                                                                                                                       Sequencing of Mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Project Information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Summary Statistics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
                                                                                                                                                                                seq_name: gb_htg17:AC079432
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                                                                                                                                                                                                                                                                                                                             Mus musculus
                                                                                                                                                                                                                                                                                                                  house mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished
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6545
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9200
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1322
2451
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3735
3835
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TITLE
JOURNAL
REFERENCE
                                                                                                                                                                                                                                                                                    VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                         REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                 AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMMENT
                                                                                                                                                                                                                                                                                                                 SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
Submitted (16-JUL-1999) Department of Pulmonary Medicine, Institute
of Clinical Medicine, University of Tsukuba, 1-1-1 Tennoudai,
Tsukuba, Ibaraki 305-8575, Japan
                                                                                                                                     AF169347 278 bp mRNA ROD 15-AUG-1999
Cavia porcellus transforming growth factor-beta mRNA, partial cds.
AF169347
                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
                                                                                                                                                                                                                                                                                                                          Guinea-pig transforming growth factor-beta expression in injured
                                                                                                                                                                                                                                                                              1 (bases 1 to 278)
Morishima,Y., Uchida,Y., Nomura,A., Ishii,Y., Sakamoto,T. and
                                                                                                                                                                                                                                                                                                                                                                      2 (bases 1 to 278)
Morishima,Y., Uchida,Y., Nomura,A., Ishii,Y., Sakamoto,T. and
2 LeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysValAr 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValHisG 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue_type="trachea"
/note="obtained from injured tissue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length: 91
Gaps: 0
Percent Identity: 74.725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Cavia porcellus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Align seg 1/1 to: AF169347 from: 1 to: 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /strain="Hartley"
/db_xref="taxon:10141"
/cell_type="epithelium"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                          AF169347.1 GI:5732935
                                                                                                                                                                                                                       domestic guinea pig.
Cavia porcellus
                                                                                                                                                                                                                                                                                                                                         tracheal epithelium
Unpublished
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85.714
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                                                                                                    seq_name: gb_rol:AF169347
                                                                                                                                  seq_documentation_block:
                                                                                                                                                                                                                                                                                                            Sekizawa, K.
                                                                                                                                                                                                                                                                                                                                                                                                  Sekizawa, K.
                                                                        252 CACCCAAG 259
                                             95 hrProLys 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99
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BASE COUNT

ORIGIN

CDS

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Consensus quality: 130929 bases at least 040
Consensus quality: 155193 bases at least 030
Consensus quality: 155193 bases at least 020
Estimated insert size: 1213300; agarose-fp estimation
Estimated insert size: 211087; sum-of-contigs estimation
Quality coverage: 4.98 in 020 bases; agarose-fp estimation

* NOTE: This is a "working draft" sequence. It currently

* consists of 43 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N. but the exact sizes of the gaces such on whoow.

* This record will be updated which the finished sequence

* as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (01-SEP-2000) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 215287)
DOE Joint Genome Institute.
                                                                                                                                                                                                                                                                                                                                                                        seq_documentation_block:
LOCUS AC079432 215287 bp DNA HTG 01-SEP-2000
DEFINITION Mus musculus chromosome 16 clone RP23-235H2, WORKING DRAFT
SEQUENCE, 43 unordered pieces.
                                                                                                                      204 CAACCCGGCGCTTCGCGCGCCCTTGCTGTGCCGCAGGCGTTGGAGC 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1221: contig of 1221 bp in length
1321: gap of unknown length
2450: contig of 1129 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    unknown length
of 1414 bp in length
unknown length
of 1096 bp in length
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68 uAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuGluP
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of 1327 h
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source

121268 AGCCATGTGCACACACATGCAGAGTTCCCACCATAGTTTCAAGCATCCTT 121219 121168 TCACTCTGTGTCACAGATGTATGCACCTGGTTGGTAAGATGTGGGGCCCCA 121119 121118 GAGAAGTITCTACCTCCGTTAAGACAGAATGACGCATGTAGGAAAGGAAT 121069 121468 TGTTGAATGAATGGTAATCTTGGATGAGAAAATCCCTGTAACAACGTTCT 121419 121418 GATCTTGGCAGGCTGGTCCACTGCTACTCAGCTGCACTCTGCAATTTAAA 121369 121368 TCCCTACCACGGGGACTAGCACATGGGTAAAACGTATGCTTAGTGTGTGC 121319 121318 CATGCTCTGGATTCAGTCTCTAGCAAACACACTTACCTGAACATGCACAC 121269 121218 TTFATTTGTCTAAAGCTTCTGTACTATGAAAGTTATTCAGCTGTCGCATG 121169 59 59 59 59 /chromosome="16" /clone="RP23-239H2" /clone="RPCI mouse BAC library 23" 1 45866 c 52114 g 52335 t 7588 others 38 lyTyrTyrAlaAsnPheCysSerGlyProCysProTyrLeuArgSerAla 54 7 CysPhe....ArgAsnLeuGluGluAsnCysCysValArgProLeuTy 21 Align seg 1/1 to reverse of: AC079432 from: 1 to: 215287 Length: 429 Gaps: 3 Percent Identity: 24.476 /organism="Mus musculus" /db\_xref="taxon:10090" 55 AspThrThrHisSer..... 401.00 3.819 24.476 59 alignment\_block: TGFB3P x AC079432/rev 57382 a Quality: Ratio: Percent Similarity: alignment\_scores: BASE COUNT 59 59 59 59 59 59 29 ORIGIN

JOURNAL Fish Shell			TITLE Direct Suk	Carolina 5 27606, US	FEATURES source			dene	SQD						sig_peptide	misc_feature	misc_feature	misc_feature	misc_feature ( mat_peptide (	BASE COUNT 448 a ORIGIN		alignment_scores: Quality: Ratio: Retio: Percent Similarity: alignment_block: TGFB3P x AF140363	Align seg 1/1 to: AF 13 GluAsnCysCysV	29 YTPLySTTPVal           ::: 985 ATGGAAGTGGATA 46 LyProCysProTy 1035 GGTCCTGCACCTI
8 AGCGATAGAAAGGGCGGAGGGTCCGCAGCCTCAGCAACCTACCT		8 GGTICGGGGGGGGGAAIACIGAGIAGGGCGGIAGGCIGIGAGCCAGII 120969	59 59	8 CCAGGCAGCACCATCACTACATCCCGTCTGGGGCACACATTCTTAC 120919	65	8 AACTACTAAATGTGCCAAAGCAGTGCTGAGTGTGCACATTACCCAACT 120869	65 59	8 GTGGAAACTTACAGACAGGAAGACCTTTTGGAGGAGTTTCTTATCAACTG 120819	65 59	8 CTCCTTCGGGTGCTTCAGTTAGGAACATAATGCAGTCCATGGGTTATGCC 120769	65 69	8 ITCTGCCATACTGGATGACTGCAGCTCGTCTTATTCAAACAGTTCCCA 120719	65 69	8 CAATCCCTTTTAAGCAGATCTCCCATGGCCACTCTGCCTTAGGGTAGC 120669	6 59	8 CCCCACAACTTGCATGGTTTCTGGGTCACAGGCTCAAGGCTTGGCTTTTT 120619	0Thr.ValLeuGlyLeuTyrAsnThr 67 	8 LeuasnProGlualaSeralaSerProCysCysValProGlnAspLeuGl 84	4 uProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGlnL 101 	1 euserasnmetvalvallysserCyslyscysser 112 	e: gb_ov:AF140363	seq_documentation_block: LOCUS AF140363 1514 bp mRNA VRT 18-FEB-2000 DEFINITION Morone chrysops x Morone saxatilis transforming growth factor-beta ACCESSION AP140363. GIGF-beta) mRNA, complete cds. WERSION AF140363.1 GI:5690245	Σ	Percoide; Moronidae; Morone.  Et i (bases 1 to 1514)  RS Harms, C.A., Kennedy-Stoskopf, S., Horne, W.A., Fuller, F.J. and Tompkins, W.A.  Cloning and sequencing hybrid striped bass (Morone saxatilis x M. chrysops) transforming growth factor-beta (TGF-beta), and development of a reverse transcription quantitative competitive polymerase chain reaction (RT-qcPCR) assay to measure TGF-beta mRNA
121068	S	121018	Σ.	120968	ίΩ	120918	5	120868	5	120818	59	120768	53	120718	59	120668	60 120618	68 120568	84 120518	101	sed_name:	seq_docume LOCUS DEFINITION ACCESSION	SOURCE ORGANISM	REFERENCE AUTHORS TITLE

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791. .799
                                                                                                                            North
                                                                                                                      d (05-APR-1999) MPP, College of Veterinary Medicine, State University, 4700 Hillsborough St., Raleigh, NC
                                       s 1 to 1514)
A., Kennedy-Stoskopf,S., Horne,W.A., Fuller,F.J. and
                                                                                                                                                                                                                           /organism="Morone chrysops x Morone saxatilis"
/db_xref="taxon:45352"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            887. .898
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899. .1234
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359 c 378 g 329 t
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llfish Immunol. 10 (1), 61-85 (2000)
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Gaps: 0
Percent Identity: 69.000
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89. 1237
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4.714
84.000
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tqfb3p.rge

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                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 (bases 1 to 270)
Melby.P.C., Tryon,V.V., Chandrasekar,B. and Freeman,G.L.
Cloning of Syrian hamster (Mesocricetus auratus) cytokine cDNAs and
analysis of cytokine mRNA expression in experimental visceral
leishmaniasis
                                                                                                                                                                                                                                               Mesocricetus auratus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 (bases 1 to 270)
Melby, P.C. and Tryon, V.V.
Direct Submission
Submitted (0-FEB-1998) Medicine, UTHSCSA, 7703 Floyd Curl Drive,
San Antonio, TX 78284, USA
Location/Qualifiers
79 lProGlnAspLeuGluProLeuThrIleLeuTyrTyrValGlyArgThrP 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Identity: 74.444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Mesocricetus auratus"
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/note="Syrian hamster (outbred)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Immun. 66 (5), 2135-2142 (1998)
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AF046214.1 GI:3005106
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88
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eArgGlnAspLeuGlyTrpLysTrpValHisGluProLysGlyTyrTyrA 41

24

8 PheArgAsnLeuGluGluAsnCysCysValArgProLeuTyrIleAspPh 24 

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GASAHPCCVPQVLEPLPIIXYVGRQHKVEQVPNMIVMSCRCS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (30-JUL-1996) C.J. Secombes, Univ. of Aberdeen, Dept. of Zoology and Medicine, Therapeutics,, Tillydrone Avenue, Aberdeen AB24 2TZ, UK On Aug 2, 1996 this sequence version replaced gi:1438515.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (11-JUL-1996) C.J. Secombes, Univ. of Aberdeen, Dept. of 
Zoology and Medicine, Therapeutics,, Tillydrone Avenue, Aberdeen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene:
                                                                                                                                                                                                                                                                                                                                                                                                             17-JUL-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hardie, L.J., Laigy, K.J., Daniels, G.D., Grabowski, P.S., Cunningham, C. and Secombes, C.J.
Isolation of the first piscine transforming growth factor B analysis reveals tissue specific expression and a potential regulatory sequence in rainbow trout (Oncorhynchus mykiss)
Cytokine In press
2 (bases 1 to 1152)
                                                                               201 GTCTCCGTGCTGTGTGCCCCCAGGCGCTGGAGCCGCTGCCCATCGTGTACT 250
                                       101 ccaactrefereneggecergreceracatregageerggacacacag 150
                                                                                                                                                                         91
                                                                                                                                                                                                                                                                                                                                                                                                          OMTGFB 1152 bp mRNA VRT O.mykiss mRNA for transforming growth factor beta.
aSerProCysCysValProGlnAspLeuGluProLeuThrIleLeuTyrT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TGF-beta; transforming growth factor beta.
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<1. <1.
                                                                                                                                                                                                                                                                                                   251 ACGTGGGTCGCAAGCCCAAG 270
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revised by [3]
3 (bases 1 to 1152)
                                                                                                                                                                                                                                                         yrValGlyArgThrProLys 97
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                                                                                                                                                                                                                                                                                                                                                                                    seq_documentation_block:
LOCUS
                                                                                                                                                                                                                                                                                                                                               seq_name: gb_ov:OMTGFB
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7e-51 9e-48

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1e-48 1e-48 .1e-48 le-48 1e-48

1017. 1017. 1017.

\$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$25.00 \$2

1017. 1017. 1003.

```
seq_name: /SIDS1/gcgdata/geneseq/geneseqn/NA1991.DAT:AAQ11995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TGF-beta3; biologically active protein production;
Encodes Transforming Growth Factor beta 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           /SIDS1/gcgdata/geneseq/geneseqn/NA1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                     /SIDS1/gcgdata/geneseq/geneseqn/NA1998.
/SIDS1/gcgdata/geneseq/geneseqn/NA1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      qenesedn/NA1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ВР
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_documentation_block:
ID AAQ11995 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     /SIDS1/gcgdata/geneseg/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29-AUG-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAQ11995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EXEXEXEXEX EXE
                                                                                                                                                                                                                                                                                                                                                                                                               2530
2676
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2669
2671
498
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4382
                                                            -WODEL-frame+p20.model -DEV-x1h
-Q-Cgn2_1/USPTO_spool/DUFFY097/runat_29102001_165247_25287/app_query.fasta_1.159
-Q-Cgn2_1/USPTO_spool/DUFFY097/runat_29102001_165247_25287/app_query.fasta_1.159
-DB-N_Geneseq_0601_-OFMT=fastap_-SUFFIX=rng_-GAPOP=12.000
-GAPEXT=4.000 -WINMATCH=0.100 -LOOPCL=0.000 -LOOPEXT=0.000
-GAPEXT=4.000 -GAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500
-FGAPOP=4.500 -GGAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500
-FGAPOP=6.000 FGAPEXT=7.000 -YGAPOP=1.000 -YGAPEXT=0.500
-TRANS=human40.cdi -LIST=100 -DOCALIGN=200 -THR_SCORE=pct
-THR_MAX_100 -THR_MIN=0 -ALIGN=100 -MODE=LOCAL -OUTFMT-Pfs
                                                                                                                                                                                                                                                          900-04
900-04
900-04
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100-04
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8e-62
                                                                                                                                                                                                                                                                                                                                                                                         3e-61
3e-61
5e-62
                                                                                                                                                                                                                                                                                                                                                                                                              16-61
56-50
56-59
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36-59
76-57
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         e-
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                                  software, version 4.5,
                                                                                                                                                                                                                                                                         NORM=ext -MINLEN=0 -MAXLEN=2000000000
-USER=DUFFY097_@CGGN1_1_254 -NCPU=6 -ICPU=3 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -NO_XLPXY -WAIT -THREADS=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              888
                                                                                                                                                                                                                                                                                                                                                          630.
                                                                                                                                                                                                                                                     out_format : pfs
                                Results were produced by the GenCore Copyright (c) 1993-2000 Compugen Ltd.
  of: TGFB3P to: N_Geneseq_0601:*
                                                                                                                                                                            Query length: 113
Database: N. Geneseq_0601:*
Database sequences: 730101
Database length: 313950809
Search time (sec): 76.040000
                Date: Oct 30, 2001 9:13 AM
                                                    Command line parameters:
                                                                                                                                                               Search information block:
                               About: Results
                                                                                                                                                                      Query: TGFB3P
                                                                                                                                                                                                                                          score_list:
                                                                                                                                                                                                                                                  Sequence
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10095 225089 225089 225089 225089 225089 225089 225089 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339 23339

4e-47

4e-48

.5e-40 .0e-38 .2e-25 .1e-18

50 50 50 50

1009. 1008. 1004.

.1e-18 .1e-18

4e-17 le-15 4e-16

50

208.00 207.50 207.50

```
This coding sequence was isolated from the CI-215 human glioma cell line. It was incorporated into an appropriate vector to transform Saccharomyces cerevisiae or E.Coli. Monomeric TGF-betal was purified, denatured and dissolved in 140ml 50mm Tris/HCl pH8. IM NaCl, 5mm EDTA, 2mm reduced glutathione, 1mm oxidised glutathione and 33mm Chaps. After 72 hrs at 4 deg C, pH was adjusted to 2.5 and the mixture was conc. 10 times. The conc. soln was diluted to the original vol. with 10mm HCl and conc to a final vol of 10 ml. The supernatant from
                                                                                                                                                                                                                                                                     Prodn. of Transforming Growth Factor type-beta-like proteins subjecting denatured monomeric form to refolding conditions
                                                                                                                                                                                                Schmitz A, Meyhack B;
                                                                                                                                                                                                Cox D,
                                                                                                                                                                                                                                                                                                                  Example; Page 27; 35pp; English.
                                                                                                     90EP-0810922
                                                                                                                                  89GB-0027546
                                                                                                                                                                                              Cerletti N, McMaster GK,
                                                                                                                                                               (CIBA ) CIBA GEIGY AG
                                                                                                                                                                                                                        WPI; 1991-180005/25.
                                                                                                                                                                                                                                         P-PSDB; AAR12404
                Homo sapiens
                                                                                                                                  06-DEC-1989;
                                                                                                     27-NOV-1990;
                                                                        19-JUN-1991
                                         EP433225-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IGF-beta3
```

- by

other; Sequence 339 BP; 74 A; 104 C; 86 G; 75 T; 0

Percent Identity: 100.000 Gaps: Length: Ratio: 5.652 Percent Similarity: 100.000 633.00 Quality: alignment\_scores

TGFB3P x AAQ11995 alignment\_block

to: 339 Align seg 1/1 to: AAQ11995 from: 1 1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17

1 GCTTTGGACACCAATTACTGCTTCCGCAACTTGGAGGAGAACTGCTGTGT

17 largProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34

isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 34 101

151 51

rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 67

201 84

LeuSerAsnMetValValLysSerCysLysCysSer 112 101

251

The invention covers hybrid TGF-beta molecules consisting of parts of the human isoforms TGF-beta1, TGF-beta2 and TGF-beta3 (see AAQ41599, AAQ41600 and AAQ41601, respectively). The hinge points between parts derived from different parent isoforms are pref. between amino acids 44 and 45, 56 and 57, 79 and 80, 90 and 91, or 22 and 23. The hybrid melecules promote cell migration, inhibit the growth of A375 melanoma cells, accelerate the healing of partial-thickness burn wounds and full-thickness incisional wounds and increase formation wounds and full-thickness incisional wounds and increase formation of fibrous granular tissue. See e.g. AAQ41602-Q41607 for pref. hybrids. New hybrid transforming growth factor-beta molecules - comprise portions of mature TGF-beta isoforms; useful as wound healants, cardioprotective, antiinflammatory and immunosuppressive agents etc. nTGF-beta3; hybrid protein; wound healing; cancer treatment; bone repair; growth regulation; ss. seq\_name: /SIDS1/gcgdata/geneseq/geneseqn/NA1993.DAT:AAQ41601 Sequence 339 BP; 74 A; 104 C; 86 G; 75 T; 0 other; Mature human Transforming Growth Factor-beta3, 301 CTCTCCAACATGGTGGTGAAGTCTTGTAAATGTAGC 336 Kuhla J; Location/Qualifiers 1..336 /\*tag= a Cerletti N, Claim 4; Page 24; 48pp; English. seq\_documentation\_block:
ID AAQ41601 standard; cDNA; 339 92EP-0810845. 91EP-0810870 (first entry) (CIBA ) CIBA GEIGY AG Cox D, WPI; 1993-161126/20. P-PSDB; AAR39640. McMaster GK, 03-NOV-1992; 11-NOV-1991; Homo sapiens 26-AUG-1993 mat\_peptide 19-MAY-1993 EP542679-A. AAQ41601; 

20 1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17 17 largProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34 Percent Identity: 100.000 to: 339 Align seg 1/1 to: AAQ41601 from: 1 Quality: 633.00 Ratio: 5.652 Percent Similarity: 100.000 alignment\_block: TGFB3P x AAQ41601 alignment\_scores:

Length:

```
The coding sequence (AAT17234) of human transforming growth factor TGF-beta 3 (AAR92772) was cloned into plasmid pGEM-52F(+) (Promega) and the construct used to transform E. coli Y1090. Subcloning in pPLMu yielded plasmid pPLMu.hTGF-beta 3. Non-soluble, monomeric TGF-beta 3 was recovered from E. coli LC 137/ppLMu.hTGF-beta 3 (DSM FGFS) transformants. A biologically active, dimeric form of TGF-beta 3 was obtd. by refolding this monomer in detergent-free buffer contg. DMSO and/or DMF. Dimers of TGF-beta 1 (AAR92773) and TGF-beta 2 (AAR92774), and hybrid dimers (see also AAR927775-77), were
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Prodn. of dimeric biologically active transforming growth factor by refolding denatured monomer in detergent-free folding buffer contg. specific organic solvent to improve yield
                                                                              84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
                                                                                                                                                                                                           101 ATGAACCTAAGGGCTACTATGCCAACTTCTGCTCAGGCCCTTGCCCATAC 150
                                                                 67
                                                                                                                            84
                                                                                                                                                                                                                                                                                                                        seq_name: /SIDS1/gcgdata/geneseq/geneseqn/NA1996.DAT:AAT17234
34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr
                                                              LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh
                                                                                                                            67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Transforming growth factor type beta; TGF-beta 3; protein renaturation; protein folding; ds.
                                                                                                                                                                                                                                                           LeuSerAsnMetValValLysSerCysLysCysSer 112
                                                                                                                                                                                                                                                                                       301 CTCTCCAACATGGTGGTGAAGTCTTGTAAATGTAGC 336
                                                                                                                                                                                                                                                                                                                                                     seq_documentation_block:
ID AAT17234 standard; cDNA to mRNA; 339 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 1B; Page 34; 54pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            95WO-EP02719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94EP-0810439
                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human TGF-beta 3 cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (CIBA ) CIBA GEIGY AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1996-117000/12.
P-PSDB; AAR92772.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  also produced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25-JUL-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO9603433-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .2-JUL-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                    17-JUL-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             08-FEB-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cerletti N;
                                                                                                                                                                                                                                                                                                                                                                                                     AAT17234;
                                                                                           151
                                                                                                                                                                                                                                                         101
                                                              21
                                                                                                                                                                                                                        251
                                                                                                                                                          201
```

Sequence 339 BP; 74 A; 104 C; 86 G; 75 T; 0 other;

alignment\_scores

```
200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Transforming growth factor beta; TGF; regulator; method; proliferation; differentiation; wound healing; solvent; ds
                                                                                                                                                                                   250
                                                                                                                                                                                                                                                                                                   84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
                                                                                                                                                                                                                                                                                                              20
                                                                                                                                                                                                                  67
                                                                                                                                                                                                                                                           84
                                                                                                                                                                                                                                                                                                                                                                                  seq_name: /SIDS1/gcgdata/geneseq/genesegn/NA1996.DAT:AAT15464
                                                                                                                                                                                                                                                        34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr
                                                                                                                                                                                                                  51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human transforming growth factor beta 3 encoding cDNA.
                     Percent Identity: 100.000
 112
                                                                                                                                                                                                                                                                                                                                                     301 CTCTCCAACAIGGIGGIGGAAGTCTIGIAAAIGIAGC 336
                                                                                                                                                                                                                                                                                                                                           LeuSerAsnMetValValLysSerCysLysCysSer 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  human_TGF-beta-3
                                                                      Align seg 1/1 to: AAT17234 from: 1 to: 339
                                                                                                                                                                                                                                                                                                                                                                                                                вЬ
                                                                                                                                                                                                                                                                                                                                                                                                     seq_documentation_block:
ID AAT15464 standard; cDNA to mRNA; 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                95WO-EP02718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94EP-0810438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1..339
/*tag= a
/product= }
                                                                                                                                                                                                                                                                                                                                                                                                                                                         10-JUN-1996 (first entry)
Ouality: 633.00
Ratio: 5.652
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1996-116999/12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GEIGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P-PSDB; AAR91958
                                                   TGFB3P x AAT17234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (CIBA ) CIBA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25-JUL-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO9603432-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12-JUL-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           08-FEB-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cerletti N;
                                         alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                     AAT15464;
                                                                                                                                                                                                                                                                                                                                          101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Key
```

```
AATI5462-T15464 encode transforming growth factor (TGF) beta-1,
TGF beta-2 and TGF beta-3 which are produced using recombinant
DNA technology and used to produce TGF beta-like proteins in
Cdimeric form. The TGF beta-like proteins produced are hybrids of
C different types of TGF beta e.g. TGF beta-13, TGF beta-23, etc.
C different types of TGF beta e.g. TGF beta-1-3, TGF beta-2-3, etc.
C and eusing a new process of producing dimeric, biologically active
TGF beta monomers with folding buffer contg. a mild detergent (CHAPS,
CHAPSO or digitonin) and at least one of the solvents DMSO (dimethyl
C sulphoxide), DMSO2 (dimethylsulphone) and DMF (dimethyl formamide).
C The detergent allows folding of the monomer such that, after
dimerisation, the TGF beta-like protein retains biological activity
and remains in soluble form. The method allows relatively high yields
C form. TGF-beta-like proteins in their native dimeric
C form. TGF-beta-like proteins are multifunctional regulators of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cellular activity and a typical use is to stimulate wound healing.
Prodn. of dimeric, biologically active transforming growth f
beta - by refolding denatured monomer in buffer contg. mild
detergent and specific organic solvents to improve yields
                                                                                                            Page 36-37; 59pp; English.
                                                                                                            Example 1;
```

Sequence 339 BP; 74 A; 104 C; 86 G; 75 T; 0 other;

```
Percent Identity: 100.000
             Length:
                              Gaps:
          Ouality: 633.00
Ratio: 5.652
Percent Similarity: 100.000
alignment_scores
```

alignment\_block: TGFB3P x AAT15464

Align seg 1/1 to: AAT15464 from: 1 to: 339

```
1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa
```

```
17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH
```

```
34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr
```

```
seq_name: /SIDS1/gcgdata/geneseq/geneseqn/NA1997.DAT:AAT80110
                                                                       seq_documentation_block:
ID AAT80110 standard; cDNA to mRNA; 339 BP.
```

AAT80110;

28-NOV-1997 (first entry) DX SX E

Mature transforming growth factor beta3 coding sequence.

sforming growth factor beta3; TGF-beta3; human; mature protein; stable; heat-stable; homodimer; mitogenesis; cell proliferation; growth; wound; oral mucositis; intestinal mucositis; osteoarthritis; disease; bone repair; therapy; ds. Transforming acid-stable; pone cell

Homo sapiens

WO9705166-A1

13-FEB-1997

96WO-EP03140. 17-JUL-1996;

95EP-0810484 25-JUL-1995;

(CIBA ) CIBA GEIGY AG

Mittl P; Grutter M, Arvinte T,

WPI; 1997-145621/13. P-PSDB; AAW26173 Crystalline form of transforming growth factor beta-3 - useful in compsns. as slow release form of TGF, e.g. for wound healing, and for structure determn. in rational drug design

Example 1; Page 25-26; 34pp; English.

This sequence represents the coding sequence for human transforming growth factor beta3 (TGF-beta3 is one of five distinct homodimeric TGFDeta's. TGF-beta3 is a acid-stable and heat-stable disulphide linked homodimer. All the TGF-beta's are produced as 390-412 amino acid precursors, which undergo proteolytic cleavage to produce mature forms which consist of the C-terminal 112 amino acids. Depending upon cell and tissue type, and the presence of other growth factors, TGF-beta may either stimulate mitogenesis, cell proliferation and growth, or inhibit these processes. Many of the actions of TGF-beta are related to the response of cells or tissues to stress or injury, and to the repair of resultant damage. A crystalline form of TGF-beta3 is useful in produced by a method of the invention. Crystalline TGF-beta3 is useful in slow release compositions for treatment of conditions such as wounds, calls in intestinal mucositis, osteoarthritis, bone disease and repair, generally wherever TGF-beta3 is normally used. The crystalline form is also used for structure determination in rational drug design. adsorb on the walls of vials and is more stable against oxidation. Variation of the properties, e.g. size, of the crystals allows control over the rate at which active TGF is released in vivo. 

Sequence 339 BP; 74 A; 104 C; 86 G; 75 T; 0 other;

Quality: 633.00 Ratio: 5.652 Percent Similarity: 100.000 alignment\_scores:

Percent Identity: 100.000 Gaps:

alignment\_block: TGFB3P x AAT80110

to: 339 Align seg 1/1 to: AAT80110 from: 1

<sup>51</sup> LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67

<sup>151</sup> 

<sup>84</sup> rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 29

<sup>84</sup> luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100 

<sup>101</sup> LeuSerAsnMetValValLysSerCysLysCysSer 112 301 CTCTCCAACATGGTGTGAAGTCTTGTAAATGTAGC 336

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20-JAN-1999
   8.566666666888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          useful to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      comprises a purification tag and a TGF active fragment. The present sequence encodes a specifically claimed TGF active fragment. Additionally, the fusion protein may comprise proteinase-sensitive linker sites and binding domain so the protein sequence may contain some or all of the following elements: purification tag:proteinase site:ECM binding site:proteinase site:TGF-beta. TGF-beta promotes wound healing, and the fusion protein can be used to reduce surgery
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       novel transforming growth factor-beta (TGF-beta) fusion protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TGF active fragment of a TGF-beta fusion protein encoding cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Transforming growth factor-beta fusion protein; wound healing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Prepn. of transforming growth factor-beta fusion protein - \iota reduce surgery recovery time and to prepare artificial skin
                  84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
                                                                                                                                                                                                                                  67
                                                                                                                                             84
                                                                                                                                                                                                                                                                                                                                                             seq_name: /SIDS1/gcgdata/geneseq/geneseqn/NA1997.DAT:AAT42773
34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr
                                                                  51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh
                                                                                                                                           rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /*tag= a
/function= TGF active fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Мu
                                                                                                                                                                                                                                                                                      101 LeuSerAsnMetValValLysSerCysLysCysSer 112
                                                                                                                                                                                                                                                                                                           301 CTCTCCAACATGGTGGTGAAGTCTTGTAAATGTAGC 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 artificial skin; surgery recovery time; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tuan I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
1..339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 48; 59pp; English.
                                                                                                                                                                                                                                                                                                                                                                                               seq_documentation_block:
ID AAT42773 standard; cDNA; 339 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nimni ME,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      96WO-US08973
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (CHEU/) CHEUNG D T.
(HALL/) HALL F L.
(NIMN/) NIMNI M E.
(TUAN/) TUAN T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1997-043065/04
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO9639430-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         06-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26-AUG-1997
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recovery time and in the preparation of artificial skin. The inclusion of a purification tag facilitates purification of the fusion protein. The proteiness site is included to permit cleavage and release of the purification tag after purification if desired. The extracellular matrix binding site facilitates delivery of the fusion protein to the desired site of action. Delivery of the TGF-beta to the site to be treated reduces the amount of TGF-beta required to be administered to be effective and reduces the concentration of circulating TGF-beta which may result in undesirable effects.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cDNA encoding the mature form of transforming growth factor-beta-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Transforming growth factor-beta-3; TGF-beta-like protein; S-sulphonated TGF-beta-like protein; wound treatment; cancer; bone repair; tissue repair; bone marrow protective agent; cardioprotection; anti-inflammatory; immunosuppressive; ulcer; bed sore; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              51 GCGCCCCTCTACATTGACTTCCGACAGGATCTCGGCTGGAAGTGGGTCC 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       250
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AGCCCCTGACCATCCTGTACTAGGAGGACCCCCAAAGTGGAGCAG 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_name: /SIDS1/gcgdata/geneseq/geneseqn/NA1999.DAT:AAX15247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TCTGAACCCTGAAGCATCTGCCTCGCCTTGCTGCGTGCCCCAGGACCTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length: 112
Gaps: 0
Percent Identity: 100.000
                                                                                                                                                                                                                                                                Sequence 339 BP; 74 A; 104 C; 86 G; 75 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LeuSerAsnMetValValLysSerCysLysCysSer 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Align seg 1/1 to: AAT42773 from: 1 to: 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BP.
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ID AAX15247 standard; cDNA; 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                    Quality: 633.00
Ratio: 5.652
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alignment_block:
TGFB3P x AAT42773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-APR-1999
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                                                                                                                                                                                                                                                                                                                                              alignment_scores:
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Proteinase site; bone morphogenetic fusion protein; bone binding site; bone morphogenetic protein; transforming growth factor beta; active fragment; wound healing; bone growth; purification tag; ds.

· 98WO-US11189

02-JUN-1998;

10-DEC-1998.

Homo sapiens W09855137-A1

cDNA encoding a transforming growth factor beta active fragment.

(first entry)

25-MAR-1999

AAV99377;

BP.

seq\_documentation\_block:
ID AAV99377 standard; cDNA; 339

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The present sequence encodes the mature form of transforming growth factor-beta-3. Dimeric, biologically active TGF-beta-like protein can be produced by subjecting the denatured monomeric form to refolding conditions. The new monomeric S-subjehonated TGF-beta-like protein is useful for the production of the dimeric, biologically active TGF-beta-like protein, which is useful for the treatment of wounds (surface or internal) and cancer in a mammal, in bone and tissue
                                                                                                                                                                                                                                                                                                                                                                                                                  repair, as a bone marrow protective agent, a mediator of cardioprotection, for the production of an anti-inflammatory or immunosuppressive preparation. Treatment is useful for animals, especially humans, and wound treatment (e.g. ulcers, bed sores etc.) is particularly useful for the elderly.
                                                                                                                                                                                                                      refolding new monomeric Transforming Growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
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                                                                                                                                                                                                   Producing biologically active dimeric Transforming Growth
                                                                                                                    Schmitz A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG
                                                                                                                                                                                                                                   Factor-beta, useful for treatment of wounds and cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Identity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 339 BP; 74 A; 104 C; 86 G; 75 T; 0 other;
                                                                                                                    Meyhack B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Align seg 1/1 to: AAX15247 from: 1 to: 339
                                                                                                                McMaster GK,
                                                                                                                                                                                                                                                                    Example 1; Page 30; 32pp; English.
               90EP-0810922
                                               89GB-0027546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Quality: 633.00
Ratio: 5.652
Percent Similarity: 100.000
                                                                                (NOVS ) NOVARTIS AG
                                                                                                                  Cox D,
                                                                                                                                                 WPI; 1999-083520/08
                                                                                                                                                                  P-PSDB; AAW97093
                                                                                                                                                                                                                      Factor-beta - by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TGFB3P x AAX15247
               27-NOV-1990;
                                               06-DEC-1989;
                                                                                                                Cerletti N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      51
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The present sequence encodes a transforming growth factor beta active fragment. The protein can be used in place of a bone morphogenetic active fragment to create the fusion proteins of the invention. When a bone morphogenetic active fragment is used, the fusion proteins are designated bone morphogenetic fusion proteins. The bone morphogenetic fusion proteins. The bone morphogenetic fusion proteins are purification and some or all of the following elements: a purification tag, a proteinase site, an ECM/bone binding site, a second proteinase site, and a bone morphogenetic protein active fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 New bone morphogenetic fusion proteins - comprising a purification tag and a bone morphogenetic active fragment, used for enhancing wound healing or bone growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 GCTTTGGACACCAATTACTGCTTCGCAACTTGGAGGAGAACTGCTGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length: 112
Gaps: 0
Percent Identity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 339 BP; 74 A; 104 C; 86 G; 75 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                  Mu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 43; 64pp; English.
                                                                                                                                                                                                                                                                                                                                                                                 Shors
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                                                                                                                                                                                                                                                                       97US-0868452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ratio: 5.652
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       633.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        healing or bone growth.
                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1999-059875/05.
P-PSDB; AAW84209.
                                                                                                                                                                                                                                                                                                              HAN B.
NIMNI M E.
SHORS E C.
                                                                                                                                                                                                                                                                                                 (HALL/) HALL F L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         alignment_block:
TGFB3P x AAV99377
                                                                                                                                                                                                                                                                     03-JUN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alignment_scores:
                                                                                                                                                                                                                                                                                                              (HANB/)
(NIMN/)
                                                                                                                                                                                                                                                                                                                                          (SHOR/)
                                                                                                                                                                                                                                                                                                                                                     (MULL/)
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seq\_name: /SIDS1/gcgdata/geneseq/geneseqn/NA1999.DAT:AAV99377

251 101

LeuSerAsnMetValValLysSerCysLysCysSer 112 CTCTCCAACATGGTGGTGAAGTCTTGTAAATGTAGC 336

tqfb3p.rng

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This 2529bp full-length TGF-beta3 gene sequence was obtained from three shorter overlapping clones derived from human placental, humsumbilical cord and A673 cells cDNA libraries, respectively. The predicted amino acid sequence of the gene encoding TGF-beta3 shows
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Transforming growth factor beta 3 proteins, precursors and mutants - obtd. from polypeptide and antibodies, with optimal therapeutic use due to genetic manipulation of coding sequence
                                                                              321 GCGCCCCCTCTACATTGACTTCCGACAGGATCTGGGCTGGAAGTGGGTCC 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_name: /SIDS1/gcgdata/geneseq/geneseqn/NA1992.DAT:AAQ20576
                                                                                                                                           LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh
                                                                                                                                                                                                                                                                                                                                 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG
                                                                                                                                                                                                                                                                                                                                                34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Transforming Growth Factor beta 3 coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         LeuSerAsnMetValValLysSerCysLysCysSer 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tendijke P, Haley
                                                 to: AAQ05774 from: 1 to: 609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 2; Fig 1; 107pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_documentation_block:
ID AAQ20576 standard; cDNA; 2529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      91WO-US04541.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     90US-0543348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TGF-beta 3; homodimer; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (ONCO-) ONCOGENE SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Foulkes JG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1992-041510/05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P-PSDB; AAR20621
      alignment_block:
TGFB3P x AAQ05774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              05-MAY-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25-JUN-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25-JUN-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO9200318-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09-JAN-1992
                                                 Align seg 1/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   wata KK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAQ20576;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         101
                                                                                                                                                                                                                                                                    21
                                                                                                                                                                                                                                                                                                 121
                                                                                                                                                                                                                                                                                                                                29
                                                                                                                                                                                                                                                                                                                                                                                                                           521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gene product may be used to inhibit growth of tumour cells, to treat proliferative type disorders, burns and other wounds, and may also be used as an immune modulator. Detection of proteins and of TGF-alpha can indicate presence of a tumour.

Proteins may be produced from a bacterial or eukaryotic expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cancer; carcinoma; melanoma; leukaemia; arteriosclerosis; psoriasis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence encoding protein with tumour growth inhibitory activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tissue-derived tumour growth inhibitors - used in diagnosis and treatment of tumours and treatment of proliferative type
84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
                                                                                                                                                                                                      84
                                                                                                                                                                                                                                                                                                                seq_name: /SIDS1/gcgdata/geneseq/geneseqn/NA1990.DAT:AAQ05774
                                                                                                                         other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length: 112
Gaps: 0
Percent Identity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             T; 0
                                                                                                                                                                                                                                                Sequence 609 BP; 154 A; 172 C; 158 G; 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ε;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Fig 29; 81pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gold
                                                                                                                                                                                                                                                                                                                                                              ВP
                                                                                                                                                                                                                                                                                                                                            seq_documentation_block:
ID AAQ05774 standard; cDNA; 609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              87EP-0106772
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             90EP-0106772
86US-0922121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     disorders, burns and wounds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         JR,
                                                                                                                                                                                                                                                                                                                                                                                                                         03-JAN-1991 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (ONCO-) ONCOGENE SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Quality: 633.00
Ratio: 5.652
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Iwata KK, Stephenson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1990-262507/35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P-PSDB; AAR06548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGF-alpha; ds;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20-OCT-1987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JAN-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20-OCT-1986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29-AUG-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alignment_scores:
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AAQ05774;

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tgfb3p.rng

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The present sequence encodes human transforming growth factor-beta 3 (TGF-beta3). The specification describes a composition for regulating trophoblast invasion which comprises an inhibitor of TGF-beta 1. TGF-beta family cytokine receptors, hypoxia inducible factor 1 alpha (HIF-1 alpha) or oxygen tension. The composition is used in methods of diagnosing, monitoring, preventing or treating conditions requiring regulation of trophoblast invasion, especially preeclempsia in pregnant
                                                                                                                                                                                        Regulation of trophoblast invasion - by, e.g. transforming growth factor-beta3 inhibitor, useful for detecting or treating preeclempsia in pregnant women
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1404 AGCCCCTGACCATCCTGTACTATGTTGGGAGGACCCCCAAAGTGGAGCAG 1453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1154 GCTTTGGACACCAATTACTGCTTCCGCAACTTGGAGGAGAACTGCTGTGT 1203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq_name: /SIDS1/gcgdata/geneseq/geneseqn/NA2001.DAT:AAF55131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2574 BP; 629 A; 680 C; 666 G; 599 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps: 0
Percent Identity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LeuSerAsnMetValValLysSerCysLysCysSer 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       to: 2574
                                          (HOSP-) HOSPITAL FOR SICK CHILDREN
                                                              (MOUN ) MOUNT SINAI HOSPITAL CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Align seg 1/1 to: AAV63209 from: 1
                                                                                                                                                                                                                                                                   Disclosure; Fig 1; 59pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seq_documentation_block:
ID AAF55131 standard; DNA; 4382
                                                                                                Post M;
     97US-0039919
                                                                                                                                                                                                                                                                                                                                                                                                                                            women or choriocarcinomas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Quality: 633.00
Ratio: 5.652
Percent Similarity: 100.000
                                                                                               Caniggia I, Lye S,
                                                                                                                                   WPI; 1998-520837/44
P-PSDB; AAW80417.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                alignment_block:
TGFB3P x AAV63209
     07-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAF55131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29
     Human transforming growth factor-beta 3; TGF-beta3; oxygen tension; trophoblast invasion regulation; inhibitor; HIF-1 alpha; TGF-beta family cytokine receptor; hypoxia inducible factor 1 alpha; preeclempsia; pregnanancy; choriocarcinoma; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleic acid sequence of human transforming growth factor-beta 3.
                                                                                                                                                                                                                                                                                                                      1163 GCTTTGGACACCAATTACTGCTTCCGCAACTTGGAGGAGAACTGCTGTGT 1212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         67
                                                                                                                                                                                                                                                                                                                                                                              34
                                                                                                                                                                                                                                                                                                  1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq_name: /SIDS1/gcgdata/geneseq/geneseqn/NA1998.DAT:AAV63209
                                                                                                                                                                                                                                                                                                                                                                          34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG
                                                          other;
                                                                                                                                Length: 112
Gaps: 0
Percent Identity: 100.000
                                                        G; 581 T; 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1463 CTCTCCAACATGGTGGTGAAGTCTTGTAAATGTAGC 1498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       101 LeuSerAsnMetValValLysSerCysLysCysSer 112
                                                                                                                              Length:
 beta
                                                                                                                                                                                                                                                                to: 2529
extensive homology to TGF-beta 1 and See also AAQ22229 and AAR20622.
                                                    Sequence 2529 BP; 617 A; 670 C; 661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
254..1492
/*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /*tag= a
/product= TGF-beta3
                                                                                                                                                                                                                                                              to: AAQ20576 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_documentation_block:
ID AAV63209 standard; DNA; 2574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98WO-CA00180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                            Quality: 633.00
Ratio: 5.652
Percent Similarity: 100.000
                                                                                                                                                                                                                       TGFB3P x AAQ20576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-MAR-1998;
                                                                                                            alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14-JAN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO9840747-A1
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                                                                                                                                                                                                       alignment_block
                                                                                                                                                                                                                                                            Align seg 1/1
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1313 67

112

67

Key

Tue Oct,30 12;56:48 2001

(first entry)

29-MAY-2001

(CHEN/) CHEN 24 - AUG-1999;

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01-MAR-2001

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Nucleic acid sequences encoding transforming growth factor-beta diagnostic probes, and for use in therapeutics
                                                                                                                                                                                                                                                                                                                                TGF-beta-1; TGF-beta-2; transforming growth factor beta-1; transforming growth factor beta-3; recombinant; wound healing;
                                  AGCCCCTGACCATCTTGTACTATGTGGGCAGAACCCCCAAGGTGGAGCAG 1657
seq_name: /SIDS1/gcgdata/geneseq/geneseqn/NA1994.DAT:AAQ56926
                                                                                    LeuSerAsnMetValValLysSerCysLysCysSer 112
                                                                                                                                                                                           AAQ56926 standard; cDNA; 2157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              85US-0715142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               87US-0025423.
89US-0389929.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               85US-0715142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 92US-0845893
                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ratio: 5.625
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Goeddel
                                                                                                                                                                         seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1994-056343/07
                                                                                                                                                                                                                                                                                                 Human TGF-beta-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P-PSDB; AAR46229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Quality:
                                                                                                                                                                                                                                                                                                                                                                     vulnerary; ss
                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22-MAR-1985;
13-MAR-1987;
                                                                                                                                                                                                                                                           09-JUL-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22-MAR-1985;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Derynk RMA,
                                                                                                                                                                                                                                                                                                                                                                                                                                        US5284763-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 04-MAR-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  04-AUG-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          08-FEB-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alignment_scores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              alignment_block
                                                                                                                                                                                                                           AAQ56926;
                                1608
                                                                                                    1658
84
                                                                  101
                                                                                                                                                                                                         The specification describes a method for growing stem cells. The method involves providing stem cells with supporters which are genetically modified in order to provide externally regulatable interactions between the supporters and the stem cells, and applying an external signal for starting or stopping the interactions. The cells are useful for curing diseases by gene therapy and/or cell therapy in combination with tissue engineering, when the functional expression of stem cells is helped with engineered architecture of the tissue, which diseases are related to insufficient and/or lack and/or disorders of stem cells. The present sequence represents a vector, which is used in the method of the
                                                                                                                                                                                                                                                                                                                                                                              Growing stem cells useful as therapeutic, involves providing stem cells with supporters which are genetically modified to provide externally regulatable interactions, and applying an external signal
                                                                Stem cell; gene therapy; cell therapy; stem cell disorder; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 4382 BP; 1153 A; 1120 C; 1091 G; 1018 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps: 0
Percent Identity: 100.000
                              Nucleotide sequence of the vector puhd10-3-tgf
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Align seg 1/1 to: AAF55131 from: 1 to: 4382
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Fig 26; 92pp; English.
                                                                                                                                                                                                       24-AUG-2000; 2000WO-EP08247
                                                                                                                                                                                                                                           99EP-0116533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ratio: 5.652
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Quality: 633.00
                                                                                                                                                                                                                                                                                                                                                WPI; 2001-218440/22
                                                                                                                                   WO200114530-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            alignment_block:
TGFB3P x AAF55131
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alignment\_scores:

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cDNA sequences were determined for human pre-TGF-beta-1 (AAQ56923), pig TGF-beta-3 (AAQ56926), and the corresponding amino acid sequences were determined (AAG56927-29, respectively). A genomic fragment corresponding to a human TGF-beta-1 exon (AAQ56924) was also isolated and its amino acid sequence determined (AAR46230). The sequences have been used in the onstruction of vectors for the expression of recombinant TGF-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         278 GCTTTGGACACCAATTACTGCTTCCGCAACTTGGAGGAGAACTGCTGGT 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa
                                                                                                                                                                                                                                                                                                                                                    0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length: 112
Gaps: 0
Percent Identity: 99.107
                                                                                                                                                                                                                                                                                                                                                    Sequence 2157 BP; 621 A; 462 C; 492 G; 582 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             to: 2157
Disclosure; Fig 4a-c; 25pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Align seg 1/1 to: AAQ56926
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 630.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TGFB3P x AAQ56926
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1558 CCTGAACCCAGAGGGGTCTGCCTCGCCATGCTGCTGCCTCCCCCAGGACCTGG 1607

rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG

1458

1508 51

tgfb3p.rng

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of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA encoding transforming growth factor-beta precursor sequence useful for analysis to perform manipulations to increase yield crecombinant production of the protein
         427
                                                                                             477
                                                                                                                                                   luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
                                                                           67
                                                                                                                 84
  34
                                                                                                                                                                                                                              seq_name: /SIDS1/gcgdata/geneseq/geneseqn/NA1998.DAT:AAV52935
lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH
                                    LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh
                                                                                                               rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG
                                                                                                                                                                                                                                                                                                                                     Transforming growth factor-beta 3; TGF-beta 3; human;
                                                                                                                                                                                                                                                                                                                                                                                           /*tag= a
/transl_except= (pos:50..52, aa:Thr)
                                                                                                                                                                                                                                                                                                                  Human transforming growth factor-beta 3 cDNA.
                                                                                                                                                                                          LeuSerAsnMetValValLysSerCysLysCysSer 112
                                                                                                                                                                                                            CTCTCCAACATGGTGGTGAAGTCTTGTAAATGTAGC 613
                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 6; Fig 4a-c; 26pp; English.
                                                                                                                                                                                                                                                           ВÞ
                                                                                                                                                                                                                                               seq_documentation_block:
ID AAV52935 standard; cDNA; 2157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             87US-0025423.
85US-0715142.
89US-0389929.
92US-0845893.
93US-0147364.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            85US-0715142
                                                                                                                                                                                                                                                                                               (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                   ..616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (GETH ) GENENTECH INC.
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P-PSDB; AAW78787.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RMA,
                                                                                                                                                                                                                                                                                              21-DEC-1998
                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                            22-MAR-1985;
                                                                                                                                                                                                                                                                                                                                                                                                                        US5801231-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13-MAR-1987
22-MAR-1985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 04-AUG-1989
04-MAR-1992
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30-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                         01-SEP-1998
                                                                                                                                                                                                                                                                           AAV52935,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Derynck
                                                                          21
                                                                                            428
                                                                                                                                  478
                                                                                                                                                                      528
                                                                                                               67
                                                                                                                                                    84
                                                                                                                                                                                         101
                                                                                                                                                                                                           578
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This nucleotide sequence, hu4, codes for a human partial transforming growth factor-beta 3 (TGF-beta 3) sequence including

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all of the mature sequence. Clone hu4 was isolated from a human ovarian cDNA library using porcine TGF-beta 3 cDNA (see AAV52934) as probe. The invention relates to the recombinant production of TGF-beta. Biologically active TGF-beta is defined as being capable of inducing EGF-potentiated anchorage independent growth of target cell lines and/or growth inhibition of neophastic cell lines. Nucleic acids encoding TGF-beta have been isolated and cloned into vectors which are replicated in bacteria and expressed in euclaryotic cells. TGF-beta recovered from transformed cells is used in known therapeutic applications. TGF-beta nucleic acids are also used in diagnosis and identification of TGF-beta clones.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              growth factor beta-3 (TGF beta 3); tumour cells; growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        327
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             84
                                                                                                                                                                                                                                                                                                                                                                                                     1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_name: /SIDS1/gcgdata/geneseq/geneseqn/NA1990.DAT:AAQ02820
                                                                                                                                                                                                                                                                                                                                                                                                                       17 largProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG
                                                                                                                                                                                             Sequence 2157 BP; 621 A; 462 C; 492 G; 582 T; 0 other;
                                                                                                                                                                                                                                                           112
0
99.107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LeuSerAsnMetValValLysSerCysLysCysSer 112
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                                                                                                                                                                                                                                                             Length:
                                                                                                                                                                                                                                                                                                                                                                       to: 2157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cDNA sequence encoding human TGF-beta 3.
                                                                                                                                                                                                                                                                                                                                                                       from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seq_documentation_block:
ID AAQ02820 standard; DNA; 2158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          88WO-US01945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                          Quality: 630.00
Ratio: 5.625
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                       Align seg 1/1 to: AAV52935
                                                                                                                                                                                                                                                                                                                                        TGFB3P x AAV52935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Transforming inhibition.
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                                                                                                                                                                                                                                             alignment_scores:
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                                                                                                                                                                                                                                                                                                                      alignment_block:
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    222222222222XX
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This sequence has been compiled from the description of a mutant TGF-beta3 contained in the claims. The sequence coding for the Factor Xa cleavage site may be replaced by one encoding a similar protease recognition site, e.g. for collagenase. The coding sequence may also include a region encoding a hydrophobic transmembrane amino acid sequence, e.g. from c-erbB2 cDNA and a "stop transfer" sequence. The protease recognition site is located between the C-terminal of the transmembrane region and the N-terminal of the TGF-beta 3 precursor. Mature TGF-beta 3 can then be efficiently cleaved from the membrane. See also AAQ20576 and AAR20622.
                                                                                                                                                                                                                                             /*tag= d
/note= "wild-type codon = ATG. May be replaced by
any other codon to give mutant sequence"
1216..1239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mutants - obtd. from polypeptide and antibodies, with optimal therapeutic use due to genetic manipulation of coding sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /*tag= e
/note= "nucleotides 1475-1498 of TGF-beta3"
                                                                                                                                                                                            /*tag= c
/note= "nucleotides 1163-1471 of TGF-beta3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Transforming growth factor beta 3 proteins, precursors and mutants - obtd. from polypeptide and antibodies, with optin
                                                                       **tag= a
note= "nucleotides 263-1150 of TGF-beta3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17
                                                                                                                 /*tag= b
/note= "encodes Factor Xa cleavage site
/note= followed by a methionine residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1239 BP; 308 A; 348 C; 328 G; 248 T; 7 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length: 112
Gaps: 0
Percent Identity: 99.107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Haley JD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             to: 1239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tendijke P,
                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 12; Page 66; 107pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             to: AAQ22229 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          90US-0543348.
                                                                                                                                                                                                                           misc_difference 1213.:1215
                                                                                                        889..903
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5.649
99.107
                                                     . 888
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1992-041510/05
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ratio:
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                                                     misc_feature
                                                                                                        misc_feature
                                                                                                                                                                            misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                        25-JUN-1991;
                                                                                                                                                                                                                                                                                                   misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25-JUN-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                   WO9200318-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           aliqnment_block
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Align seg 1/1
   Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Iwata KK,
   This sequence encodes human transforming growth factor-beta 3 (TGF-beta 3) polypeptide. The nucleic acid sequence encoding this subtype is useful as a probe or to produce TGF-beta 3 for both normal and neoplastic cell growth inhibition.
                                                                                                                                          ø
                                                                                                                                     Nucleotide sequence encoding transforming growth factor beta-3 -used as probe; or to produce TGF beta 3, for inhibition of growth of normal and neoplastic cells, eg A549.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Factor beta 3 coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_name: /SIDS1/gcgdata/geneseq/genesegn/NA1992.DAT:AAQ22229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   528 AGCCCCTGACCATCCTGTACTATGTTGGGAGGACCCCCAAAGTGGAGCAG
                                                                                                                                                                                                                                                                                                                                   other;
                                                                                                                                                                                                                                                                                                                                                                                                    Length: 112
Gaps: 0
Percent Identity: 99.107
                                                                                                                                                                                                                                                                                                                                Sequence 2158 BP; 621 A; 462 C; 493 G; 582 T; 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     101 LeuSerAsnMetValValLysSerCysLysCysSer 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       578 CTCTCCAACATGGTGGTGAAGTCTTGTAAATGTAGC 613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            from: 1 to: 2158
                                                                                                                                                                                                           Disclosure; Fig. 4; 61pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq_documentation_block:
ID AAQ22229 standard; cDNA; 1239
88WO-U001945.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Align seg 1/1 to: AAQ02820
                                                                    Goeddel DV;
                                                                                                                                                                                                                                                                                                                                                                                                                      Ratio: 5.625
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                    Quality: 630.00
                                  (GETH ) GENENTECH INC
                                                                                                    WPI; 1990-007474/01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        alignment_block:
TGFB3P x AAQ02820
08-JUN-1988;
                                                                                                                                                                                                                                                                                                                                                                                     alignment_scores:
                                                                    Dernyck RM,
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51

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Quality:
Ratio:
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                                                                                                                                                 Sequence 2639
                                                                                                                                                                                                                                                        alignment_block:
TGFB3P x AAV52934
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                                                                                                                                                                                         alignment_scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                67
This nucleotide sequence, termed 10+11.3, codes for the porcine transforming growth factor-beta 3 precursor (preTGF-beta 3, see AAW78786). A porcine ovarian cDNA library was screened using human TGF-beta 1 cDNA (see AAW52933) as probe. A hybridising clone, designated lambda 11.3, was used to rescreen the library to identify clone lambda 10. The was combined with clone lambda 11.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 precursor sequence -
                      luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
                                                                67
                                                                                                                   84
                                                                                                                                                                                                                                                                                 seq_name: /SIDS1/gcgdata/geneseq/geneseqn/NA1998.DAT:AAV52934
                                                                            51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh
         isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr
                                                                                                                  rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG
                                                                                                                                                                                                                                                                                                                                                                                                                                       pig; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /*tag= a
/transl_except= (pos:481..483, aa:Met)
                                                                                                                                                                                                                                                                                                                                                                                                                                    Transforming growth factor-beta 3; TGF-beta 3;
                                                                                                                                                                                                                                             CTCTCCAACNNNGTGGTGAAGTCTTGTAAATGTAGC 1239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA encoding transforming growth factor-beta useful for analysis to perform manipulations recombinant production of the protein
                                                                                                                                                                                                                              LeuSerAsnMetValValLysSerCysLysCysSer 112
                                                                                                                                                                                                                                                                                                                                                                                                         transforming growth factor-beta 3 cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
127..1497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 6; Fig 4a-c; 26pp; English
                                                                                                                                                                                                                                                                                                                           BP
                                                                                                                                                                                                                                                                                                          seq_documentation_block:
ID AAV52934 standard; cDNA; 2639
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89US-0389929.
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                                                                                                                                                                                                                                                                                                                                                                               21-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22-MAR-1985;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US5801231-A.
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04-AUG-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               04-MAR-1992
05-NOV-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               scrofa
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                                                                                        1054
                                                                                                                                             1104
                                                                                                                                                                      84
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sus
                                                                                                                  67
                                                                                                                                                                                                                            101
                                                                                                                                                                                                                                                                                                                                                                                                           Pig
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to provide the 10+11.3 sequence. The invention relates to the recombinant production of TGF-beta. Biologically active TGF-beta is defined as being capable of inducing EGF-potentiated anchorage independent growth of target cell lines and/or growth inhibition of meoplastic cell lines. Nucleic acids encoding TGF-beta have been isolated and cloned into vectors which are replicated in bacteria and expressed in eukaryotic cells. TGF-beta recovered from TGF-beta nucleic acids are also useful in diagnosis and identification of TGF-beta clones.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TGF-beta-1; TGF-beta-2; transforming growth factor beta-1; transforming growth factor beta-3; recombinant; wound healing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1159 GCCCTGGACACCAACTACTGCTTCCGCAATTTGGAGGAGAACTGCTGTGT 1208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1409 AGCCCCTGACCATCCTGTACTACGTCGGAGGACCGCCAAGGTGGAGCAG 1458
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     84
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG
                                                                                                                                                                                                                                                                                                 G; 563 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                  Length: 112
Gaps: 0
Percent Identity: 98.214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           to: 2639
                                                                                                                                                                                                                                                                                              BP; 677 A; 702 C; 697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ВР
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CDNA; 2669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09-JUL-1994 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                  621.00
5.595
99.107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Align seg 1/1 to: AAV52934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_documentation_block:
ID AAQ56925 standard;
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cDNA sequences were determined for human pre-TCF-beta-1 (AAQ56923), plg TGF-beta-3 (AAQ56925) and human TGF-beta-3 (AAQ56926), and the corresponding amino acid sequences were determined (AAR46227-29, respectively). A genomic fragment corresponding to a human TGF-beta-1 exon (AAQ56924) was also isolated and its amino acid sequence determined (AAR46230). The sequences have been used in the construction of vectors for the expression of recombinant TGF-
                                                                                                                                                                                                              encoding transforming growth factor-beta for use in therapeutics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1259 ATGAACCTAAGGCTACTATGCCAACTTCTGCTCAGGCCCTTGCCGTAC 1308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1359 CCTGAACCCCGAAGCCTCGGCCTCTCCGTGCTGCTGCCCCAGGACCTGG 1408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_name: /SIDS1/gcgdata/geneseq/geneseqn/NA1990.DAT:AAQ03303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr
                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2669 BP; 706 A; 702 C; 697 G; 564 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length: 112
Gaps: 0
Percent Identity: 98.214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          101 LeuSerAsnMetValValLysSerCysLysCysSer 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Align seg 1/1 to: AAQ56925 from: 1 to: 2669
                                                                                                                                                                                                                                                        Disclosure; Fig 4a-c; 25pp; English
                             85US-0715142.
87US-0025423.
89US-0389929.
92US-0845893.
 85US-0715142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     621.00
5.595
99.107
                                                                                                                                  Derynk RMA, Goeddel DV;
                                                                                                                                                                                                             Nucleic acid sequences diagnostic probes, and
                                                                                                      (GETH ) GENENTECH INC.
                                                                                                                                                                WPI; 1994-056343/07
                                                                                                                                                                                 P-PSDB; AAR46228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                alignment_block:
TGFB3P x AAQ56925
                           22-MAR-1985;
13-MAR-1987;
04-AUG-1989;
04-MAR-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        alignment_scores:
22-MAR-1985
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cDNA library to find
                                                                 Entire porcine transforming growth factor (TGF) beta-3 cDNA sequence
                                                                                                   Porcine transforming growth factor (TGF) beta-3; human ovarian cDNA; human transforming growth factor (TGF) beta-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleic acid encoding transforming growth factor-beta -
cloned into expression vectors for expression in eukaryotic host
cells for therapeutic use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1209 GCGCCCTCTCTACATIGACTICCGACAGGATCTGGGCTGGAAGTGGGTCC 1258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1259 ATGAACCTAAGGGCTACTATGCCAACTTCTGCTCAGGCCCTTGCCCGTAC 1308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTCCGCAGTGCAGACACAACCCACAGCTCGGTGCTGGGGCTGTACAACAC 1358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                34 isGluproLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LeuargSeralaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            It was used to screen plaques from a human ovarian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Percent Identity: 98.214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                T; 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2671 BP; 706 A; 705 C; 699 G; 561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           to: 2671
                                                                                                                                                                                                                                                                                             87US-0025423, US-715142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fig 4a-c; 28pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            to: AAQ03303 from: 1
                                                                                                                                                                                                                                                             87US-0U25423
                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                    DV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   621.00
5.595
99.107
                                                                                                                                                                                                                                                                                                                                                                    Goeddel
                                                                                                                                                                                                                                                                                                                                (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1990-051338/07.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                human TGF-beta-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TGFB3P x AAQ03303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure;
                                                                                                                                                                                                                                                             13-MAR-1987;
                                                                                                                                                                                                                                                                                             13-MAR-1987;
                                05-AUG-1990
                                                                                                                                                                                                                                                                                                                                                                  Derynck RMA,
                                                                                                                                                                                        US4886747-A
                                                                                                                                                                                                                          12-DEC-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alignment_scores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        alignment_block
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Align seg 1/1
AAQ03303
                                                                                                                                                         Porcine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1309
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101 LeuSerAsnMetValValLysSerCysLysCysSer 112

seq\_documentation\_block:
ID AAQ03303 standard; DNA; 2671 BP

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alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tissue-derived growth inhibitor and corresponding genes - useful for detection of tumours, inhibition of tumour growth, treatment of proliferative disorders and healing of burns and wounds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The sequence encodes a 112 amino acid tumor growth inhibitor (TGI) (AAR86770) or a 205 precursor TGI (AAR86771) comprising TGI with an additional 93 amino acid residues at the N-terminus. However, the nucleotides representing codons -40 to -1 of the precursor TGI are not specified in Figure 29, i.e. the cDNA is 498 nucleotides in length, but should be 615 nucleotides long. The DNA is used to produce the inhibitors by recombinant methods i.e. vector expression in bacterium or eukaryotic host cells. The proteins can be used to inhibit the growth of human tumour cells, e.g. carcinoma, melanoma or leukamenia cells, in the treatment of proliferative disorders e.g. arteriosclerosis, inflammation and proliferative disorders e.g. arteriosclerosis, inflammation and pooriasis, or for the treatment of burns to facilitate wound
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            t positions -40 to -1 (i.e. 117 are not given in the
                                                                                                                                                                                                                                                                                                                                                                                                            Tumour growth inhibitor; carcinoma; melanoma; leukaemia; arteriosclerosis; inflammation; psoriasis; therapy; vulnerary; immunomodulator; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product= tumour_growth_inhibitor_precursor
/note= "see AAR86771"
159..160
                                                                                                                                                                                                                                                                                                                                                                      Tissue-derived tumour growth inhibitor-1 coding sequence
                                                                                           seq_name: /SIDS1/gcgdata/geneseq/geneseqn/NA1996.DAT:AAT06496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /*tag= c
/product= mature_tumour_growth_inhibitor
/note= "see AAR86770"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /*tag= b
/note= "the codons at positions
specfication"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nucleotides)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Stephenson JR;
                                                                                                                                                   seq_documentation_block:
ID AAT06496 standard; cDNA; 498 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 6; Fig 29; 83pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         87EP-0109866
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                                                                                                                                                                                                                                                                                                              (first entry)
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/*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gold LI, Iwata KK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1996-000991/01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20-0CT-1987;
                                                                                                                                                                                                                                                                                                           12-JUN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20-OCT-1986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EP684260-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29-NOV-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mat_peptide
                                                                                                                                                                                                                                               AAT06496;
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healing. They can also be used as immunomodulators. Although the proteins have tumour growth inhibitory activity, they are not transforming growth factor-beta-1 or -beta-2.

Sequence 498 BP; 122 A; 136 C; 129 G; 111 T; 0 other;

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TGI; carcinoma; melanoma; leukaemia; arteriosclerosis; inflammation;
                                                                                                                                                                                   84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
                                                                                                                                                               210 GCGCCCCCTCTACATTGACTTCCGACAGGATCTGGGCTGGAAGTGGGTCC 259
                                                                                                                                          17 lArgProLeuTyrlleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
                                                                                                                                                                                                                                67
                                                                                                                                                                                                                                                                         84
                                                                                                                                                                                                                                                                                                                                                                                                     seq_name: /SIDS1/gcgdata/geneseq/geneseqn/NA1990.DAT:AAQ06845
                                                                                                                                                                                                                               LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh
                                                                                                                                                                                                                                                                        67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG
Length: 112
Gaps: 0
Percent Identity: 98.214
                                                                                                                                                                                                                                                                                                                                                           101 LeuSerAsnMetValValLysSerCysLysCysSer 112
                                                                                                                                                                                                                                                                                                                                                                        460 CTCTCCAACATGTCGTGAAGTCTTGTAAATGTAGC 495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence encoding tumour growth inhibitor.
                                                                           to: 498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
263..1501
                                                                           Align seg 1/1 to: AAT06496 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                            seq_documentation_block:
ID AAQ06845 standard; cDNA; 2530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               89US-0353410.
85US-0725003.
86US-0847931.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            90WO-US02753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /*tag= a
2506..2511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               05-MAR-1991 (first entry)
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620.00
5.586
99.107
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2529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /*tag=
                     Percent Similarity:
             Ratio:
                                          alignment_block:
TGFB3P x AAT06496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      psoriasis; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17-MAY-1989;
19-APR-1985;
07-APR-1986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               polyA_signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17-MAY-1990;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29-NOV-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   polyA_site
                                                                                                                                                                                                                               51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Key
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20-0CT-1986; 20-0CT-1987; 20-APR-1988;

KK,

Iwata

wounds.

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This sequence encodes porcine transforming growth factor-beta 3 (TGF-beta 3) polypeptide. The nucleic acid sequence encoding this subtype is useful as a probe or to produce TGF-beta 3 for both normal and neoplastic cell growth inhibition.
                                                                                                                                                                                                                                                                                                                                                                                                            Nucleotide sequence encoding transforming growth factor beta-3 -used probe, or to produce TGF beta 3, for inhibition of growth of normal and neoplastic cells, eg A549.
                                                                                                               Transforming growth factor beta-3 (TGF beta 3); tumour cells; growth inhibition.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2676 BP; 704 A; 705 C; 699 G; 568 T; 0 other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length: 112
Gaps: 0
Percent Identity: 97.321
                                                                                   cDNA sequence encoding porcine TGF-beta 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          to: 2676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Fig. 4; 61pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Align seg 1/1 to: AAQ02819 from: 1
                                                                                                                                                                                                                                                              88WO-UO01945.
                                                                                                                                                                                                                                88WO-US01945
                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       612.00
5.564
98.214
                                                                                                                                                                                                                                                                                                                              Dernyck RM, Goeddel DV;
                                                                                                                                                                                                                                                                                              (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                             WPI; 1990-007474/01.
                                                                                                                                                                                                                                                                                                                                                                            P-PSDB; AAR04080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TGFB3P x AAQ02819
                                                   31-MAY-1989
                                                                                                                                                                                                                                08-JUN-1988;
                                                                                                                                                                                                                                                              08-JUN-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alignment_scores:
                                                                                                                                                              WO8912101-A
                                                                                                                                                                                                 14-DEC-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        alignment_block
                   AAQ02819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1225
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      Foulkes JG;
                                                                                                                                                                                                                                                                     The plasmid was isolated from a human cDNA library prepd. from the DNA of a chronic myelocytic leukaemia cell line (K562). The sequence can be used to produce the tumour growth inhibitor (TGI) by recombinant techniques. The protein may also be isolated from human umbilical cord and placental tissues. It can be used to inhibit tumour cell growth, to treat burns, to facilitate the healing of wounds or to treat proliferative disorders. The protein and Abs raised to it can be used for detection and typing the TGI.
                                                                                                                                                                             Tissue-derived tumour growth inhibitors - comprise specified protein sequences used to detect, and treat tumours, burns and
                                                                                                  ĽI,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1213 GCGCCCCCTCTACATTGACTTCCGACAGGATCTGGGCTGGAAGTGGGTCC 1262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17 largProLeuTyrIleaspPheargGlnAspLeuGlyTrpLysTrpValH 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_name: /SIDS1/gcgdata/geneseq/genesegn/NA1990.DAT:AAQ02819
                                                                                                  Gold
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2530 BP; 619 A; 671 C; 659 G; 581 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps: 0
Percent Identity: 97.321
                                                                                                  ď,
                                                                                                  Franco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1463 CTCTCCAACATGGTGGTGAAGTCTTGTAAATGTAGC 1498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LeuSerAsnMetValValLysSerCysLysCysSer 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        to: 2530
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                                                                                              Tendijke
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Align seg 1/1 to: AAQ06845 from: 1
                                                                                                                                                                                                                                            Claim 10; Fig 41; 190pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_documentation_block:
ID AAQ02819 standard; DNA; 2676 BP
86US-0992121.
87US-0111022.
88US-0183224.
                                                                                              Stephenson JR,
                                                                (ONCO-) ONCOGENE SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        617.00
5.559
99.107
                                                                                                                              WPI; 1990-375949/50
                                                                                                                                               P-PSDB; AAR08264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Quality:
Ratio:
Percent Similarity:
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TGFB3P x AAQ06845

1313 ( 21

101

alignment\_block

alignment\_scores:

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29 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh

34

lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH

17

20 34

101 51 151 29

34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr

LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh

67

84

luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100 251 AGCCCCTGACCATCCTGTACTATGTTGGGAGGACCCCCAAAGTGGAGCAG 300

84

LeuSerAsnMetValValLysSerCysLysCysSer 112 301 CTCTCCAACATGGTGGTGAAGTCTTGTAAATGTAGC 336

101

rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG

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The invention covers hybrid TGF-beta molecules consisting of parts of the human isoforms TGF-beta1, TGF-beta2 and TGF-beta3 (see AAQ41599, AAQ41601 and AAQ41601, respectively). The hinge points between parts derived from different parent isoforms are pref. between amino acids 44 and 45, 56 and 57, 79 and 80, 90 and 91, or 22 and 23. Of the 30 possible hyprids using these hinge points and one part each from two of the isoforms, 6 are preferred including the hybrid TGF-beta1(44/45)beta3. The hybrid molecules promote cell migration, inhibit the growth of A375 melanoma cells, accelerate the healing of partial-thickness burn wounds and full-thickness incisional wounds and full-takeness incisional wounds and scenarios.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                portions of mature TGF-beta isoforms; useful as wound healants, cardioprotective, antiinflammatory and immunosuppressive agents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New hybrid transforming growth factor-beta molecules - comprise
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /*tag= a
/note= "TGF-beta1=1-132, TGF-beta3=133-336"
                                                                                                                                                  seq_name: /SIDS1/gcgdata/geneseq/geneseqn/NA1993.DAT:AAQ41603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hTGF-betal; hTGF-beta3; hybrid protein; wound healing; cancer treatment; bone repair; growth regulation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Transforming Growth Factor-beta1(44/45)beta3 hybrid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 336 BP; 75 A; 109 C; 86 G; 66 T; 0 other;
                                                                       1475 CTCTCTAACATGGTGGTGAAGTCCTGCAAGTGCAGC 1510
101 LeuSerAsnMetValValLysSerCysLysCysSer 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cerletti N, Kuhla J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 8; Page 26-27; 48pp; English.
                                                                                                                                                                                                                                                               BP.
                                                                                                                                                                                                                                                               AAQ41603 standard; cDNA; 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        92EP-0810845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               91EP-0810870
                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (CIBA ) CIBA GEIGY AG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1993-161126/20.
                                                                                                                                                                                                                             seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P-PSDB; AAR39642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              McMaster GK,
                                                                                                                                                                                                                                                                                                                                                                                                      26-AUG-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        03-NOV-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11-NOV-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19-MAY-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EP542679-A
                                                                                                                                                                                                                                                                                                                                  AAQ41603;
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A DNA sequence (AAT17237) codes for a recombinant hybrid of human transforming growth factor-beta, TGF-beta 1-3 (AAR92775), in which the N-terminal 44 amino acids are from TGF-beta 1 (see also AAR92773) and the C-terminal 68 amino acids from TGF-beta 3 (see also AAR92772). The DNA was subcloned in pPLMu, yielding plasmid pPLMu.hTGF-beta 1 (44.45)beta3. Non-soluble, monomeric hybrid TGF-beta 1-3 was recovered from E. coli transformants. A biologically active, dimeric form of the hybrid was obtd. by refolding the monomer in detergent-free buffer contg. DMSO and/or DMF. Hybrid dimers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Prodn. of dimeric biologically active transforming growth factor by refolding denatured monomer in detergent-free folding buffer contg. specific organic solvent to improve yield
                                                                                                                                                                                    Transforming growth factor type beta; TGF-beta 1; TGF-beta 3; protein renaturation; protein folding; ds.
seq_name: /SIDS1/gcgdata/geneseq/geneseqn/NA1996.DAT:AAT17237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 10; Page 36-37; 54pp; English.
                                seq_documentation_block:
ID AAT17237 standard; DNA; 336 BP
                                                                                                                                                                                                                                                                                                                                        95WO-EP02719
                                                                                                                                                                                                                                                                                                                                                                       94EP-0810439
                                                                                                                  17-JUL-1996 (first entry)
                                                                                                                                                   Hybrid TGF-beta 1-3 DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1996-117000/12.
                                                                                                                                                                                                                                                                                                                                                                                                        (CIBA ) CIBA GEIGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P-PSDB; AAR92775
                                                                                                                                                                                                                                                                                                                                                                       25-JUL-1994;
                                                                                                                                                                                                                                                                                                                                      12-JUL-1995;
                                                                                                                                                                                                                                                                    WO9603433-A1
                                                                                                                                                                                                                                                                                                     08-FEB-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                         Cerletti N;
                                                                                                                                                                                                                                     Synthetic.
                                                                                 AAT17237;
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1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17

Align seg 1/1 to: AAQ41603 from: 1 to: 336

Gaps: 0 Percent Identity: 92.857

595.00 5.459 97.321

Quality: Ratio:

alignment\_scores

Percent Similarity:

TGFB3P x AAQ41603

alignment\_block

Length:

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TGF-beta 2-3 (AAR92776) and TGF-beta 3-2 (AAR92777) were similarly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /*tag= c
/note= "encodes C-terminal 68 amino acids of
                                                                                                                                                                                              300
                                                                                                                                                                                                                                                                                                                                     84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
                                                                                                                                                                   20
                                                                                                                                                                                  17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
                                                                                                                                                                                                                       34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
                                                                                                                                                                                                                                                                                                  84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "encodes N-terminal 44 amino acids
                                                                                                                                                1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17
                                                                                                                                                                                                                                                             LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
                                                                                                                                                                                                                                                                                                                                                                                                             seq_name: /SIDS1/gcgdata/geneseq/genesegn/NA1996.DAT:AAT15465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Transforming growth factor beta; TGF; regulator; method; proliferation; differentiation; wound healing; solvent;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              encoding human TGF-beta-like protein, TGF-beta-1-3.
                                                                                                                                                                                                                                                                                                                                               rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG
                                                                        Gaps: 0
Percent Identity: 92.857
                          66 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /*tag= a
/product= hybrid_TGF-beta-1-3
                                                                                                                                                                                                                                                                                                                                                                                   LeuSerAsnMetValValLysSerCysLysCysSer 112
                                                               Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                          BP
                                                                                                                               to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Transforming growth factor beta; TGF;
                                                                                                                                                                                                                                                                                                                                                                                                                               seq_documentation_block:
ID AAT15465 standard; cDNA to mRNA; 336
                           ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TGF-beta-1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGF-beta-3"
                          Sequence 336 BP; 75 A; 109 C; 86
                                                                                                                             Align seg 1/1 to: AAT17237 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
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                                                                       5.459
97.321
                                                              595.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1..132
/*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1..336
/*tag=
                                                             Quality:
                                                                               Percent Similarity:
                                                                        Ratio
                                                                                                           TGFB3P x AAT17237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10-JUN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                      alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mat_peptide
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                                                                                                   alignment_block:
         produced
                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAT15465
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                                                                                                                                                                                                                                                            21
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AAT15465 encodes transforming growth factor (TGF) beta-like protein, TGF-beta-1-3. TGF beta-1-3 is a hybrid of TGF-1 and TGF-3. TGF beta hybrids were made using a new process of producing dimeric, blologically active TGF beta-like proteins. The new process involves treating denatured TGF beta-like proteins. The new process involves treating denatured TGF beta-like proteins. The new process involves mild detergent (CHAPS, CHAPSO or digitonin) and at least one of the solvents DMSO (dimethyl sulphoxide), DMSO2 (dimethylsulphone) and DMF (dimethyl formamide). The detergent allows folding of the monomer such that, after dimerisation, the TGF beta-like protein retains biological activity and remains in soluble form. The method allows relatively high yields of biologically active TGF beta-like proteins in their native dimeric form. TGF-beta like proteins are multifunctional regulators of cellular activity and a typical use is to stimulate wound
                                                                                                                                                                                                                                                                                                                                 factor
                                                                                                                                                                                                                                                                                                                           Prodn. of dimeric, biologically active transforming growth f
beta - by refolding denatured monomer in buffer contg. mild
detergent and specific organic solvents to improve yields
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    51 GCGCCAGCTGTACATTGACTTCCGCAAGGACCTCGGCTGGAAGTGGATCC 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percent Identity: 92.857
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 336 BP; 75 A; 109 C; 86 G; 66 T; 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            to: 336
                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 17; Page 39-40; 59pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Align seg 1/1 to: AAT15465 from: 1
                                              95WO-EP02718
                                                                                               94EP-0810438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              595.00
5.459
97.321
                                                                                                                                                                                                                                                   WPI; 1996-116999/12.
                                                                                                                                                GEIGY
                                                                                                                                                                                                                                                                             P-PSDB; AAR91959
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alignment_block:
TGFB3P x AAT15465
                                              12-JUL-1995;
                                                                                               25-JUL-1994;
                                                                                                                                                (CIBA ) CIBA
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08-FEB-1996
                                                                                                                                                                                                    Cerletti N;
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51

 34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50

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The invention covers hybrid TGF-beta molecules consisting of parts of the human isoforms TGF-beta1, TGF-beta2 and TGF-beta3 (see AAQ41599, AAQ41600 and AAQ41601. TGF-beta2, TGF-beta2 and TGF-beta3 (see AAQ41599, derived from different parent isoforms are pref. between parts possible hybrids using these hinge points and one part each from two of the isoforms, 6 are preferred including the hybrid TGF-beta2(44/45)beta3. The hybrid molecules promote cell migration, inhibit the growth of A375 melanoma cells, accelerate the healing of partial-thickness burn wounds and full-thickness incisional wounds and full-thickness incisional wounds and increase formation of fibrous granular tissue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New hybrid transforming growth factor-beta molecules - comprise portions of mature TGF-beta isoforms; useful as wound healants, cardioprotective, antiinflammatory and immunosuppressive agents etc.
                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
1.336
7.tag= a
/note= "TGF-beta2=1-132, TGF-beta3=133-336"
                                                               seq_name: /SIDS1/gcgdata/geneseq/geneseqn/NA1993.DAT:AAQ41605
                                                                                                                                                                                                                                           hTGF-beta2; hTGF-beta3; hybrid protein; wound healing; cancer treatment; bone repair; growth regulation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New hybrid transforming growth factor-beta molecules
                                                                                                                                                                                                             Transforming Growth Factor-beta2(44/45)beta3 hybrid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 336 BP; 81 A; 94 C; 84 G; 77 T; 0 other;
LeuSerAsnMetValValLysSerCysLysCysSer 112
                Cerletti N, Kuhla J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 8; Page 29-30; 48pp; English.
                                                                                             seq_documentation_block:
ID AAQ41605 standard; cDNA; 336 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           92EP-0810845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         91EP-0810870
                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (CIBA ) CIBA GEIGY AG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1993-161126/20.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        McMaster GK,
                                                                                                                                                                             26-AUG-1993
                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           03-NOV-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11-NOV-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                           19-MAY-1993
                                                                                                                                                                                                                                                                                                                                            mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                           EP542679-A
                                                                                                                                             AAQ41605;
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A DNA sequence (AAT17238) codes for a recombinant hybrid of human transforming growth factor-beta, TGF-beta 2-3 (AAR92776), in which the N-terminal 44 amino acids are from TGF-beta 2 (see also AAR92774) and the C-terminal 68 amino acids from TGF-beta 3 (see also AAR92772). The DNA was subcloned in pPLMu, yielding plasmid pPLMu.hTGF-beta 2 (44/45)beta3. Non-soluble, monomeric hybrid TGF-beta 1-3 was recovered from E. coli LC137 transformants. A biologically active, dimeric form of the hybrid was obdd. by refolding the monomer in detergent-free buffer contg. DMSO and/or DMF. Hybrid dimers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Prodn. of dimeric biologically active transforming growth factor by refolding denatured monomer in detergent-free folding buffer contg. specific organic solvent to improve yield
                                                                                                                                                                                                                                                                                                                                                                                                                          Transforming growth factor type beta; TGF-beta 2; TGF-beta 3; protein renaturation; protein folding; ds.
                                                                                                                                                   67
                                                                                                 84
                                                                                                                                                                                                                                                                    seq_name: /SIDS1/gcgdata/geneseq/geneseqn/NA1996.DAT:AAT17238
                                                                                             LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh
                                                                                                                                                                                                           Example 10; Page 39-40; 54pp; English.
                                                                                                                                                                                                                                                                                               seq_documentation_block:
ID AAT17238 standard; DNA; 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         95WO-EP02719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94EP-0810439
                                                                                                                                                                                                                                                                                                                                                                 17-JUL-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                              Hybrid TGF-beta 2-3 DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (CIBA ) CIBA GEIGY AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1996-117000/12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P-PSDB; AAR92776.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO9603433-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12-JUL-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25-JUL-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           08-FEB-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cerletti N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic
                                                                                                                                                                                                                                                                                                                                        AAT17238;
                                      51
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1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17

to: 336

to: AAQ41605 from: 1

Length: 112 Gaps: 0 Percent Identity: 91.071

591.00 5.373 98.214

Quality: Ratio:

alignment\_scores

Percent Similarity:

TGFB3P x AAQ41605

Align seg 1/1

alignment\_block;

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251 AGCCCCTGACCATCCTGTACTATGTTGGGAGGACCCCCAAAGTGGAGCAG
 TGF-beta 1-3 (AAR92775) and TGF-beta 3-2 (AAR92777) were similarly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     of
                                                                                                                                                                                             luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
                                                                                                                                                                                                                                                                                                                                             84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /*tag= c
/note= "encodes C-terminal 68 amino acids
TGF-beta-3"
                                                                                                                                                1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17
                                                                                                                                                        51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     amino acids
                                                                                                                                                                                                                                                                                                                                                                                                            seq_name: /SIDS1/gcgdata/geneseq/geneseqn/NA1996.DAT:AAT15466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cDNA encoding human TGF-beta-like protein, TGF-beta-2-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Transforming growth factor beta; TGF; regulator; method; proliferation; differentiation; wound healing; solvent;
                                                                                                                                                                                   17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH
                                                                                                                                                                                                                                                                                               rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG
                                                                                                                                                                                                                        34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr
                                                               Length: 112
Gaps: 0
Percent Identity: 91.071
                           G; 77 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /*tag= b
/note= "encodes N-terminal 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product= hybrid_TGF-beta-2-3
                                                                                                                                                                                                                                                                                                                                                                        LeuSerAsnMetValValLysSerCysLysCysSer 112
                                                                                                                                                                                                                                                                                                                                                                                 Align seg 1/1 to: AAT17238 from: 1 to: 336
                                                                                                                                                                                                                                                                                                                                                                                                                             seq_documentation_block:
ID AAT15466 standard; cDNA to mRNA; 336 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                growth factor beta; TGF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
1..336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TGF-beta-2"
                          84
                          ΰ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10-JUN-1996 (first entry)
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                                                              591.00
5.373
98.214
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                          81 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /*tag=
                          BP;
                                                               Quality:
                                                                               Percent Similarity:
                                                                        Ratio
                                                                                                 alignment_block:
TGFB3P x AAT17238
                          Sequence 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Transforming
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                      alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mat_peptide
        produced
                                                                                                                                                                                                                                                                                                                                   84
                                                                                                                                                                                                                                                                                                                                                                        101
                                                                                                                                                                                                                                                                                                                                                                                         301
                                                                                                                                                                                                                                                                             151
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55 X 88
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AAT15466 encodes transforming growth factor (TGF) beta-like protein, TGF-beta-2-3. TGF beta-2-3 is a hybrid of TGF-2 and TGF-3. TGF beta byblids were made using a new process of producing dimeric, biologically active TGF beta-like proteins. The new process involves treating denatured TGF beta-nonemers with folding buffer contg. a mild detergent (CHAPS, CHAPSO or digitonin) and at least one of the solvents DMSO (dimethyl sulphoxide), DMSO2 (dimethylsulphoxel) and DMF (dimethyl formamide). The detergent allows folding of the monomer such that, after dimerisation, the TGF beta-like protein retains biological activity and remains in soluble form. The method allows relatively high yields of biologically active TGF beta-like proteins in their native dimeric form. TGF-beta like proteins are multifunctional requiators of cellular activity and a typical use is to stimulate wound
                                                                                                                                                                                                                                                                                                                                        Prodn. of dimeric, biologically active transforming growth f
beta - by refolding denatured monomer in buffer contg. mild
detergent and specific organic solvents to improve yields
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GCTTTGGATGCGGCCTATTGCTTTAGAAATGTGCAGGATAATTGCTGCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       51 ACGTCCACTTTACATTGATTTCAAGAGGGATCTAGGGTGGAAATGGATAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Identity: 91.071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          84 G; 77 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 17; Page 42; 59pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Align seg 1/1 to: AAT15466 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 336 BP; 81 A; 94 C;
                                                                                       95WO-EP02718
                                                                                                                                  94EP-0810438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5.373
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                                                                                                                                                                              (CIBA ) CIBA GEIGY AG
                                                                                                                                                                                                                                                                      WPI; 1996-116999/12.
P-PSDB; AAR91960.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TGFB3P x AAT15466
WO9603432-A1
                                                                                     12-JUL-1995;
                                                                                                                                  25-JUL-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alignment_scores:
                                          08-FEB-1996
                                                                                                                                                                                                                           Cerletti N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alignment_block
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   34
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The invention covers hybrid TGF-beta molecules consisting of parts of the human isoforms TGF-beta1, TGF-beta2 and TGF-beta3 (see AAQ41599, AAQ41601, respectively). The hinge points between parts derived from different parent isoforms are pref. between amino acids 44 and 45, 56 and 57, 79 and 80, 90 and 91, or 22 and 23. Of the 30 possible hybrids using these hinge points and one part each from two of the isoforms, 6 are preferred, esp. the hybrid TGF-beta3(44/45)beta2. The hybrid molecules promote cell migration, inhibit the growth of A375 melanoma cells, accelerate the healing of partial-thickness burn wounds and full-thickness incisional wounds and increase formation of fibrous granular tissue.

See AAQ41602-Q41606 for the other pref. hybrids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New hybrid transforming growth factor-beta molecules - comprise portions of mature TGF-beta isoforms; useful as wound healants, cardioprotective, antiinflammatory and immunosuppressive agents etc.
                                                                                                                                                                                                                                                                                                                                                  /*tag= a
/note= "TGF-beta3=1-132, TGF-beta2=133-336"
                                                              seq_name: /SIDS1/gcgdata/geneseq/geneseqn/NA1993.DAT:AAQ41607
                                                                                                                                                                                                                                    hTGF-beta2; hTGF-beta3; hybrid protein; wound healing; cancer treatment; bone repair; growth regulation; ss.
                                                                                                                                                                                                        Transforming Growth Factor-beta3(44/45)beta2 hybrid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 336 BP; 88 A; 87 C; 71 G; 90 T; 0 other;
Cerletti N, Kuhla J;
                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                             _documentation_block:
AAQ41607 standard; cDNA; 336 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 9; Page 32; 48pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            92EP-0810845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           91EP-0810870
                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                  1..336
/*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cox D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1993-161126/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (CIBA ) CIBA GEIGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P-PSDB; AAR39646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        McMaster GK,
                                                                                                                                                                          26-AUG-1993
                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                            03-NOV-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11-NOV-1991;
                                                                                                                                                                                                                                                                                                                    Key
mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                              19-MAY-1993
                                                                                                                                                                                                                                                                                                                                                                                              EP542679-A.
                                                                                                                                           AAQ41607;
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LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh

51

84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100

51

34

```
A DNA sequence (AAT17239) codes for a recombinant hybrid of human transforming growth factor-beta, TGF-beta 3-2 (AAR92777), in which the N-terminal 44 amino acids are from TGF-beta 3 (see also AAR92772) and the C-terminal 68 amino acids from TGF-beta 2 (see also AAR92774). The DNA was subcloned in pPLMu, yielding plasmid pPLMu.hTGF-beta 3(4445)beta2. Non-soluble, monomeric hybrid TGF-beta 3-2 was recovered from E. coli LC137 transformants. A biologically active, dimeric form of the hybrid was obtd. by refolding the monomer in detergent-free buffer contg. DMSO and/or DMF. Hybrid dimers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Prodn. of dimeric biologically active transforming growth factor
by refolding denatured monomer in detergent-free folding buffer
contg. specific organic solvent to improve yield
                                                                                                                                                                                        Transforming growth factor type beta; TGF-beta 2; TGF-beta 3; protein renaturation; protein folding; ds.
seq_name: /SIDS1/gcgdata/geneseq/geneseqn/NA1996.DAT:AAT17239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 10; Page 41-42; 54pp; English.
                                                 AAT17239 standard; DNA; 336 BP
                                                                                                                                                                                                                                                                                                                                             95WO-EP02719
                                                                                                                                                                                                                                                                                                                                                                               94EP-0810439
                                                                                                                     17-JUL-1996 (first entry)
                                                                                                                                                      Hybrid TGF-beta 3-2 DNA
                                                                                                                                                                                                                                                                                                                                                                                                                 (CIBA ) CIBA GEIGY AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1996-117000/12.
                                   seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P-PSDB; AAR92777
                                                                                                                                                                                                                                                                                                                                                                               25-JUL-1994;
                                                                                                                                                                                                                                                                           WO9603433-A1
                                                                                                                                                                                                                                                                                                                                           12-JUL-1995;
                                                                                                                                                                                                                                                                                                           08-FEB-1996.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cerletti N;
                                                                                                                                                                                                                                          Synthetic.
                                                                                   AAT17239;
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1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17

to: 336

Align seg 1/1 to: AAQ41607 from: 1

Percent Identity: 88.393

577.00 5.393 95.536

Percent Similarity:

TGFB3P x AAQ41607

alignment\_block:

Quality: Ratio:

alignment\_scores

Gaps:

Length:

TGF-beta 1-3 (AAR92775) and TGF-beta 2-3 (AAR92776) were similarly produced. of of 51 GCGCCCCTCTACATTGACTTCCGACAGGATCTGGGCTGGAAGTGGGTCC 100 84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100 50 84 acids /\*tag= c /note= "encodes C-terminal 68 amino acids 1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17 17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34 51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67 seq\_name: /SIDS1/gcgdata/geneseq/geneseqn/NA1996.DAT:AAT15467 cDNA encoding human TGF-beta-like protein, TGF-beta-3-2. regulator; method; proliferation; differentiation; wound healing; solvent; 34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG amino Length: 112 Gaps: 0 Percent Identity: 88.393 90 T; 0 other; /\*tag= b /note= "encodes N-terminal 44 /product= hybrid\_TGF-beta-3-2 LeuSerAsnMetValValLysSerCysLysCysSer 112 301 CTTTCTAATATGATTGTAAAGTCTTGCAAATGCAGC 336 Align seg 1/1 to: AAT17239 from: 1 to: 336 ВÞ Transforming growth factor beta; TGF; seq\_documentation\_block:
ID AAT15467 standard; cDNA to mRNA; 336 Location/Qualifiers TGF-beta-3" TGF-beta-2" Ü C; 71 (first entry) Sequence 336 BP; 88 A; 87 ø 577.00 5.393 95.536 133..336 /\*tag= Quality: Percent Similarity: alignment\_block: TGFB3P x AAT17239 Homo sapiens alignment\_scores: 10-JUN-1996 mat\_peptide mat\_peptide 101 Key SSXS 

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AAT15467 encodes transforming growth factor (TGF) beta-like protein, TGF-beta-3-2. TGF beta-3-2 is a hybrid of TGF-3 and TGF-2. TGF beta blybrids were made using a new process of producing dimeric, biologically active TGF beta-like proteins. The new process involves treating denatured TGF beta monomers with folding buffer contg. a mild detergent (CHAPS, CHAPSO or digitonin) and at least one of the solvents DMSO (dimethyl sulphoxide), DMSO2 (dimethylsulphone) and DMF (dimethyl formamide). The detergent allows folding of the monomer such that, after dimerisation, the TGF beta-like protein retains biological activity and remains in soluble form. The method allows relatively high yields of biologically active TGF beta-like proteins in their native dimeris form, TGF-beta like proteins are multifunctional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               requiators of cellular activity and a typical use is to stimulate wound
                                                                                                                                                                                                                                                                                                                                                                                                        factor
                                                                                                                                                                                                                                                                                                                                                                                                   Prodn. of dimeric, biologically active transforming growth f
beta - by refolding denatured monomer in buffer contg. mild
detergent and specific organic solvents to improve yields
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TTATGGAGTTCAGACACTCAGCACAGGGTCCTGAGCTTATATAC 200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 GCTTTGGACACCAATTACTGCTTCCGCAACTTGGAGGAGCTGCTGTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         isGluProLysGlyTyrAlaAsnPheCysSerGlyProCysProTyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    201 CATAAATCCAGAAGCATCTGCTTCTCCTTGCTGCGTGTCCCAAGATTTAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length: 112
Gaps: 0
Percent Identity: 88.393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 336 BP; 88 A; 87 C; 71 G; 90 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Align seg 1/1 to: AAT15467 from: 1 to: 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 17; Page 44-45; 59pp; English.
                                                                                                    95WO-EP02718
                                                                                                                                                          94EP-0810438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         577.00
5.393
95.536
                                                                                                                                                                                                               (CIBA ) CIBA GEIGY AG
                                                                                                                                                                                                                                                                                                                 WPI; 1996-116999/12.
P-PSDB; AAR91961.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TGFB3P x AAT15467
W09603432-A1
                                                                                                    12-JUL-1995;
                                                                                                                                                          25-JUL-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alignment_scores:
                                                  08-FEB-1996
                                                                                                                                                                                                                                                                    Cerletti N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alignment_block
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            34
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34

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17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH
                                                                                                                                                    51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention covers hybrid TGF-beta molecules consisting of parts AQ41509 of the human isoforms TGF-beta1, TGF-beta2 and TGF-beta3 (see AAQ4159), AAQ41600 and AAQ41601, respectively). The hinge points between parts derived from different parent isoforms are pref. between amino acids 44 and 45, 56 and 57, 79 and 80, 90 and 91, or 22 and 23. Of the 30 possible hybrids using these hinge points and one part each from two of the isoforms, 6 are preferred including the hybrid TGF-beta1(44/45)beta2. The hybrid molecules promote cell migration, inhibit the growth of A375 melanoma cells, accelerate the healing of partial-thickness burn wounds and full-thickness incisional wounds and full-traisme. See also AAQ41603-Q41607 for the other pref. hybrids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New hybrid transforming growth factor-beta molecules - comprise portions of mature TGF-beta isoforms; useful as wound healants, cardioprotective, antiinflammatory and immunosuppressive agents etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /*tag= a
/note= "TGF-betal=1-132, TGF-beta2=133-336"
                                                                                                                 seq_name: /SIDS1/gcgdata/geneseq/geneseqn/NA1993.DAT:AAQ41602
                                                                                                                                                                                                                                                                                                                                                                                                                            hTGF-betal; hTGF-beta2; hybrid protein; wound healing; cancer treatment; bone repair; growth regulation; ss.
                                                                                                                                                                                                                                                                                                                                                                       Transforming Growth Factor-betal(44/45)beta2 hybrid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 336 BP; 90 A; 92 C; 72 G; 82 T; 0 other;
Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cerletti N, Kuhla J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 8; Page 25-26; 48pp; English.
                                                                                                                                                                                                     BP
                                                                                                                                                                        _documentation_block:
AAQ41602 standard; cDNA; 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    92EP-0810845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        91EP-0810870
                                                                                                                                                                                                                                                                                                                   (first entry)
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92.857
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1993-161126/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (CIBA ) CIBA GEIGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P-PSDB; AAR39641
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   McMaster GK,
                                                                                                                                                                                                                                                                                                                   26-AUG-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11-NOV-1991;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mat_peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EP542679-A
                                                                                                                                                                                                                                                            AAQ41602;
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NO YOU COULD COULD BE A STANK A STANK

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The invention covers hybrid TGF-beta molecules consisting of parts of the human isoforms TGF-beta1, TGF-beta2 and TGF-beta3 (see AAQ41599, AAQ41600 and AAQ41601, respectively). The hinge points between parts derived from different parent isoforms are pref. between amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New hybrid transforming growth factor-beta molecules - comprise portions of mature TGF-beta isoforms; useful as wound healants, cardioprotective, antiinflammatory and immunosuppressive agents etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1..336
/*tag= a
/note= "TGF-beta3=1-132, TGF-beta1=133-336"
                                                                                          luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
                                                                                                                                                                seq_name: /SIDS1/gcgdata/geneseq/geneseqn/NA1993.DAT:AAQ41606
                                       LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh
                                                                                                                                                                                                                                                                                                                                                                                                            hTGF-betal; hTGF-beta3; hybrid protein; wound healing; cancer treatment; bone repair; growth regulation; ss.
                                                                                                                                                                                                                                                                                                                                                                                   Transforming Growth Factor-beta3(44/45)betal hybrid.
                                                                                                                                                                                                       LeuSerAsnMetValValLysSerCysLysCysSer 112
                                                                                                                                                                                                                                 301 CTTTCTAATATGATTGTAAAGTCTTGCAAATGCAGC 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cerletti N, Kuhla J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 8; Page 30-31; 48pp; English.
                                                                                                                                                                                                                                                                                        seq_documentation_block:
ID AAQ41606 standard; cDNA; 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        92EP-0810845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   91EP-0810870
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cox D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1993-161126/20.
P-PSDB; AAR39645.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        McMaster GK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        03-NOV-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11-NOV-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19-MAY-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EP542679-A.
                                                                                                                                                                                                                                                                                                                              AAQ41606;
                                                                                                                                                                                                       101
                                       21
                                                                                                                                                   84
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1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17

Align seg 1/1 to: AAQ41602 from: 1 to: 336

Percent Identity: 81.250

Percent Similarity:

TGFB3P x AAQ41602

alignment\_block:

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44 and 45, 56 and 57, 79 and 80, 90 and 91, or 22 and 23. Of the 30 possible hybrids using these hinge points and one part each from two of the isoforms; 6 are preferred including the hybrid TGF-beta3(44/45)beta1 The hybrid molecules promote cell migration, inhibit the growth of A375 melanoma cells, accelerate the healing of partial-thickness burn wounds and full-thickness incisional wounds and increase formation of fibrous granular tissue. See AAQ41602-Q41607 for the most pref. hybrids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 201 GCATAACCCGGGGGCGCTCGGCGCGCGTGCTGCGTGCCGCAGGCGCTGG 250
                                                                                                                                                                                                                                                                                                                                 84
                                                                                                                                                                                                                                                                                                                                                                                             lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                      34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_name: /SIDS1/gcgdata/geneseq/geneseqn/NA1991.DAT:AAQ11994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SS
                                                                                                                                                                                                                             Percent Identity: 83.929
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGF-beta2; biologically active protein production;
                                                                                                                                     Sequence 336 BP; 63 A; 109 C; 98 G; 66 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LeuSerAsnMetValValLysSerCysLysCysSer 112
||||||||||||||||
|CGTCCAACATGATCGTGCGCTCCTGCAAGTGCAGC 336
                                                                                                                                                                                                                 Gaps:
                                                                                                                                                                                                 Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Encodes Transforming Growth Factor beta 2.
                                                                                                                                                                                                                                                                                                       to:
                                                                                                                                                                                                                                                                                                     from: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              90EP-0810922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                     Align seg 1/1 to: AAQ41606
                                                                                                                                                                                              538.00
5.327
90.179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_documentation_block
                                                                                                                                                                                                Quality:
                                                                                                                                                                                                                            Percent Similarity:
                                                                                                                                                                                                               Ratio
                                                                                                                                                                                                                                                                       TGFB3P x AAQ41606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
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                                                                                                                                                                                alignment_scores
                                                                                                                                                                                                                                                          alignment_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAQ11994;
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    8888888888
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This coding sequence was isolated from the CI-215 human glioma cell line. It was incorporated into an appropriate vector to transform Sacchamyces cerevisiae or E.Coli. Monomeric TGF-betal was purified, denatured and dissolved in 140ml 50mm Tris/HCl pH8. IM NaCl, 5mM EDTA, 2mM reduced glutathione, 1mM oxidised glutathione and 33mM Chaps. After 72 hrs at 4 deg C, pH was adjusted to 2.5 and the mixture was conc. 10 times. The conc. soln was diluted to the original vol. with 10mM HCl and conc to a final vol of 10 ml. The supernatant from centrifugation at 5000g for 30 min contained disulphide-linked dimeric
                                                                                                                  bγ
                                                                                                                Prodn. of Transforming Growth Factor type-beta-like proteins subjecting denatured monomeric form to refolding conditions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17
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                                B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq_name: /SIDS1/gcgdata/geneseq/geneseqn/NA1993.DAT:AAQ41600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACGAACCCAAAGGGTACAATGCCAACTTCTGTGCTGGAGCATGCCCGTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Identity: 79.464
                                                                                                                                                                                                                                                                                                                                                                                  Sequence 339 BP; 98 A; 77 C; 70 G; 94 T; 0 other;
                                Schmitz A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                101 LeuSerAsnMetValValLysSerCysLysCysSer 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        to: 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  301 CTTTCTAATATGATTGTAAAGTCTTGCAAATGCAGC
                                á
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Align seg 1/1 to: AAQ11994 from: 1
                                                                                                                                                                 Example; Page 27; 35pp; English.
                                Cox
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                                GK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                    535.00
5.095
93.750
(CIBA ) CIBA GEIGY AG
                                  McMaster
                                                                WPI; 1991-180005/25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seq_documentation_block:
                                                                                 P-PSDB; AAR12403
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percent Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TGFB3P x AAQ11994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26-AUG-1993
                               Cerletti N,
                                                                                                                                                                                                                                                                                                                                                                                                                                          alignment_scores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       alignment_block
                                                                                                                                                                                                                                                                                                                                                   rGF-betaŽ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            101
 AXXXXXX
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251 84

seq\_name: /SIDS1/gcgdata/geneseq/geneseqn/NA1996.DAT:AAT17236

to mRNA; 339

seq\_documentation\_block:
ID AAT17236 standard; cDNA

5;

Transforming growth factor type beta; TGF-beta protein renaturation; protein folding; ds.

(first entry)

17-JUL-1996

AAT17236;

Human TGF-beta 2 cDNA

95WO-EP02719. 94EP-0810439

12-JUL-1995; 25-JUL-1994;

WO9603433-A1 Homo sapiens

08-FEB-1996

AG

(CIBA ) CIBA GEIGY

Cerletti N;

WPI; 1996-117000/12.

201 CATAAATCCAGAAGCATCTGCTTCTCCTTGCTGCGTGTCCCAAGATTTAG 250

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The invention covers hybrid TGF-beta molecules consisting of parts of the human isoforms TGF-beta1, TGF-beta2 and TGF-beta3 (see AAQ41599, AAQ41601, respectively). The hinge points between parts derived from different parent isoforms are pref. between amino acids 44 and 45, 56 and 57, 79 and 80, 90 and 91, or 22 and 23. The hybrid molecules promote cell migration, inhibit the growth of A375 melanoma cells, accelerate the healing of partial-thickness burn wounds and full-thickness incisional wounds and increase formation of fibrous granular tissue. See e.g. AAQ41602-Q41607 for pref. hybrids.
                                                                                                                                                                                                                                                                                                                                                                                          New hybrid transforming growth factor-beta molecules - comprise portions of mature TGF-beta isoforms; useful as wound healants, cardioprotective, antiinflammatory and immunosuppressive agents etc.
                            hTGF-beta2; hybrid protein; wound healing; cancer treatment;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percent Identity: 79.464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 339 BP; 98 A; 77 C; 70 G; 94 T; 0 other;
Mature human Transforming Growth Factor-beta2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps:
                                                                                                                                                                                                                                                                                                                    Cerletti N, Kuhla J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           to: 339
                                             bone repair; growth regulation; ss.
                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 4; Page 22-23; 48pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Align seg 1/1 to: AAQ41600 from: 1
                                                                                                                                                                                                                            92EP-0810845.
                                                                                                                                                                                                                                                          91EP-0810870
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5.095
93.750
                                                                                                                     1..336
/*tag=
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                                                                                                                                                                                                                                                                                                                                              WPI; 1993-161126/20.
P-PSDB; AAR39639.
                                                                                                                                                                                                                                                                                      (CIBA ) CIBA GEIGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TGFB3P x AAQ41600
                                                                                                                                                                                                                                                                                                                    McMaster GK,
                                                                                                                                                                                                                                                       11-NOV-1991;
                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alignment_scores:
                                                                                                                  mat_peptide
                                                                                                                                                                                              19-MAY-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             alignment_block:
                                                                                                                                                               EP542679-A
                                                                                                        Key
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The coding sequence (AAT17236) of human transforming growth factor TGF-beta 2 (AAR92774) was cloned into plasmid pGEM-52F(+) (Promega) and the construct used to transform E. coli Y1090. Subcloning in pPLMu yielded plasmid ppLMu.hTGF-beta 2. Non-soluble, monomeric TGF-beta 2 was recovered from E. coli LC 137/ppLMu.hTGF-beta 2 (DSM 5657) transformants. A biologically active, dimeric form of TGF-beta 2 was obtd. by refolding this monomer in detergent-free buffer contg. DMSO and/or DMF. Dimers of TGF-beta 1 (AAR92773) and TGF-beta 3 (AAR92772), and hybrid dimers (see also AAR92775-77), were
                                                                                                                                                                                                                                                                                                                                                                              Prodn. of dimeric biologically active transforming growth factor by refolding denatured monomer in detergent-free folding buffer contg. specific organic solvent to improve yield
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps: 0
Percent Identity: 79.464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 339 BP; 98 A; 77 C; 70 G; 94 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               to: 339
                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 1B; Page 31-32; 54pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Align seg 1/1 to: AAT17236 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               535.00
5.095
93.750
                                                                                                                                                                                                                                                                                                                                                    P-PSDB; AAR92774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                also produced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alignment_scores:
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51 ACGTCCACTTTACATTGATTTCAAGAGGGATCTAGGGTGGAAATGGATAC 100

isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50

51 121 67

rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84

51

29

101

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or bone morphogenic proteins e.g. BMP-2. The TGF beta hybrids were made using a new process of producing dimeric, biologically active TGF beta-1ike proteins. The new process involves treating denatured TGF beta monomers with folding buffer contg. a mild detergent (CHAPS, CHAPS, or digitonin) and at least one of the solvents DMSO (dimethyl sulphoxide), DMSO2 (dimethylsulphone) and DMF (dimethyl formamide). The detergent allows folding of the monomer such that, after dimethyl the TGF beta-like protein retains blological activity and remains in soluble form. The method allows relatively high yields of blologically active TGF beta-like proteins in their native dimeric form. TGF-beta like proteins are multifunctional regulators of ellular activity and a typical use is to stimulate wound healing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGF active fragment of a TGF-beta fusion protein encoding cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Transforming growth factor-beta fusion protein; wound healing; artificial skin; surgery recovery time; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seq_name: /SIDS1/gcgdata/geneseq/genesegn/NA1997.DAT:AAT42772
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               201 CATAAATCCAGAAGCATCTGCTTCTCCTTGCTGCGTGTCCCAAGATTTAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       251 AACCTCTAACCATTCTCTACTACATTGGCAAAACACCCAAGATTGAACAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG
                                                                                                                                                                                                                                                                                                                                                                                                                                         Percent Identity: 79.464
                                                                                                                                                                                                                                                                                                 Sequence 339 BP; 98 A; 77 C; 70 G; 94 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    101 LeuSerAsnMetValValLysSerCysLysCysSer 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           301 CTTTCTAATATGATTGTAAAGTCTTGCAAATGCAGC 336
                                                                                                                                                                                                                                                                                                                                                                                               Length:
                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            to:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         to: AAT15463 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BP
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ID AAT42772 standard; cDNA; 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
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5.095
93.750
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                          alignment_scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alignment_block
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Align seg 1/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAT42772;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21
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       AAT15462-T15464 encode transforming growth factor (TGF) beta-1, TGF beta-2 and TGF beta-3 which are produced using recombinant DNA technology and used to produce TGF beta-1ike proteins in dimeric form. The TGF beta-1ike proteins produced are hybrids of 2 different types of TGF beta e.g. TGF beta-1-3, TGF beta-2-3, etc,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Prodn. of dimeric, biologically active transforming growth factor beta - by refolding denatured monomer in buffer contg. mild detergent and specific organic solvents to improve yields
                                                                                                                                                                                                                                                                                                                                                                                                        regulator; method;
healing; solvent; ds.
                                                                                                                                                            201 CATAAATCCAGAAGCATCTGCTTCTCTTGCTGCGTGTCCCAAGATTTAG 250
                                                                                                                                  34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
                                                                                                                                                                                                                                                                                                                         84
                                            lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
                                                                                                                                                                                                                           LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_name: /SIDS1/gcgdata/geneseq/geneseqn/NA1996.DAT:AAT15463
GCTTTGGATGCGGCCTATTGCTTTAGAAATGTGCAGGATAATTGCTGCCT
                                                                                                                                                                                                                                                                                                                    rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human transforming growth factor beta 2 encoding cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LeuSerAsnMetValValLysSerCysLysCysSer 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product= human_TGF-beta-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAT15463 standard; cDNA to mRNA; 339 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Transforming growth factor beta; TGF; proliferation; differentiation; wound
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 1; Page 34-35; 59pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94EP-0810438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         95WO-EP02718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1..339
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1996-116999/12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seq documentation block:
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10-JUN-1996

AAT15463

Homo sapiens

WO9603432-A1

08-FEB-1996

12-JUL-1995; 25-JUL-1994;

Cerletti N;

100

50

200

67

150

20

250

84

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A novel transforming growth factor-beta (TGF-beta) fusion protein comprises a purification tag and a TGF active fragment. The present sequence encodes a specifically claimed TGF active fragment.

C Additionally, the fusion protein may comprise proteinase-sensitive linker sites and binding domain so the protein sequence may contain some or all of the following elements: purification tag:proteinase site: ECW binding site:proteinase site:TGF-beta TGF-beta promotes wound healing, and the fusion protein can be used to reduce surgery recovery time and in the preparation of artificial skin. The inclusion of a purification tag facilitates purification of the fusion protein. The proteinase site is included to permit cleavage and release of the purification tag after purification if desired. The extracellular matrix binding site facilitates delivery of the fusion protein to the cleared site of action. Delivery of the TGF-beta to the site to be traced to trace and the amount of TGF-beta required to be administered to
                                                                                                                                                                                                                                                                                                                                                                                            Prepn. of transforming growth factor-beta fusion protein - useful to reduce surgery recovery time and to prepare artificial skin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      be effective and reduces the concentration of circulating {\tt TGF-beta} which {\tt may} result in undesirable effects.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 339 BP; 98 A; 77 C; 70 G; 94 T; 0 other;
/function= TGF active fragment
                                                                                                                                                                                                                                                                                                    Tuan T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 46-47; 59pp; English.
                                                                                                                                                                                                                                                                                                  Nimni ME,
                                                                                                             96WO-US08973.
                                                                                                                                                95US-0470837.
                                                                                                                                                                                  CHEUNG D T. HALL F L. NIMNI M E.
                                                                                                                                                                                                                                                                                                  Cheung DT, Hall FL,
                                                                                                                                                                                                                                                                                                                                       WPI; 1997-043065/04.
                                                                                                                                                                                                                                                                                                                                                          P-PSDB; AAW08174
                                                                                                                                                                                                                                          TUAN T.
                                                                                                                                                06-JUN-1995;
                                                                                                           05-JUN-1996;
                                    WO9639430-A1
                                                                       12-DEC-1996
                                                                                                                                                                                                                                          (TUAN/) TUAN
(WULL/) WU 1
                                                                                                                                                                                    (CHEU/)
                                                                                                                                                                                                        (HALL/)
(NIMN/)
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Gaps: 0
Percent Identity: 79.464 Length: 535.00 5.095 93.750 Quality: Ratio: Percent Similarity: alignment\_scores:

TGFB3P x AAT42772 alignment\_block:

Align seg 1/1 to: AAT42772 from: 1 to: 339

34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50

51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67

84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100 

LeuSerAsnMetValValLysSerCysLysCysSer 112 101

301 CTTTCTAATATGATTGTAAAGTCTTGCAAATGCAGC 336

seq\_name: /SIDS1/gcgdata/geneseq/geneseqn/NA1999.DAT:AAX15246

AAX15246 standard; cDNA; 339 seq\_documentation\_block:

BP.

AAX15246;

Ľ;

3

28-APR-1999 (first entry) 

cDNA encoding the mature form of transforming growth factor-beta-2.

Transforming growth factor-beta-2; TGF-beta-like protein; S-sulphonated TGF-beta-like protein; wound treatment; cancer; bone repair; tissue repair; bone marrow protective agent; cardioprotection; anti-inflammatory; immunosuppressive;

ulcer; bed sore; ds

Homo sapiens

EP891985-A1

20-JAN-1999

90EP-0810922 27-NOV-1990; 89GB-0027546 06-DEC-1989;

(NOVS ) NOVARTIS AG.

Schmitz A; Meyhack B, McMaster GK, Cerletti N, Cox D,

WPI; 1999-083520/08 P-PSDB; AAW97092 Producing biologically active dimeric Transforming Growth Factor-beta - by refolding new monomeric Transforming Growth Factor-beta, useful for treatment of wounds and cancer

Example 1; Page 29; 32pp; English.

The present sequence encodes the mature form of transforming growth factor-beta-2. Dimeric, biologically active TGF-beta-like protein can be produced by subjecting the denatured monomeric form to refolding conditions. The new monomeric S-sulphonated TGF-beta-like protein is useful for the production of the dimeric, biologically active (surface or internal) and cancer in a mammal, in bone and tissue repair, as a bone marrow protective agent, a mediator of cardioprotection, for the production of an anti-inflammatory or faminosouppressive preparation. Treatment is useful for animals, especially humans, and wound treatment (e.g. ulcers, bed sores etc.) is particularly useful for the elderly.

98 A; 77 C; 70 G; 94 T; 0 other; Sequence 339 BP;

Length: Gaps: 535.00 5.095 93.750 Quality: Percent Similarity: Ratio: alignment\_scores:

Percent Identity: 79.464

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Proteinase site; bone morphogenetic fusion protein; bone binding site; bone morphogenetic protein; transforming growth factor beta; active fragment; wound healing; bone growth; purification tag; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New bone morphogenetic fusion proteins - comprising a purification tag and a bone morphogenetic active fragment, used for enhancing wound healing or bone growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    encoding a transforming growth factor beta active fragment.
                                                                                                                                                                                                                                                              84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
                                                                                                                             51 ACGTCCACTTTACATTGATTTCAAGAGGGATCTAGGGTGGAAATGGATAC 100
                                                                               50
                                                                                                                                                                                                                                                  84
                                                                                                      LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
                                                        1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17
                                                                                                                                                                                                                                                                                                                                                                                             seq_name: /SIDS1/gcgdata/geneseq/geneseqn/NA1999.DAT:AAV99376
                                                                       34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr
                                                                                                                                                                                                                                                rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG
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                                                                                                                                                                                                                                                                                                                                              LeuSerAsnMetValValLysSerCysLysCysSer 112
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to
                                  to: AAX15246 from: 1
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ID AAV99376 standard; cDNA; 339
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
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NIMNI M E.
SHORS E C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (HALL/) HALL F L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hall FL, Han B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P-PSDB; AAW84208
         TGFB3P x AAX15246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO9855137-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      03-JUN-1997;
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aliqnment_block
                                 Align seg 1/1
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(SHOR/) S
(WULL/) V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HANB/)
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The present sequence encodes a transforming growth factor beta active fragment. The protein can be used in place of a bone morphogenetic active fragment to create the fusion proteins of the invention. When a bone morphogenetic active fragment is used, the fusion proteins are designated bone morphogenetic fusion proteins. The bone morphogenetic fusion proteins. The bone morphogenetic fusion proteins. The bone morphogenetic proteins are purification and proteins sale for the following elements: a proteinase site, and a bone morphogenetic protein active fragment. The bone morphogenetic fusion proteins can be used for enhancing wound
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               macrophage inducible nitric oxide synthase; iNOS; constitutive NOS; interleukin-1-beta; transforming growth factor-beta; TGF-beta; IL1-beta; nitric oxide production; hypotension; inflammation; septic shock;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AACCTCTAACCATTCTCTACTACATTGGCAAAACACCCAAGATTGAACAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 G; 94 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cDNA encoding transforming growth factor-beta 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length:
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Disclosure; Page 42; 64pp; English
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ID AAT05877 standard; cDNA; 1695
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93.750
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Ratio:
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\begin{smallmatrix} \mathbf{A} & \mathbf{X} & \mathbf{C} & \mathbf{C}
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The cDNA encodes transforming growth factor-beta 2 (TGF-beta 2) which has been found to inhibit inducible nitric oxide synthase (INOS) gene transcription, spp. in interleukin-1-beta (ILI-beta) stimulated rat smooth muscle cells, and a dose which does not inhibit constitutive NOS. TGF-beta 1 or 2 (AAR83055) or their active fragments, can be used in the treatment of hypotension, such as that associated with severe
                                                                                                                                                                                                                                                                                 Treatment of hypotension, esp. in septic shock - by administering transforming growth factor-beta e.g. to inhibit inducible nitric oxide synthase gene transcription
                                7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1288 CATAAATCCAGAAGCATCTGCTTGCTGCTGCTGCTCCCAAGATTAG 1337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product= transforming growth factor-beta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1695 BP; 523 A; 386 C; 354 G; 432 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length: 112
Gaps: 0
Percent Identity: 79.464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            101 LeuSerAsnMetValValLysSerCysLysCysSer 112
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                                                                                                                                                                                                                                                                                                                                              Disclosure; Fig 16; 52pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Align seg 1/1 to: AAT05877 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      inflammation or septic shock.
                                                                                                                       94WO-US03705
                                                                                                                                                   94WO-US03705
182..1426
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5.095
93.750
                                                                                                                                                                                (HARD ) HARVARD COLLEGE.
                 /*tag=
                                                                                                                                                                                                             Perrella MA;
                                                                                                                                                                                                                                        WPI; 1995-358443/46.
P-PSDB; AAR83055.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         alignment_scores:
Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Similarity:
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                                                                                                                                                 05-APR-1994;
                                                          W09526745-A1
                                                                                                                     05-APR-1994;
                                                                                        12-0CT-1995
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CDS
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A new method for treating hypertension comprises administering a transforming growth factor (TGF)-beta to an individual at a dose effective for lowering blood pressure; the TGF-beta may be e.g. mature TGF-beta, TGF-beta2, a mature TGF-beta1/beta2 hybrid, TGF-beta1 precursor, a latent TGF-beta2 precursor, hybrid TGF-beta1/TGF-complex.
                                                                                                                                 Hypertension therapy; hypotensive agent; blood pressure modulator;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             their
treating
                                                                                                   Sequence encoding hybrid transforming growth factor (TGF).
seq_name: /SIDS1/gcgdata/geneseq/geneseqn/NA1992.DAT:AAQ20291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2208 BP; 599 A; 576 C; 534 G; 499 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length: 112
Gaps: 0
Percent Identity: 79.464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Use of transforming growth factor (TGF)-beta and antagonists - for modulating blood pressure, for hypertension and hypotension
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       to: 2208
                                                                                                                                                                                     Location/Qualifiers
262..282
/*tag= a
283..324
/*tag= b
325..1095
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                                  ВЪ
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                     seq_documentation_block:
ID AAQ20291 standard; cDNA; 2208
                                                                                                                                                                                                                                                                                                                                                                     91WO-US04449
                                                                                                                                                                                                                                                                                                                                                                                          90US-0541221
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1096..1434
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2208
                                                                            (first entry)
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5.095
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                                                                                                                                                                 Homo sapiens and monkey.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1992-024199/03.
P-PSDB; AAR20126.
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Ratio:
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                                                                                                             beta-1/beta-2.
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                                                                           16-APR-1992
                                                                                                                                                                                                                                                                                                                                                                     20-JUN-1991;
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                                                                                                                                                                                                                                                                   mat_peptide
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                                                                                                                                                                                                                                                                                         polyA_site
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                                                      AAQ20291;
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1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17

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17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
       misc_difference 1143
     /*tag= c
1456.1794
/*tag= d
811..897
/*tag= e
//note="This entire SQ is replaced with AAT in simian
TGF-beta-2-414 cDNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence of human transforming growth factor (TGF) beta-2 precursor 442 cDNA in pPC-21.
17 largProLeuTyrileAspPheArgGlnAspLeuGlyTrpLysTrpValH 34 :|||||||||||||||||::||
146 ACGTCCACTTTACATTCAAGAGGATCTAGGGTGGAAATGGATAC 1195
                                                                                                                                                                                                                                                                               84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq_name: /SIDS1/gcgdata/geneseq/geneseqn/NA1989.DAT:AAN90767
                                                                                                                             /note="Possible sequencing error"
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942
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misc_difference 1077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
466..1791
/*tag a
/note="Claimed"
466..1794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_documentation_block:

XX
AAN90767;
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AAN90767;
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AAN90767;
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Call differentiation, cell prolifer
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Cell differentiation, cell prolifer
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Cell difference 466..1794
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X+tag= 
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PolyA-RNA was isolated from the tamoxifen-treated, human prostatic adenocarcinoma cell line PC-3 and converted to cDNA. TGF DNA is used for control of the SV40 promoter and expressed in CHO cells. The simian SQ is also claimed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New DNA sequence encoding transforming growth factor beta used for large scale expression in eucaryotic cells
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Gaps: 0
Percent Identity: 79.464
/label=T
/note="Possible sequencing error"
misc_difference 1282
                                                                                                                                                                                                                                                                                                                                 /*tag= o
/label=T
/note="Possible sequencing error"
                                                                                                                                                                                                                                                                 /labél=C
/note="Possible sequencing error"
misc_difference 1017
                                                                                                                                                                                                        /labe_=A
/note="Possible sequencing
misc_difference 1698
                                                                                                                                              /note="Possible sequencing
misc_difference 1566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Align seg 1/1 to: AAN90767 from: 1 to: 2568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Fig 1a; 27pp; German.
                                                                              /note="Possible
misc_difference 1509
                                                                                                                                                                                                                                                                                                                                                                                                        /*tag= p
1456..1791
/*tag= q
/note="Claimed"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Webb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               88DE-3833897
                                                                            /label=T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              535.00
5.095
93.750
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1989-138796/19.
P-PSDB; AAP91889.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (ONCO-) ONCOGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alignment_block:
TGFB3P x AAN90767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18-AUG-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                           misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               05-OCT-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DE3833897-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               03-MAY-1989.
                                                                                                                                                                                                                                                                                                                                                                                          polyA_site
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to: 2569

29

84

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Hypertension therapy; hypotensive agent; blood pressure modulator;
                                                                                                                                                                                                                                                                                                      1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence encoding human transforming growth factor (TGF)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                seq_name: /SIDS1/gcgdata/geneseq/geneseqn/NA1992.DAT:AAQ20290
                                                                                                                                                                                  17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH
                                                                                                                                                                                                                                   34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr
                                                                                                                                                                                                                                                                                       LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh
                                                                                                                                                                                                                                                                                                                                         rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG
               Length: 112
Gaps: 0
Percent Identity: 79.464
                                                                                                                                                                                                                                                                                                                                                                                                                                                            LeuSerAsnMetValValLysSerCysLysCysSer 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                       from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ВР
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seq_documentation_block:
ID AAQ20290 standard; cDNA; 2569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           91WO-US04449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /*tag= b
526..1456
/*tag= c
1457..1792
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2569
/*tag= e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /*tag= a
478..525
             535.00
5.095
93.750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  467..475
                                                                                                         Align seg 1/1 to: AAQ05126
                                       Percent Similarity:
                             Ratio:
                                                                              TGFB3P x AAQ05126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20-JUN-1991;
   alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-APR-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO9119513-A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26-DEC-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              beta-2-442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      polyA_site
                                                                  alignment_block
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAQ20290;
                                                                                                                                                                                                                                                                                                                                                                                                                                             101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TGF-Beta2 may be used in treatment of tumors at effective doses, and may also be useful in augmenting wound healing by stimulating cell proliferation. The growth factor can be produced at high levels from a CHO expression system.
           1506 ACGTCCACTTTACATTGATTTCAAGAGGGATCTAGGGTGGAAATGGATAC 1555
                                  51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
                                                                                                                                                                                                                                                                                                  seq_name: /SIDS1/gcgdata/geneseq/geneseqn/NA1990.DAT:AAQ05126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2569 BP; 772 A; 598 C; 512 G; 687 T; 0 other;
Cloning and expression of transforming growth factor used for treatment of tumors or for augmenting wound
                                                                                                                                                                                                                                                                                                                                                                                                                                           Human TGF-Beta2 precursor; cancer; tumorcide; ss
                                                                                                                                                                                                                                                            101 LeuSerAsnMetValValLysSerCysLysCysSer 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
467..1792
/*tag= a
1457..1792
/*tag= b
                                                                                                                                                                                                                                                                                                                                                                                                                Human TGF-Beta2-442 precursor cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ż
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Webb
                                                                                                                                                                                                                                                                                                                         seq_documentation_block:
ID AAQ05126 standard; DNA; 2569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         89EP-0403480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  88US-0285140
89US-0446020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (ONCO-) ONCOGEN LTD PARTNER,
                                                                                                                                                                                                                                                                                                                                                                                        02-NOV-1990 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Purchio AF, Madisen L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1990-203127/27.
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.4-DEC-1989; 16-DEC-1988; 05-DEC-1989;

04-JUL-1990 EP376785-A.

mat\_peptide

Synthetic

AAQ05126;

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This DNA sequence is expressed in a host cell, preferably a COS or CHO cell, containing a recombinant vector encoding this sequence under the control of a 2nd nucleotide sequence that regulates gene expression, preferably the SV40 promoter, so the host cell produces active TGF-beta2. The produced TGF-beta2 protein can be used to regulate cellular differentiation and proliferation.
                                                              TGF-betal; TGF-betal; transforming growth factor; protein; cell differentiation; cell proliferation; CHO; Chinese hamster; ovary; COS; monkey kidney; animal; mammal; ss.
                                                                                                                                                                                                                                                                                                                                                                                                               /*tag= c
/note= "putative signal sequence cleavage site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hybrid transforming growth factor beta-1/TGF-beta-2 precursor to produce biologically active, mature TGF-beta-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1634 TTATGGAGTTCAGACACTCAGCACAGGGTCCTGAGCTTATATAATAC 1683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1484 GCTTTGGATGCGGCCTATTGCTTTAGAAATGTGCAGATAATTGCTGCCT 1533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length: 112
Gaps: 0
Percent Identity: 79.464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              to: 2592
           Human transforming growth factor-2 cDNA.
                                                                                                                                                                                                                                     Location/Qualifiers
503..550
/*tag= a
1484..1819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Fig.1a; 52pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Align seg 1/1 to: AAT04116 from: 1
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88US-0285140
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5.095
93.750
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553
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1995-346094/45.
P-PSDB; AAR79922.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (ONCO ) ONCOGEN LP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        alignment_block:
TGFB3P x AAT04116
                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                    misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14-DEC-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               alignment_scores:
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                                                                                                                                                                                                                                                             sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-DEC-1988;
                                                                                                                                                                                                                                                                                                                           mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11-0CT-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EP676474-A1
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        NEW YORK WANTED THE FEET THE F
                                                                                                                                                                                                                                                                                                                                                                                                                                 A new method for treating hypertension comprises administering a transforming growth factor (TGF)-beta to an individual at a dose effective for lowering blood pressure; the TGF-beta may be e.g. mature TGF-beta, TGF-beta, a mature TGF-betal/beta2 hybrid, TGF-betal precursor, a latent TGF-betal precursor, hybrid TGF-betal/TGF-betal precursor, a latent TGF-betal complex or a latent TGF-betal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
                                                                                                                                                                                                                                                          Use of transforming growth factor (TGF)-beta and their antagonists - for modulating blood pressure, for treating hypertension and hypotension
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq_name: /SIDS1/gcgdata/geneseq/geneseqn/NA1995.DAT:AAT04116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2569 BP; 772 A; 598 C; 513 G; 686 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Identity: 79.464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LeuSerAsnMetValValLysSerCysLysCysSer 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            to: 2569
                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Fig 2; 42pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Align seg 1/1 to: AAQ20290 from: 1
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                                                           (BRIM ) BRISTOL-MYERS SQUIB
  90US-0541221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     535.00
5.095
93.750
                                                                                                                    Oleson FB, Comereski
                                                                                                                                                                         1992-024199/03.
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                                                                                                                                                                                                       P-PSDB; AAR20125.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         alignment_block:
TGFB3P x AAQ20290
20-JUN-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28-MAY-1996
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1507

1557 51 1607 1657

29

1707

84

1757

XXXXXX

101

complex

host

67

- used

1094 GCTTTGGATCCGGCCTATTGCTTTAGAAATGTGCAGCATAATTGCTGCCT 1143

84

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TGF-beta may be used in vivo to prevent formation of synctia and inhibit HIV infection. TGF may also be used with other HIV treatments (AZT, soluble CD4 etc.).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Compsns. contg. transforming growth factor beta - used for inhibitions of HIV infection and replication in vivo.
                               1294 CATAAATCCAGAAGCATCTGCTTCTCCTTGCTGCGTGTCCCAAGATTTAG 1343
                                                                                                                                                                                                                                                           LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seq_name: /SIDS1/gcgdata/geneseq/geneseqn/NA1990.DAT:AAQ03511
                                                                                                                                                                                                                                                                                                                                                                     67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2207 BP; 600 A; 576 C; 532 G; 499 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HIV; AIDS; SIV; vaccine; A2T; CD4; cytokines; growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hybrid transforming growth factor TGF-betal/beta2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
267..1437
/*tag= a
1103..1437
/*tag= b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Brankovan V, Lioubin M, Purchio A;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq_documentation_block:
ID AAQ03511 standard; DNA; 2207 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            89EP-0115719.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14-AUG-1990 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1990-068723/10.
P-PSDB; AAR05666.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25-AUG-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25-AUG-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        factors; ds
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mat_peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAQ03511;
                                                                                                                                                                                                                                                           51
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGF-beta may be used in vivo to prevent formation of synctia and inhibit HIV infection. TGF may also be used with other HIV treatments (AZT, soluble CD4 etc.).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Compsns. contg. transforming growth factor beta - used for inhibitions of HIV infection and replication in vivo.
84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human Transforming growth factor from TGF-Beta2-442 cDNA.
                                                                                                                                                                                                                                                                                                                                        seq_name: /SIDS1/gcgdata/geneseq/geneseqn/NA1990.DAT:AAQ03510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2206 BP; 600 A; 577 C; 530 G; 499 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HIV; AIDS; SIV; vaccine; AZT; CD4; cytokines; growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length: 112
Gaps: 0
Percent Identity: 79.464
                                                                                                                                                                                                                      Align seg 1/1 to: AAQ03510 from: 1 to: 2206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
260..1429
/*tag= a
1091..1429
/*tag= b
label= mature TGF-Beta2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Purchio A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Fig 2; 20pp; English.
                                                                                                                                                                                                                                                                                                                                                                                            seq_documentation_block:
ID AAQ03510 standard; DNA; 2206 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      89EP-0115719
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Brankovan V, Lioubin M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      532.00
5.115
92.857
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P-PSDB; AAR05665
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Ratio:
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TGFB3P x AAQ03510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25-AUG-1989;
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EP356935-A.

AAQ03510;

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1095 GCTTTGGATCCGGCCTATGCTTTAGAAATGTGCAGCATAATTGCTGCCT 1144
                                                                                                                     84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
                                                                                                                                                                                                                                                                                                     Human TGF-Betal/TGF-Beta2 hybrid precursor cDNA expressing
                                                                                                                                          67
                                                            1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17
                                                                                                                                                                                                                                             seq_name: /SIDS1/gcgdata/geneseq/geneseqn/NA1990.DAT:AAQ05127
                                                                                                                                         LeuargSeralaaspThrThrHisSerThrValLeuGlyLeuTyrAsnTh
                                                                                                               34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr
            Gaps: 0
Percent Identity: 79.464
                                                                                                                                                                                                                           Human TGF-Beta2 precursor; cancer; tumorcide;
                                                                                                                                                                                                                    101 LeuSerAsnMetValValLysSerCysLysCysSer 112
     Length:
                                                Align seg 1/1 to: AAQ03511 from: 1 to: 2207
                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
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                                                                                                                                                                                                                                                      BP
     532.00
5.115
92.857
       Quality:
           Ratio:
Percent Similarity:
                              alignment_block:
TGFB3P x AAQ03511
alignment_scores
                                                                                                                                         51
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Sequence of human transforming growth factor (TGF) beta-1/TGF-beta-2
                                                                                                                                      TGF-Beta2 may be used in treatment of tumors at effective doses, and may also be useful in augmenting wound healing by stimulating cell proliferation. The growth factor can be produced at high levels from a CHO expression system.
                                                 Cloning and expression of transforming growth factor beta 2 -used for treatment of tumors or for augmenting wound healing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seq_name: /SIDS1/gcgdata/geneseq/geneseqn/NA1989.DAT:AAN90768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh
                                                                                                                                                                                                                                Sequence 2207 BP; 600 A; 577 C; 532 G; 498 T; 0 other;
                                                                                                                                                                                                                                                                                                   Length: 112
Gaps: 0
Percent Identity: 79.464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     101 LeuSerAsnMetValValLysSerCysLysCysSer 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cell differentiation; cell proliferation; ss
                                                                                                                                                                                                                                                                                                                                                                                                                               to: 2207
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198..2025
                                                                                                                                                                                                                                                                                                                                                                                                                                Align seg 1/1 to: AAQ05127 from: 1
                                                                                                      Claim 15; Fig 1b; 58pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23-DEC-1990 (first entry)
                                                                                                                                                                                                                                                                                                   532.00
5.115
92.857
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_documentation_block:
ID AAN90768 standard; DNA;
WPI; 1990-203127/27.
P-PSDB; AAR05749.
                                                                                                                                                                                                                                                                                                       Quality:
                                                                                                                                                                                                                                                                                                                                     Percent Similarity:
                                                                                                                                                                                                                                                                                                                        Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     precursor DNA.
                                                                                                                                                                                                                                                                                                                                                                                            TGFB3P x AAQ05127
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misc_feature
                                                                                                                                                                                                                                                                                     alignment_scores:
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                                                                                                                                                                                                                                                                                                                                                                           alignment_block:
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PolyA-RNA was isolated from the tamoxifen-treated, human prostatic adenocarcinoma cell line PC-3 and converted to cDNA. TGF DNA is prefused for control of the SV40 promoter. and expressed in CHO cells.
                                                                                                                                                                                                                                                                                                                               7
                                                                                                                                                                                                                                                                                                                             New DNA sequence encoding transforming growth factor beta used for large scale expression in eucaryotic cells
                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2217 BP; 600 A; 577 C; 531 G; 499 T; 10 other;
                                                                 /*tag= e
/label=G
/note="Possible sequencing error"
1218
                                                                                                                                              /*tag= g
1114..1116
/*tag= h
/codon=(seq:ccg,aa:Ala)
                                                                                                          /label=A
/note="As above"
2217
                                                                                                                                                                                                                                                                                                                                                         Disclosure; Fig 1b; 27pp; German.
/note="Claimed"
268..1443
/*tag= b
289..330
                                                                                                                                                                                                                                                                                   Webb N;
                                     /*tag= c
1102..1440
/*tag= d
1161
                                                                                                                                                                                                                              88DE-3833897
                                                                                                                                                                                                                                               88US-0234065
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                                                                                                                                                                                                                                                                                  Purchio AF, Madisen
                                                                                                                                                                                                                                                                                                   WPI; 1989-138796/19
                                                                                                                                                                                                                                                                                                             P-PSDB; AAP91900
                                                                                                  misc_difference
                                                              misc_difference
                                                                                                                                                                                                                                                                 ONCO-) ONCOGEN
                                                                                                                                                                                                                             05-OCT-1988;
                                                                                                                                                                                                                                               18-AUG-1988;
                            sig_peptide
                                              mat_peptide
                                                                                                                                                                                           DE3833897-A
                                                                                                                                                                                                            03-MAY-1989
                                                                                                                                      polyA_site
                                                                                                                                                       CDS
           CDS
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Length: 112 Gaps: 0 Percent Identity: 79.464 532.00 5.115 92.857 Quality: Ratio: Percent Similarity: alignment\_scores:

TGFB3P x AAN90768 alignment\_block:

Align seg 1/1 to: AAN90768 from: 1 to: 2217

- LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67 21

84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100

seq\_name: /SIDS1/gcgdata/geneseq/geneseqn/NA1995.DAT:AAT04115

BP. AAT04115 standard; DNA; 2200 seq\_documentation\_block:

AAT04115;

26-MAR-1996 (first entry)

Simian-human hybrid TGF-beta1/TGF-beta2 precursor DNA.

TGF-betal; TGF-betal; transforming growth factor; protein; cell differentiation; cell proliferation; CHO; Chinese hamster; ovary; COS; monkey kidney; animal; mammal; ss.

Homo sapiens

/\*tag= a /note= "hybrid TGF-betal/TGF-beta2 precursor" 257..1084 /\*tag= c /note= "human TGF-beta2 precursor" /78..319 /\*tag= d TGF-betal Location/Qualifiers /\*tag= b /note= "simian T 1085..1423 ..1423 mat\_peptide mat\_peptide mat\_peptide 

EP676474-A1

sig\_peptide

11-0CT-1995

89EP-0104223 14-DEC-1989; 89US-0446020. 88US-0285140. 05-DEC-1989; 16-DEC-1988;

(ONCO ) ONCOGEN LP.

Webb Purchio AF, Madisen L,

ż

P-PSDB; AAR79921

WPI; 1995-346094/45.

Hybrid transforming growth factor beta-1/TGF-beta-2 precursor - used to produce biologically active, mature TGF-beta-2

Claim 1, 2 and 3; Fig.1b; 52pp; English.

This hybrid DNA sequence is expressed in a host cell, preferably a COS or CHO cell, containing a recombinant vector encoding this sequence under the control of a 2nd nucleotide sequence that regulates gene expression, preferably the SV40 promoter, so the host cell produces active TGF-beta2. The produced TGF-beta2 protein can be used to regulate cellular differentiation and proliferation.

Sequence 2200 BP; 597 A; 588 C; 517 G; 498 T; 0 other;

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51 LeuargSeralaaspThrThrHisSerThrValLeuGlyLeuTyrasnTh 67
||| |||:::|||||| ||||||
|1238 TTATGGAGTTCAGACACTCAGCAGAGGGTCCTGAGCTTATATAATAC 1287
                                                                                                                                                                                                                                               84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
                                                                                            1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17
                                                                                                                                                                                                                                                                                                                                             seq_name: /SIDS1/gcgdata/geneseq/geneseqn/NA1990.DAT:AAQ04908
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /*tag= a
/note="Sequence derived from TGF-beta2."
                                                                                                                                                               34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr
                                                                                                                                                                                                                                     67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG
                                                                                                                                                                                                                                                                                                                                                                                                                                              ds.
              Length: 112
Gaps: 0
Percent Identity: 76.786
                                                                                                                                                                                                                                                                                                                                                                                                                                             Transforming growth factor; TGF-beta; cancer; CHO;
                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence encoding chimeric simian TGF-beta1/beta2
                                                                                                                                                                                                                                                                                                                    101 LeuSerAsnMetValValLysSerCysLysCysSer 112
                                                                           to: 2200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                          from: 1
                                                                                                                                                                                                                                                                                                                                                              _documentation_block:
AAQ04908 standard; DNA; 1561 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                89EP-0403463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (ONCO-) ONCOGEN LTD PARTNER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 88US-0284972
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        262..1431
/*tag= b
1120..1155
                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
             507.00
5.070
89.286
                                                                          Align seg 1/1 to: AAT04115
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Circopithecus aethiops.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Madisen L;
                       Ratio:
Percent Similarity:
              Quality:
                                                         TGFB3P x AAT04115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          insertion_seq
                                                                                                                                                                                                                                                                                                                                                                                                          18-OCT-1990
     alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13-DEC-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-DEC-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Purchio AF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20-JUN-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EP374044-A
                                                alignment_block
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Key
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Transforming growth factor; TGF; TGF-beta; TGF-5 beta; simian; Simian virus 40; SV40; expression vector; Chinese Hamster ovary; CHO; vascular endothelial cell; ss.
                                                                                                                                                                                                           Chimeric gene has TGF activity and may be more desirable than its parents TGF-betal. CHO cells expressing the product from a plasmid vector (p5beta/dhr) are 2.5 times more bioactive than normal. The product is useful in treatment of cancer and wound
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1346 AGCCACTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAG 1395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        84
                                                                    New chimeric transforming growth factor - with TGF-beta biological activity and increased secretion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq_name: /SIDS1/gcgdata/geneseq/geneseqn/NA1992.DAT:AAQ29177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1296 GCATAACCCGGGCGCCTCGGCGCGCGCGTGCTGCGTGCCGCAGGCGCTGG
                                                                                                                                                                                                                                                                                                                                                                              Sequence 1561 BP; 304 A; 543 C; 443 G; 271 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length: 112
Gaps: 0
Percent Identity: 75.893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1396 CTGTCCAACATGATCGTGCGCTCCGTCAAATGCAGC 1431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          101 LeuSerAsnMetValValLysSerCysLysCysSer 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          to: 1561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        to: AAQ04908 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGF-beta 1/beta 2 chimeric gene.
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                                                                                                                                                               Claim 2; Fig 1; 18pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_documentation_block:
ID AAQ29177 standard; DNA; 1561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    503.00
5.030
89.286
WPI; 1990-187401/25.
P-PSDB; AAR05492.
                                                                                                                                                                                                                                                                                                                                See also EP-373994
                                                                                                                                                                                                                                                                                                                                                                                                                                                alignment_scores:
Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percent Similarity:
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                                                                                                                     efficiency
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                                                                                                                                                                                                                                                                                                            healing
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Synthetic

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The sequence given encodes a hybrid transforming growth factor (TGF)-beta termed TGF-beta 1/beta 2 (or TGF-5 beta). The mutations indicated in the features table represent replacements of TGF-beta 1 bases with those from the corresponding positions of TGF-beta 2. Simian codon usage was maintained. This DNA sequence could be placed
                                                                                                                                                                                                                                                                                                                                                                                                                            /*tag= o
/note= "Feature not labelled in the specification"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 comprising new chimeric TGF-B (TGF-beta 1-beta 2) - s proliferation of vascular endothelial cells, useful for grancer and to promote wound healing
                                                                           /*tag= c
/note= "TGF-5 beta pre-pro-protein"
                                                                                                      *tag= d
note= "TGF-5 beta pro-protein"
                                  10963.1431
/*tag= b
/note= "Mature TGF-5 beta"
                                                                                                                                                                                                                                                                                                                                                                                                ′*tag= n
'note= "Mutagenic linker"
        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Purchio AF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Fig 1; 45pp; English
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                                                                                                                                  /*tag= e
//abel= S9R
//abel= S1R
/*tag= 1
//abel= S10N
//abel= T11V
//abel= T11V
//abel= T129
//abel= T120
//abel= T11V
//abel= E120
//abel= E120
//abel= E130
//abel= E130
//abel= E130
//abel= E130
//abel= E130
//abel= E130
                                                                                                                                                                                                                                                                              /*tag= j
/label= V17L
1150..1152
/*tag= k
/label= Q19P
/label= Q19P
/*tag= 1
/label= R25K
                                                                                                                                                                                                                                                                                                                                                                    /*tag= m
/label= K26R
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                                                                                            .1095
                   ..1434
                                                                 .348
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                             *tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    L, Merwin J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1992-348938/42.
P-PSDB; AAR27522.
                                                                                              precursor_RNA
                                                                                                                                                                                                                                                                                                                                                                                      old_sequence
                                                                                                                                                                                                                                                                                                                                                                                                                 misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13-MAR-1992;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO9216228-A
                                    mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-OCT-1992
                                                                 sig_peptide
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         Key
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under the control of Simian virus 40 (SV40) expression regulatory region within an expression vector and used to transfect Chinese Hamster ovary (CHO) cells. CHO transfectants can be seen to synthesise and secrete high levels of mature TGF-5 beta. TGF-5 beta induces effects on the proliferation of vascular endothelial cells equivalent to those produced by TGF-beta 1.
                                                                                                                                                                                                                                                                                                           1196 ACGAGCCCAAGGGCTACCATGCCAACTTCTGCCTGGGGCCCTGTCCTAC 1245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1296 GCATAACCCGGGGGCGCCTGCGGGGGCGCTGCTGCCGCAGGCGCTGG 1345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_name: /SIDS1/gcgdata/geneseq/geneseqn/NA1996.DAT:AAT17235
                                                                                                                                                                                                                                                                                                                                                                                                                                 34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG
                                                                                                         Sequence 1561 BP; 306 A; 541 C; 443 G; 271 T; 0 other;
                                                                                                                                                                   Length: 112
Gaps: 0
Percent Identity: 75.893
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LeuSerAsnMetValValLysSerCysLysCysSer 112
                                                                                                                                                                                                                                                                               to: 1561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq_documentation_block:
ID AAT17235 standard; cDNA to mRNA; 339
                                                                                                                                                                                                                                                                             Align seg 1/1 to: AAQ29177 from: 1
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                                                                                                                                                                    503.00
5.030
89.286
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (CIBA ) CIBA GEIGY AG
                                                                                                                                                                      Quality:
Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                TGFB3P x AAQ29177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25-JUL-1994;
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                                                                                                                                                        alignment_scores:
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                                                                                                                                                                                                                                 alignment_block
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Cerletti N;

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Human transforming growth factor beta 1 encoding cDNA.
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87.500
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P-PSDB; AAR91956
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                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                          WO9603432-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12-JUL-1995;
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                                                                                                                                                                                                             Key
NAME OF THE PROPERTY OF THE PR
                                                                                                                                                                                                                                                                                                                                                                      TGF-beta (AAR92773) was cloned into plasmid pGEW-52F(+) (Promega) and the construct used to transform E. coli Y1090. Subcloning in PpLMu yielded plasmid pPLMu.hTGF-beta 1. Non-soluble, monomeric TGF-beta 1 was recovered from E. coli LC 137/ppLMu.hTGF-beta 1 (DSM 5656) transformants. A biologically active, dimeric form of TGF-beta 1 was obtd. by refolding this monomer in detergent-free buffer conty, DMSO, and/or DMF. Dimers of TGF-beta 3 (AAR92772) and TGF-beta 2 (AAR927774), and hybrid dimers (see also AAR92775-77), were
                                                                                                                                                                                                                                                                                                                                                coding sequence (AAT17235) of human transforming growth factor
                                                                                                                                                               Prodn. of dimeric biologically active transforming growth factor by refolding denatured monomer in detergent-free folding buffer contg. specific organic solvent to improve yield
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          201 GCATAACCCGGGCGCCTCGGCGCGCGCGTGCTGCCGCAGGCGCTGG 250
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_name: /SIDS1/gcgdata/geneseq/geneseqn/NA1996.DAT:AAT15462
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 GCCCTGGACACCAACTATTGCTTCAGCTCCACGGAGAAGAACTGCTGCGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 339 BP; 66 A; 114 C; 100 G; 59 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Identity: 76.786
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                to: 339
                                                                                                                                                                                                                                                                                  Example 1B; Page 20-30; 54pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Align seg 1/1 to: AAT17235 from: 1
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5.102
87.500
                                                                       WPI; 1996-117000/12.
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Ratio:
                                                                                                          P-PSDB; AAR92773
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alignment\_scores

alignment\_block:

AAT15462 standard; cDNA to mRNA; 339 BP

seq\_documentation\_block:

101

67

(first entry)

10-JUN-1996

AAT15462;

axexex xaxex

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AATIS462-T15464 encode transforming growth factor (TGF) beta-1,
TGF beta-2 and TGF beta-3 which are produced using recombinant
DNA technology and used to produce TGF beta-like proteins in
C dimeric form. The TGF beta alike proteins produced are hybrids of
2 different types of TGF beta e.g. TGF beta-1-3, TGF beta-2-3, etc,
c robom encrphogenic proteins e.g. BMP-2. The TGF beta hybrids were
made using a new process of producing dimeric, biologically active
TGF beta monomers with folding buffer contg. a mild detergent (CHAPS,
CHAPSO or digitonin) and at least one of the solvents DMSO (dimethyl
S sulphoxide), DMSO2 (dimethylsulphone) and DMF (dimethyl formamide).
The detergent allows folding of the monomer such that, after
and remains in soluble form. The method allows relatively high yields
of biologically active TGF beta-like proteins in their native dimeric
form, TGF-beta like proteins are multifunctional regulators of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cellular activity and a typical use is to stimulate wound healing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Prodn. of dimeric, biologically active transforming growth f
beta - by refolding denatured monomer in buffer contg. mild
detergent and specific organic solvents to improve yields
       regulator; method;
healing; solvent; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Identity: 76.786
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                                                                                                                                                                                                                                                                                                   /product= human_TGF-beta-1
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Transforming growth factor beta; TGF; proliferation; differentiation; wound
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 1; Page 32-33; 59pp; English.
                                                                                                                                                                                    Location/Qualifiers
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alignment_block:
TGFB3P x AAT42771
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8888888888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A novel transforming growth factor-beta (TGF-beta) fusion protein comprises a purification tag and a TGF active fragment. The present sequence encodes a specifically claimed TGF active fragment, TGF-betal. Additionally, the fusion protein may comprise proteinase-sensitive linker sites and binding domain so the protein sequence may contain some or all of the following elements: purification tag:proteinase site:ECM binding site:proteinase site:TGF-beta. TGF-beta promotes wound healing, and the fusion protein can be used to reduce surgery recovery time and in the preparation of artificial skin. The inclusion
                                                                                                                                                                                                                                                                                                                                                                                                                                TGF-betal active fragment of a TGF-beta fusion protein encoding cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   β
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Transforming growth factor-beta fusion protein; wound healing; artificial skin; surgery recovery time; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               of transforming growth factor-beta fusion protein - a surgery recovery time and to prepare artificial skin
                                                                                                                                                                ACGAGCCCAAGGGCTACCATGCCAACTTCTGCCTCGGGCCCTGCCCCTAC 150
                                                             201 GCATAACCCGGCGCCCTCGGCGGCGCCCTGCTGCCGTGCCGCAGGCGCTGG 250
                                                                                                       84
                                                                                                                                                                                                                                                                                          seq_name: /SIDS1/gcgdata/geneseq/geneseqn/NA1997.DAT:AAT42771
                                          LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh
                                                                                                     rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG
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                                                                                                                                                                                                                              Tuan T,
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/function= TGF
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AAT42771 standard; cDNA; 339
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HALL F L.
NIMNI M E.
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(WULL/) WU L.
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of a purification tag facilitates purification of the fusion protein. The proteinase site is included to permit cleavage and release of the purification tag after purification if desired. The extracellular matrix binding site facilitates delivery of the fusion protein to the desired site of action. Delivery of the TGF-beta to the site to be treated reduces the amount of TGF-beta required to be administered to be effective and reduces the concentration of circulating TGF-beta which may result in undesirable effects.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cDNA encoding the mature form of transforming growth factor-beta-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             S-sulphonated TGF-beta-like protein; wound treatment; cancer; bone repair; tissue repair; bone marrow protective agent; cardioprotection; anti-inflammatory; immunosuppressive; ulcer; bed sore; an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    101 ATGAGCCCAAGGGCTACCATGCCAACTTCTGCCTCGGGCCCTGCCCTAC 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               201 GCATAACCCGGGCGCCTCGGCGCGCGCGTGCTGCGTGCCGCAGGCGCTGG 250
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_name: /SIDS1/gcgdata/geneseq/geneseqn/NA1999.DAT:AAX15245
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH
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                                                                                                                                                                                                                                                                 Sequence 339 BP; 66 A; 113 C; 100 G; 60 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                 Length: 112
Gaps: 0
Percent Identity: 76.786
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87.500
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                                                                                                                                                                                                                                                                                                                                                         alignment_scores:
Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                 Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                         Percent Similarity:
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The present sequence encodes the mature form of transforming growth factor-beta-1. Dimeric, biologically active TGF-beta-like protein can be produced by subjecting the denatured monomeric form to refolding conditions. The new monomeric S-sulphonated TGF-beta-like protein is useful for the production of the dimeric, biologically active TGF-beta-like protein, which is useful for the treatment of wounds repair, as a bone marrow protective agent, a mediator of cardioprotection, for the production of an anti-inflammatory or immunosuppressive preparation. Treatment is useful for animals, especially humans, and wound treatment (e.g. ulcers, bed sores etc.) is
                                                                                                                                                                                                                                                                                              Producing biologically active dimeric Transforming Growth Factor-beta - by refolding new monomeric Transforming Growth Factor-beta, useful for treatment of wounds and cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           51 GCGCAGCTGTACATTGACTTCCGCAAGGACCTCGGCTGGAAGTGGATCC 100
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                                                                                                                                                                     Schmitz A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH
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Gaps: 0
Percent Identity: 76.786
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                                                                                                                                                                  Meyhack B,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Align seg 1/1 to: AAX15245 from: 1 to: 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     particularly useful for the elderly.
                                                                                                                                                                  McMaster GK,
                                                                                                                                                                                                                                                                                                                                                                                                               Example 1; Page 28; 32pp; English.
  90EP-0810922
                                                     89GB-0027546
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5.102
87.500
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                                                                                                             (NOVS ) NOVARTIS AG
                                                                                                                                                                                                                  WPI; 1999-083520/08
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Ratio:
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TGFB3P x AAX15245
27-NOV-1990;
                                                        06-DEC-1989;
                                                                                                                                                                  Cerletti N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               alignment_scores:
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seq\_name: /SIDS1/gcgdata/geneseq/geneseqn/NA1999.DAT:AAV99375

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The present sequence encodes a transforming growth factor beta active fragment. The protein can be used in place of a bone morphogenetic active fragment to create the fusion proteins of the invention. When a bone morphogenetic active fragment is used, the fusion proteins are designated bone morphogenetic fusion proteins. The bone morphogenetic fusion proteins. The bone morphogenetic fusion proteins are designated bone morphogenetic fusion proteins are purification tag, a proteinase site, an a bone morphogenetic protein active fragment. The bone morphogenetic fusion proteins can be used for enhancing wound
                                                                                                                              Proteinase site; bone morphogenetic fusion protein; bone binding site; bone morphogenetic protein; transforming growth factor beta; active fragment; wound healing; bone growth; purification tag; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New bone morphogenetic fusion proteins - comprising a purification tag and a bone morphogenetic active fragment, used for enhancing wound healing or bone growth
                                                                                                    cDNA encoding a transforming growth factor beta active fragment.
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Shors EC,
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             BP.
            AAV99375 standard; cDNA; 339
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87.500
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI: 1999-059875/05
seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                          HALL F L.
HAN B.
                                                                                                                                                                                                                                                                                                                                                                      (NIMN/) NIMNI M E. (SHOR/) SHORS E C. (WULL/) WU L.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Hall FL, Han B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P-PSDB; AAW84207
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGFB3P x AAV99375
                                                                                                                                                                                                                        WO9855137-A1
                                                                                                                                                                                                                                                                                   02-JUN-1998;
                                                                                                                                                                                                                                                                                                              03-JUN-1997;
                                                                                                                                                                                            Homo sapiens
                                                                       25-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alignment_scores:
                                                                                                                                                                                                                                                     10-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           aliqnment_block
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Align seg 1/1
                                                                                                                                                                                                                                                                                                                                            (HALL/) H
(HANB/) H
                                           AAV99375
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90US-0541221
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (BRIM ) BRISTOL-MYERS SQUIB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /*tag= c
1099..1436
/*tag= d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        283.324
/*tag= b
325..1098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oleson FB, Comereski CR;
     5.102
87.500
                                                                                       Align seg 1/1 to: AAQ09317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /*tag=
     Ratio:
Percent Similarity:
                                             alignment_block:
TGFB3P x AAQ09317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-APR-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20-JUN-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20-JUN-1990;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26-DEC-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAQ20289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Monkey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /*tag= b
/product=monkey transforming growth factor-beta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Inhibition of proliferation of epidermal cells - used to treat psoriasis by contacting cells with compositions containing transforming growth factor-beta.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TGF-beta may be used in the treatment of hyperplasia associated with acanthosis-categorised skin diseases, and in alleviating psoriatic symptoms associated with cytokine-induced phenomena. See also AAQ03268 and AAR03750.
201 GCATAACCCGGGCGCCTCGGCGGCGCCGTGCTGCCTGCCGCGCGCGCGCTGG 250
                                                                                                                                                     84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
                                                                                                                                                                       seq_name: /SIDS1/gcgdata/geneseq/geneseqn/NA1990.DAT:AAQ09317
                                       51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh
                                                                                               67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1303 BP; 263 A; 442 C; 378 G; 217 T; 3 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Stevens V;
                                                                                                                                                                                                                                                                                                                                                                                                                              Transforming growth factor-beta; simian; psoriasis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    112
                                                                                                                                                                                                             101 LeuSerAsnMetValValLysSerCysLysCysSer 112
                                                                                                                                                                                                                                301 CTGTCCAACATGATCGTGCGCTCCTGCAAGTGCAGC 336
                                                                                                                                                                                                                                                                                                                                                                                                    Monkey transforming growth factor-beta cDNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Purchio AF, Ranchalis JE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; fig 1; 20pp; English.
                                                                                                                                                                                                                                                                                                  seq_documentation_block:
ID AAQ09317 standard; cDNA; 1303 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            89EP-0114458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        88US-0229133
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836..1170
                                                                                                                                                                                                                                                                                                                                                                          (first entry)
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P-PSDB; AAR03743.
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                                                                                                                                                                                                                                                                                                                                                                        12-AUG-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            04-AUG-1989;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sig_peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                07-FEB-1990
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rgF-beta Monkey.

Key

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Hypertension therapy; hypotensive agent; blood pressure modulator;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence encoding simian transforming growth factor (TGF) beta-1.
                                                                                                                                                                                                                                                                                                                                                              84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
                                                                                                                                                                                                   84
                                                                                                                                                                                                                                                                                                                                         51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seq_name: /SIDS1/gcgdata/geneseq/geneseqn/NA1992.DAT:AAQ20289
                                                                                                                                                                                                                                                                                                                                                                                                          67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG
                                                                                                                              1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa
                                                                                                                                                                                                                                                                        34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr
Gaps: 0
Percent Identity: 76.786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                to: 1303
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262..282
                                                                                                    from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_documentation_block:
ID AAQ20289 standard; cDNA; 1559 BP.
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101 LeuSerAsnMetValValLysSerCysLysCysSer 112
     A new method for treating hypertension comprises administering a transforming growth factor (TGF)-beta to an individual at a dose effective for lowering blood pressure; the TGF-beta may be e.g. mature TGF-beta, TGF-beta, a mature TGF-betal/beta2 hybrid, TGF-beta1 precursor, a latent TGF-beta2 precursor, hybrid TGF-beta1 beta2 precursor, a latent TGF-beta1 complex or a latent TGF-beta1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1095 GCCTGGACACCAACTACTGCTTCAGCTCCACGGAGAACTGCTGCGT 1144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
                                                                                                        Use of transforming growth factor (TGF)-beta and their antagonists - for modulating blood pressure, for treating hypertension and hypotension
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                seq_name: /SIDS1/gcgdata/geneseq/geneseqn/NA1990.DAT:AAQ03268
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1559 BP; 300 A; 546 C; 446 G; 267 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length: 112
Gaps: 0
Percent Identity: 76.786
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Align seg 1/1 to: AAQ20289 from: 1 to: 1559
                                                                                                                                                                                                                            English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAQ03268 standard; DNA; 1561 BP
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5.102
87.500
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                             WPI; 1992-024199/03
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                                                          P-PSDB; AAR20124
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Ratio:
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TGFB3P x AAQ20289
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         complex.
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XX X DRX B D
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/product=human transforming growth factor-beta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Inhibition of proliferation of epidermal cells - used to treat psoriasis by contacting cells with compositions containing transforming growth factor-beta.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1196 ACGAGCCCAAGGCTACCATGCCAACTTCTGCCTGGGGCCCTGTGCCTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1561 BP; 301 A; 547 C; 446 G; 267 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length: 112
Gaps: 0
Percent Identity: 76.786
                                                                                                                                                                                                                                                                                                                                                                Stevens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        induced phenomena. See also AAQ03269 and AAR03750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  to: 1561
                                                                                                                                                                                                                                                                                                                                                           Purchio AF, Ranchalis JE,
Location/Qualifiers
283..324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; fig 1; 20pp; English
                                      __ay=_ a
1096..1431
/*tag=_b
/pr
                                                                                                                                                                                                                                89EP-0114458
                                                                                                                                                                                                                                                                         88US-0229133
                                                                                                                                                                                                                                                                                                                  (ONCO-) ONCOGEN LTD PARTNER
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5.102
87.500
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                                                                                                                                                                                                                                                                                                                                                                                                                          P-PSDB; AAR03743
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TGFB3P x AAQ03268
                                                                                                                                                                                                                                                                                                                                                             Twardzik DR,
                                                                                                                                                                                                                                04-AUG-1989;
                                                                                                                                                                                                                                                                         05-AUG-1988;
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                       sig_peptide
                                                              mat_peptide
                                                                                                                                                                                       07-FEB-1990
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12-AUG-1990

AAQ03269;

Homo sapiens

rGF-beta

sig\_peptide mat\_peptide

84

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The DNA sequence encodes human prepro-TGF-beta 1 which can be produced by recombinant methods, it has osteogenetic and tumoricidal activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human pro-TGF-beta 1 prodn., for osteo-genetic activity - by preparing DNA chain contg. base sequence coding for human pre:pro-TGF-beta 1, forming expression vector etc.
     seq_name: /SIDS1/gcgdata/geneseq/geneseqn/NA1991.DAT:AAQ13392
                                                                                                        67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG
                                                                                                                         51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh
                                                                                                                                                                                                                       /*tag= c
/note= "pro-TGF-beta 1"
1346..1684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
512..1684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /*tag= e
/note= "TGF-beta 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Fig 1; 16pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                               tumoricidal; ss
                                                                                                                                                                                                                                                                                                             seq_documentation_block:
ID AAQ13392 standard; DNA; 1821
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         89JP-0318243
                                                                                                                                                                                                                                                                                                                                                                                     20-NOV-1991 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /*tag= b
599..1684
                                                                                                                                                                                                                                                                                                                                                                                                                   Human pro-TGF-beta 1 gene.
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512..598
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (KIRI ) KIRIN BREWERY
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P-PSDB; AAR13813.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Osteogenetic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       07-DEC-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    07-DEC-1989;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mat_peptide
                                                                                                                                                                                                                                                                                                                                                          AAQ13392;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              misc_RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Key
                                                                                                                                                                                                                                                                                                                                                        /*tag= b
/product-human transforming growth factor-beta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Inhibition of proliferation of epidermal cells - used to treat psoriasis by contacting cells with compositions containing transforming growth factor-beta.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1106 GCCCTGGACACCAACTACTGCTTCAGCTCCACGAGAACAGAACTGCTGCGT 1155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TGF-beta may be used in the treatment of hyperplasia associated with acanthosis-categorised skin diseases, and in alleviating psoriatic symptoms associated with cytokine-induced phenomena. See also AAQ03268 and AAR03743.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17
                            seq_name: /SIDS1/gcgdata/geneseq/geneseqn/NA1990.DAT:AAQ03269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1571 BP; 299 A; 563 C; 443 G; 266 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Purchio AF, Ranchalis JE, Stevens V;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length: 112
Gaps: 0
Percent Identity: 76.786
1396 CTGTCCAACATGATCGTGCGCTCCTGCAAATGCAGC 1431
                                                                                                                                                                                      Transforming growth factor-beta; psoriasis;
                                                                                                                                                             Human transforming growth factor-beta cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 to: 1571
                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Align seg 1/1 to: AAQ03269 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; fig 1; 20pp; English.
                                                                       AAQ03269 standard; DNA; 1571
                                                                                                                                                                                                                                                                                                                                                                                                                          89EP-0114458
                                                                                                                                                                                                                                                                                                                                                                                                                                                       88US-0229133.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (ONCO-) ONCOGEN LTD PARTNER
                                                                                                                                                                                                                                                                                           /*tag= a
836..1170
                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         500.00
5.102
87.500
                                                                                                                                                                                                                                                                               . . 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1990-038499/06.
                                                          seq_documentation_block
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P-PSDB; AAR03750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ratio:
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Twardzik DR,

04-AUG-1989; 05-AUG-1988;

07-FEB-1990 EP353772-A

Sequence 1821 BP; 326 A; 679 C; 508 G; 308 T; 0 other; alignment\_scores:

34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50

17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34

alignment\_block: TGFB3P x AAQ03269

alignment\_scores:

```
Key
       37..113
/*tag= a
/note= "Sequence can form stable hairpin loops"
                                                                                                                                                                                                                                                                                                   1446 ACGAGCCCAAGGCTACCATGCCAACTTCTGCCTCGGGCCCTGCCCTAC 1495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67 ::: ||| ||||||| :::||||||||||
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        84
                                                                                                                                                                                                             1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_name: /SIDS1/gcgdata/geneseq/geneseqn/NA1986.DAT:AAN60972
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Transforming growth factor beta; cancer; wound healing
                                               Percent Identity: 76.786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1646 CTGTCCAACATGATCGTGCGCTCCTGCAAGTGCAGC 1681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LeuSerAsnMetValValLysSerCysLysCysSer 112
                          Gaps:
  Length:
                                                                                                                                                               to: 1821
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                               from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAN60972 standard; cDNA; 2537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence encoding preTGF-beta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                85US-0715142.
87US-0025423.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   86EP-0302112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 842..2014
/*tag= b
1676..2011
/*tag= c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
500.00
5.102
87.500
                                                                                                                                                               to: AAQ13392
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1986-326875/50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seq_documentation_block:
Quality:
Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   misc_structure
                                                                                                                TGFB3P x AAQ13392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RMA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22-MAR-1985;
13-MAR-1987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-MAR-1986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28-OCT-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10-DEC-1986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mat_peptide
                                                                                             alignment_block;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EP200341-A.
                                                                                                                                                               Align seg 1/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAN60972
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2
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cDNA encoding human pre-transforming growth factor-beta-1 (pre-TGF-beta-
                                                                                                                          The gene product is known to stimulate cell proliferation and inhibit anchorage-dependent growth of a variety of human cancer cell lines, it is esp. useful in treatment of burns and the promotion of surface and internal wound healing. TGF-beta may be expressed from a transformed CHO cell line.
                                    from transformed hosts - useful esp. for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1726 GCGGCAGCTGTACATTGACTTCCGCAAGGACCTCGGCTGGAAGTGGATCC 1775
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq_name: /SIDS1/gcgdata/geneseq/geneseqn/NA1990.DAT:AAQ03301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh
                                                                                                                                                                                                                                              Sequence 2537 BP; 473 A; 893 C; 739 G; 432 T; 0 other;
                                                                                                                                                                                                                                                                                                                    Length: 112
Gaps: 0
Percent Identity: 76.786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Transforming growth factor-beta-1 (TGF-beta-1); neoplastic cell line inhibition; EGF-potentiated anchorage-independent growth;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1976 CTGTCCAACATGATCGTGCGCTCCTGCAAGTGCAGC 2011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  101 LeuSerAsnMetValValLysSerCysLysCysSer 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                      to: 2537
                                                                                           Disclosure; Fig 1b; 26pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Align seg 1/1 to: AAN60972 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                    500.00
5.102
87.500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seq_documentation_block:
ID AAQ03301 standard; DNA;
                                  TGF-beta prodn. fr
wounds (J6 2/9/86)
P-PSDB; AAP61468
                                                                                                                                                                                                                                                                                                                          Quality:
                                                                                                                                                                                                                                                                                                                                        Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                              alignment_block:
TGFB3P x AAN60972
                                                                                                                                                                                                                                                                                                     alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              05-AUG-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAQ03301;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo
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Location/Qualifiers

tgfb3p.rng

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It was obtained by an analysis of several overlapping cDNAs and gene fragments, leading to the detn. of a continuous sequence corresp. to the TGF-beta-1 precursor mRNA. It is useful in constructing vectors that encode biologically active transforming growth factor (TGF-beta), operably linked to DNA that encodes a secretory leader (SL). It, or a nucleic acid capable of hybridising with it, can also be labelled and used in diagnostic assays for DNA or mRNA encoding TGF-beta or related
                                                                                                                                                                                                                                                                                                                                                                     Nucleic acid encoding transforming growth factor-beta - cloned into expression vectors for expression in eukaryotic host
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2537 BP; 473 A; 893 C; 739 G; 432 T; 0 other;
                                                                                                          /*tag= d
/note="G-C rich sequence
and a downstream TATA-like sequence"
                                                                 /*tag= c
/note="stable hairpin loops"
2015..2100
                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Fig 1b; 28pp; English
                                                                                                                                                                                                                    87US-0U25423
                                                                                                                                                                                                                                              87US-0025423
               /*tag= a
1676..2011
                                        /*tag= b
37..113
 842..2014
                                                                                                                                                                                                                                                                                                                                                                                                 cells for therapeutic use
                                                                                                                                                                                                                                                                                                      Goeddel DV;
                                                                                                                                                                                                                                                                         (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                WPI; 1990-051338/07.
                                                                                                                                                                                                                                                                                                                                             P-PSDB; AAR05258
                                                     misc_difference
                                                                                                                                                                                                                                                                                                     Derynck RMA,
                                                                                             misc_feature
                                                                                                                                                                                                                    13-MAR-1987;
                                                                                                                                                                                                                                              13-MAR-1987;
                                                                                                                                                               US4886747-A.
                          mat_peptide
                                                                                                                                                                                         12-DEC-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    proteins.
```

Percent Identity: 76.786 Length: Gaps: 5.102 87.500 500.00 Quality: Ratio: Percent Similarity: alignment\_scores

TGFB3P x AAQ03301 alignment\_block:

to: 2537 Align seg 1/1 to: AAQ03301 from: 1

Dernyck RM, Goeddel DV;

(GETH ) GENENTECH INC

largProLeuTyrIleaspPheargGlnaspLeuGlyTrpLysTrpValH 34 17

1726 GCGGCAGCTGTACATTGACTTCCGCAAGGACCTCGGCTGGAAGTGGATCC 1775

isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50 34

51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67

67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84

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Transforming growth factor beta-3 (TGF beta 3); tumour cells; growth inhibition.
1876 GCATAACCCGGCGCCCTCGGCGCGCCCTGCTGCCTGCCGCAGGCGCTGG 1925
                      1926 AGCGCTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAG 1975
               84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
                                                                              seq_name: /SIDS1/gcgdata/geneseq/geneseqn/NA1990.DAT:AAQ02814
                                                        1976 CTGTCCAACATGATCGTGCGCTCCTGCAAGTGCAGC 2011
                                              101 LeuSerAsnMetValValLysSerCysLysCysSer 112
                                                                                                                                                                                                                                                                                                           863..911
/*tag= f
/label=hydrophobic domain
                                                                                                                                                                                                                                                               /*tag= c
2093..2099
/*tag= d
/label=TATA-like sequence
                                                                                                                                                                                                                                             /label-mature TGF-beta
2015..2092
                                                                                                                                                                                              Location/Qualifiers
842..2011
                                                                                                        ВР
                                                                                                                                                       Sequence of pre-TGF-betal cDNA
                                                                                                                                                                                                                      /label=pre-TGF
1677..2011
                                                                                              seq_documentation_block:
ID AAQ02814 standard; cDNA; 2537
                                                                                                                                                                                                                                                                                                                                                                                            88WO-U001945
                                                                                                                                                                                                                                                                                                                                                                            88WO-US01945
                                                                                                                                      31-MAY-1989 (first entry)
                                                                                                                                                                                                                                                                                                      Φ
                                                                                                                                                                                                                                      /*tag= b
                                                                                                                                                                                                                                                                                             ..113
                                                                                                                                                                                                                /*tag=
                                                                                                                                                                                                                                                                                                     /*tag=
                                                                                                                                                                                                                                                                       misc_feature
                                                                                                                                                                                                                                                                                                            misc_feature
                                                                                                                                                                                                                                                                                                                                                                            08-JUN-1988;
                                                                                                                                                                                                                                                                                                                                                                                            08-JUN-1988;
                                                                                                                                                                                                                                                                                                                                            WO8912101-A.
                                                                                                                                                                                                                                                                                                                                                            14-DEC-1989
                                                                                                                                                                                                                                                       GC_signal
                                                                                                                                                                                                                                                                                              stem_loop
                                                                                                                                                                                               Key
                                                                                                                                                                                                                              CDS
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Sequence encodes the 390 amino acid (AA) precursor transforming growth factor beta 1 (pre-TGF-beta 1) polypeptide. The 5' untranslated region of the TGF-beta 1 mRNA is 841 bases long, is purine rich and has a region of potential secondary structure. The TATA-like sequence in the 3' untranslated region of the gene is presumably a polyadenylation signal. Mature TGF-beta 1 comprises the C-terminal 112 AA's of pre-TGF-beta 1 and is cleaved at the Arg-Arg dipeptide preceding its NHZ terminus. The nucleic acid encoding the second subtype of TGF-beta (TGF-beta 3) is useful as a probe or to produce TGF-beta 3 for inhibition of growth of normal and neoplastic cells. Nucleotide sequence encoding transforming growth factor beta-3 -used as a probe, or to produce TGF beta 3, for growth inhibition of certain normal and neoplastic cells, eg A549. Disclosure; Fig. 1b; 61pp; English. WPI; 1990-007474/01. P-PSDB; AAR04034.

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seg_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                       TGFB3P x AAQ56923
                                        13-MAR-1987;
04-AUG-1989;
04-MAR-1992;
                                                                                                           Derynk RMA,
           22-MAR-1985;
                                                                                                                                                                                                                                                                                                                                                       alignment_scores:
                                22-MAR-1985;
                                                                                                                                                                                                                                                                                                                                                                                                          alignment_block
                                                                                                                                                                                                                                                                                                 beta.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1726
 TGF-beta-1; TGF-beta-2; transforming growth factor beta-1; transforming growth factor beta-3; recombinant; wound healing; vulnerary; ss.
                                                                                                                                                                                                                                                    1776 ACGAGCCCAAGGCTACCATGCCAACTTCTGCCTCGGGCCCTGCCCTAC 1825
                                                                                                                                                                                                                                                                                                1826 ATTIGGAGCCTGGACACGCAGTACAGCAAGGTCCTGGCCCTGTACAACCA 1875
                                                                                                                                                                                                                                                                                                                                                                        1676 GCCCTGGACACCAACTATTGCTTCAGCTCCACGGAGAACTGCTGCGT 1725
                                                                                                                                                                                                         1876 GCATAACCCGGGCGCCTCGGCGCGCCCTGCTGCCTGCCGCAGGCGCTGG 1925
                                                                                                                                                                                               17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
                                                                                                                                                                                                                                          20
                                                                                                                                                                                                                                                                                                                                84
                                                                                                                                                    1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17
                                                                                                                                                                                                                                                                                    51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                seq_name: /SIDS1/gcgdata/geneseq/geneseqn/NA1994.DAT:AAQ56923
                                                                                                                                                                                                                                         34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr
                                                                                                                                                                                                                                                                                                                              67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG
          0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 47..113
/*tag= a
/note= "possible hairpin loop region"
                                                    Length: 112
Gaps: 0
Percent Identity: 76.786
          G; 432 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                1976 CTGTCCAACATGATCGTGCGCTCCTGCAAGTGCAGC 2011
                                                                                                                                                                                                                                                                                                                                                                                                                       LeuSerAsnMetValValLysSerCysLysCysSer 112
                                                                                                                               Align seg 1/1 to: AAQ02814 from: 1 to: 2537
          893 C; 739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ВР
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAQ56923 standard; cDNA; 2537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /*tag= b
1676..2011
/*tag= c
2515..2521
/*tag= d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            09-JUL-1994 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 842..2014
         Sequence 2537 BP; 473 A;
                                                   500.00
5.102
87.500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human pre-TGF-beta-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seg_documentation_block:
                                                    Quality:
                                                                         Percent Similarity:
                                                                Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   misc_structure
                                                                                                        TGFB3P x AAQ02814
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                         alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             polyA_signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US5284763-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   08-FEB-1994
                                                                                               alignment_block
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             vulnerary;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAQ56923;
                                                                                                                                                                                                                                                                                                                                                                                                                    101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Key
X S
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respectively). A genomic fragment corresponding to a human TGF-beta-1 exon (AAQS624) was also isolated and its amino acid sequence determined (AAR46230). The sequences have been used in the construction of vectors for the expression of recombinant TGF-
                                                                                                                                                                                                                                                                                                                                                                                             cDNA sequences were determined for human pre-TGF-beta-1 (AAQ56923), pig TGF-beta-3 (AAQ56925), and the corresponding amino acid sequences were determined (AAR46227-29,
                                                                                                                                                                                                                                                                                            Nucleic acid sequences encoding transforming growth factor-beta diagnostic probes, and for use in therapeutics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_name: /SIDS1/gcgdata/geneseq/geneseqn/NA1996.DAT:AAT15720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2537 BP; 473 A; 890 C; 742 G; 432 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length: 112
Gaps: 0
Percent Identity: 76.786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       101 LeuSerAsnMetValValLysSerCysLysCysSer 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              to: 2537
                                                                                                                                                                                                                                                                                                                                                      Disclosure; Fig 1b; 25pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Aliqn seq 1/1 to: AAQ56923 from: 1
                                       85US-0715142.
87US-0025423.
89US-0389929.
92US-0845893.
85US-0715142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          500.00
5.102
87.500
                                                                                                                                                                                        Goeddel DV;
                                                                                                                                               (GETH ) GENENTECH INC
                                                                                                                                                                                                                             WPI; 1994-056343/07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Quality:
                                                                                                                                                                                                                                                   P-PSDB; AAR46227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ratio:
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The nucleotide sequence was obtd. by an analysis of several overlapping cDNAs and gene fragments. The DNA is useful for the recombinant production of TGF beta 1, which can be used in, e.g. wound healing. (Revised entry submitted to correct sequence analysis breakdown.)
                                                                                                                                                                                                                                                                                                  34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
                                                                                                                                                                                                                                                                                   1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                seq_name: /SIDS1/gcgdata/geneseq/geneseqn/NA1998.DAT:AAV52933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /*tag= a
//*tag= b
37.113
/*tag= b
//ote= "putative stable hairpin loop"
2015..2100
/*tag= c
//ote= "CC-rich sequence"
                                                                                                                                                                                                                                                                                                                                          17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH
                                                                                                                                                                                                                                                                                                                                                                                                        34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG
                                                                                 Sequence 2537 BP; 473 A; 893 C; 739 G; 432 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Transforming growth factor-beta 1; TGF-beta 1; human;
                                                                                                                                             Length: 112
Gaps: 0
Percent Identity: 76.786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human pre-transforming growth factor-beta 1 cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    to: 2537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
842..2014
                                                                                                                                                                                                                                                     Align seg 1/1 to: AAT15720 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seq_documentation_block:
ID AAV52933 standard; cDNA; 2537 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                          500.00
5.102
87.500
                                                                                                                                             Quality:
Ratio:
                                                                                                                                                                        Percent Similarity:
                                                                                                                                                                                                        alignment_block:
TGFB3P x AAT15720
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 polyA_signal
                                                                                                                               alignment_scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          stem_loop
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAV52933;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Key
      8 × 6 6 6 6 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /*tag= b
/note= "GC-rich region forms stable hairpin loops;
similar to structural organisation of c-myc RNA,
could play role in mRNA stability or in
regulation of transcription"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The cDNA encodes the pre-transforming growth factor (TGF) beta 1 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New recombinant human transforming growth factor-beta prods. - produced using Chinese hamster ovary cells, for use in diagnostic applications or in therapy
                                                                                                                                                                                                                                                                                                                                                                                                                              /product= mature_TGF_beta_1
2015..2100
/*tag= e
/note= "GC-rich region; possibly responsible for the fact 3'0TR of mRNA could not be cloned as cDNA;
may be important for transcription efficiency"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /*tag= g
/note= "TATA-like sequence; no evidence that this
functions a promoter"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "consensus sequence immediately precedes polyA-tail (Benoist et al)"
                                                                                                                                       transforming growth factor beta 1; wound healing; recombinant production; ss.
                                                                                                         Pre-transforming growth factor beta 1 cDNA.
                                                                                                                                                                                                                                                                                                                                                                        /*tag= c
/product= pre-TGF_beta_1
1676..2011
/*tag= d
                                                                                                                                                                                                                   Location/Qualifiers
1..841
   ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 3; Fig 1; 26pp; English.
AAT15720 standard; cDNA; 2537
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85US-0715142.
89US-0389929.
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93US-0147364
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2094..2100
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/*tag= h
2529..2536
/*tag= i
                                                             (revised)
(first entry)
                                                                                                                                                                                                                                             /*tag= a
37..113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1996-076891/08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P-PSDB; AAR90827
                                                                                                                                                                                                                                                                                                                                                                                                                                                 repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13-MAR-1987;
22-MAR-1985;
04-AUG-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Derynck RMA,
                                                                                                                                                                                                                                                                misc_feature
                                                           24-JUL-1997
25-JAN-1980
                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                04-MAR-1992;
05-NOV-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     polyA_signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22-MAR-1985;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           repeat_unit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US5482851-A
                                                                                                                                                                                                                                                                                                                                                                                                     mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09-JAN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TATA_signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 misc_signal
                               AAT15720
                                                                                                                                                                                                                   Key
5'UTR
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alignment_block:
                                                                                                                                    84
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  factor-beta 1 precursor (preceding 1, see AAW78185). It is a composite of overlapping CDNA clones isolated from different cDNA libraries (placenta, A172 glioblastoma, H71080 (libroblastoma) using TGF-beta exon (see AAV52936) restriction fragments as probes.

TGF-beta exon (see AAV52936) restriction of appleation of fraget cell lines and/or growth inhibition of neophastic cell lines.

Nucleic acids encoding TGF-beta have been isolated and cloned into extrors which are replicated in bacteria and expressed in eukaryotic cells. TGF-beta recovered from transformed cells is used in known therapeutic applications. TGF-beta nucleic acids are also useful in diagnosis and identification of TGF-beta clones.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             precursor sequence -
to increase yield of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nucleotide sequence codes for the human transforming growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1826 ATTTGGAGCCTGGACACGCAGTACAGCAAGGTCCTGGCCCTGTACAACCA 1875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1726 GCGCCAGCTGTACATTGACTTCCGCAAGGACCTCGGCTGGAAGTGGATCC 1775
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2537 BP; 475 A; 895 C; 736 G; 431 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps: 0
Percent Identity: 76.786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA encoding transforming growth factor-beta useful for analysis to perform manipulations recombinant production of the protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Align seg 1/1 to: AAV52933 from: 1 to: 2537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 3; Fig 1B 1-3; 26pp; English.
                                                                                                                                                                                                                                                                                     850S-0715142
890S-0389929.
920S-0845893.
930S-0147364.
950S-0454468.
                                                                                                                                                                                             85US-0715142
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ס
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Goeddel DV;
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5.102
87.500
/*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1998-494840/42.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P-PSDB; AAW78785
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Quality:
Ratio:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TGFB3P x AAV52933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Derynck RMA,
                                                                                                                                                                                          22-MAR-1985;
                                                            US5801231-A.
                                                                                                                                                                                                                                                                                                                                                      04-MAR-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                         30-MAY-1995;
                                                                                                                         01-SEP-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                alignment_scores
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macrophage inducible nitric oxide synthase; iNOS; constitutive NOS; interleukin-1-beta; transforming growth factor-beta; TGF-beta; IL1-beta; nitric oxide production; hypotension; inflammation; septic shock;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The cDNA encodes transforming growth factor-beta 1 (TGF-beta 1) which has been found to inhibit inducible nitric oxide synthase (NOS) gene transcription, esp. in interleukin-1-beta (ILI-beta) stimulated rat smooth muscle cells, and at a dose which does not inhibit constitutive NOS. TGF-beta 1 or 2 (AAR83055) or their active fragments, can be used in the treatment of hypotension, such as that associated with severe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Treatment of hypotension, esp. in septic shock - by administering transforming growth factor-beta e.g. to inhibit inducible nitric oxide synthase gene transcription
1926 AGCCGCTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAG 1975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /*tag= a
/product= transforming growth factor-beta 1
                                                                                                           luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
                                                                                                                                                                                                                                                                                                                       seq_name: /SIDS1/gcgdata/geneseq/geneseqn/NA1995.DAT:AAT05876
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length: 112
Gaps: 0
Percent Identity: 76.786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cDNA encoding transforming growth factor-beta 1.
                                                                                                                                                                                                              Location/Qualifiers
842..2017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Fig 15; 52pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                       BP
                                                                                                                                                                                                                                                                                                                                                                                                       AAT05876 standard; cDNA; 2745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     inflammation or septic shock.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94WO-US03705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          94WO-US03705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
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5.102
87.500
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lee M, Perrella MA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1995-358443/46.
P-PSDB; AAR83054.
                                                                                                                                                                                                                                                                                                                                                                              seq_documentation_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ratio:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           treatment; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mammalian sp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      05-APR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25-JUN-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          05-APR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12-0CT-1995.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         alignment_scores
                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAT05876;
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Extracellular matrix protein; self aggregation; hydroxylated proline; AAA12498; 51 101 3497 WX DX DX CX growth factor; TGF-beta-1; collagen IA; osteogenesis; /\*tag= a /product= collagen IA/TGF-beta-1 fusion protein 2679 1679 GCCTGGACACCAACTATTGCTTCAGCTCCACGGAGAAGAACTGCTGCGT 1728 1929 AGCCGCTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAG 1978 1779 ACGAGCCCAAGGCTACCATGCCAACTTCTGCCTCGGGCCCTGCCCCTAC 1828 /\*tag= c /note= "base 2688 is not identified in the specification" 34 isGluproLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50 51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67 1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17 seq\_name: /SIDS1/gcgdata/geneseq/geneseqn/NA1996.DAT:AAT16516 /\*tag= b /note= "base 2679 is not identified specification" 1979 CTGTCCAACATGATCGTGCGCTCCTGCAAGTGCAGC 2014 101 LeuSerAsnMetValValLysSerCysLysCysSer 112 to: 2745 Collagen Al/TGF-beta-1 chimeric gene. Location/Qualifiers 20..3535 bone formation; tissue repair; ds to: AAT05876 from: 1 ВP seq\_documentation\_block: ID AAT16516 standard; DNA; 3541 95CA-2151547 94US-0259263 (first entry) (USSU ) US SURGICAL CORP. Gruskin EA; 2688 misc\_difference misc\_difference TGFB3P x AAT05876 Transforming .2-JUN-1995; 10-JUN-1994; 01-OCT-1996 CA2151547-A 11-DEC-1995 Espino P, Align seg 1/1 Synthetic. AAT16516; 

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A chimeric gene (AAT16516) codes for a fusion protein (AAR89470) between the helical region of human collagen I(a) and human transforming growth factor beta-1 (TGF-beta-1). The collagen moiety was cloned from human fibroblast AG02261A cells by PCR amplification. The construct was inserted into a pWal vector for expression in E. coli. The fusion protein provides sustained release and delivery of TGF-beta-1 to a target tissue. The TGF increases efficacy of the body's normal soft tissue repair response and also induces
                                                                             Chimaeric DNA encoding protein contg. extracellular matrix protein domain. - and cellular regulatory factor domain, partic. useful as osteogenic agents, also related vectors, transformed cells and chimaeric proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cDNA encoding a chimeric collagen 1 (alpha1)/TGF-betal protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3447 AGCCGCTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAG 3496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17 largProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq_name: /SIDS1/gcgdata/geneseq/geneseqn/NA2000.DAT:AAA12498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 3541 BP; 504 A; 1143 C; 1188 G; 704 T; 2 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length: 112
Gaps: 0
Percent Identity: 76.786
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LeuSerAsnMetValValLysSerCysLysCysSer 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           to: 3541
                                                                                                                                                                                                               Disclosure; Fig 2; 59pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BP
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ID AAA12498 standard; cDNA; 3541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
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5.102
87.500
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WPI; 1996-140144/15.
P-PSDB; AAR89470.
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Ratio:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alignment_block:
TGFB3P x AAT16516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      osteogenesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25-JUL-2000
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The specification describes a method for producing an extracellular matrix protein or its fragment. The extracellular matrix protein is capable of self aggregating in a cell which does not ordinarily violations. The method comprises optimising a nucleic acid sequence for expression in the cell by substitution of codons preferred by the cell: or naturally occurring codons not preferred by the cell: incorporating the nucleic acid sequence into the cell; and contacting the nucleic acid sequence into the cell; and contacting the cell with a hypertonic growth medium containing at least one amino caid, selected from the group consisting of trans-4-hydroxyproline and 3-hydroxyproline to allow at least one of the amino acids to be assimilated into the cell and incorporated into the extracellular matrix conception. The method may be used to make host cells assimilate and incorporate trans-4-hydroxyproline into proteins such as collagen, cuseful in the recombinant production of proteins such as collagen, concinent of the method is also useful in studying the structure and function of proteins. The method is also useful in studying the structure and function of proteins. The method is also useful in studying the structure and function of proteins. The method is also useful in studying the structure and function of proteins. The method is also useful in studying the structure and function of proteins.
trans-4-hydroxyproline; 3-hydroxyproline; recombinant protein production; collagen; fibrinogen; fibronectin; post translational hydroxylation; ss. transforming growth factor-betal; TGF-betal; chimera; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence encodes a chimeric collagen 1 (alphal)/transforming growth factor-betal (TGF-betal) protein, which may be produced using the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Production of extracellular matrix proteins containing 4-trans-hydroxyproline results in native self aggregating proteins, useful on medical implants -
                                                                                                                                                                                                                      /product= "chimeric collagen 1 (alpha1)/TGF-beta1
    protein"
/transl_except= (pos: 2591..2593, aa: Gly)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 3541 BP; 504 A; 1145 C; 1188 G; 704 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Connolly K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Fig 16A-C; 260pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Zhang G,
                                                                                                                                                        Location/Qualifiers 20..3535
                                                                                                                                                                                                                                                                                                                                                                                                       99EP-0119184.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (USSU ) US SURGICAL CORP
                                                                                    Chimeric - Homo sapiens.
Chimeric - Unidentified.
                                                                                                                                                                                                      /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2000-259138/23.
P-PSDB; AAY84538.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 09-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gruskin EA,
                                                                                                                                                                                                                                                                                                                 EP992586-A2
                                                                                                                                                                                                                                                                                                                                                          12-APR-2000
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5.102 87.500 alignment\_block: TGFB3P x AAA12498

Percent Similarity

Length: 112 Gaps: 0 Percent Identity: 76.786

500.00

Quality:

alignment\_scores:

Align seg 1/1 to: AAA12498 from: 1 to: 3541

/\*tag= a /note= "the inventor has used T instead of U in the TGFbetal full-length mRNA" /note= "the N residues at positions 3464 and 3465 each appear as the letter F in the specification" 3347 ATTTGGAGCCTGGACACGCAGTACAGCAGGTCCTGGCCCTGTACAACCA 3396 3397 GCATAACCCGGGGGCCCTGCGGGGGCGCTGCTGCCGCAGGCGCTGG 3446 84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100 Transforming Growth Factor beta 1; TGF; non-coding region; coding region; resonance; interaction; optimisation; ss. 50 29 84 seq\_name: /SIDS1/gcgdata/geneseq/geneseqn/NA1994.DAT:AAQ55624 51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 101 LeuSerAsnMetValValLysSerCysLysCysSer 112 Location/Qualifiers /note= "N1 region" /\*tag= e /note= "N2 region" TGFbeta1 /\*tag= f /note= "P region" seq\_documentation\_block: ID AAQ55624 standard; DNA; 4105 BP. /\*tag= g /product= TC 3379..4105 /\*tag= h 92FR-0007571 TGFbetal 5'-UTR-CDS-3'-UTR 2203..3378 (first entry) /\*tag=\_ b 231..631 U 911..1039 632..910 1..4105 /\*tag= 1..2202 1..230 /\*tag= /\*tag= Homo sapiens 22-JUN-1992; 12-JUL-1994 24-DEC-1993. FR2692594-A. AAQ55624; enhancer misc\_RNA misc\_RNA misc\_RNA 5'UTR 3'UTR Key mRNA 3247 3297 CDS 

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The TGFbetal mRNA was divided into 3 regions (i.e. 5'-UTR, CDS and 3'-UTR) for various "perturbation" experiments. The relative order of the 3 regions was altered, e.g. the 3'-UTR was positioned upstream of the CDS and the 5'-UTR was positioned downstream of the CDS. The experiments showed that interactions between coding and noncoding regions are destroyed by such perturbations.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1140 ACGAGCCCAAGGCTACCATGCCAACTTCTGCCTCGGCCCTGCCCTAC 3189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3240 GCATAACCCGGGCGCCTCGGCGCGCGCGTGCTGCCGCGAGGCGCTGG 3289
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                                                                                                                                                                                                                                                                                                                                                          Application of optimised gene expression - for scientific, industrial and therapeutic purposes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              84
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 4105 BP; 744 A; 1407 C; 1201 G; 751 T; 2 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq_name: /SIDS1/gcgdata/geneseq/geneseqn/NA1993.DAT:AAQ41604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps: 0
Percent Identity: 76.786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         101 LeuSerAsnMetValValLysSerCysLysCysSer 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        to: 4105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Align seg 1/1 to: AAQ55624 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Fig 1; 110pp; French
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAQ41604 standard; cDNA; 336 BP
                                        92FR-0007571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
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5.102
87.500
                                                                                                                                                                                                                                                                             WPI; 1994-028256/04
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Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              alignment_block:
TGFB3P x AAQ55624
                                                                                                                      (PERE/) PEREZ
                                        22-JUN-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26-AUG-1993
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                                                                                                                                                                                                       Perez J;
XEXEXEX
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The invention covers hybrid TGF-beta molecules consisting of parts of the human isoforms TGF-betal, TGF-beta2 and TGF-beta3 (see AAQ41899, AAQ41601, respectively). The hinge points between parts derived from different parent isoforms are pref. Detween amino acids 44 and 45, 56 and 57, 79 and 80, 90 and 91, or 22 and 23. Of the 30 possible hybrids using these hinge points and one part each from two of the isoforms, 6 are preferred including the hybrid TGF-beta2(44/45)beta1. The hybrid molecules promote cell migration, inhibit the growth of A375 melanoma cells, accelerate the healing of partial-thickness burn wounds and full-thickness incisional wounds and increase formation of fibrous granular tissue.
See AAQ41602-Q41607 for the most pref. hybrids.
                                                                                                                                                                                                                                                                                                                                                                                  New hybrid transforming growth factor-beta molecules - comprise portions of mature TGF-beta isoforms; useful as wound healants, cardioprotective, antiinflammatory and immunosuppressive agents etc.
                                                                                                           a
"TGF-beta2=1-132, TGF-beta1=133-336"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
hTGF-betal; hTGF-beta2; hybrid protein; wound healing; cancer treatment; bone repair; growth regulation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length: 112
Gaps: 0
Percent Identity: 75.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 336 BP; 71 A; 99 C; 97 G; 69 T; 0 other;
                                                                                                                                                                                                                                                                                                          Kuhla J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    to: 336
                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                           Cerletti N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Align seg 1/1 to: AAQ41604 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 8; Page 28; 48pp; English
                                                                                                                                                                                                                   92EP-0810845.
                                                                                                                                                                                                                                               91EP-0810870
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           496.00
5.010
88.393
                                                                                                         /*tag=
                                                                                                                           /note=
                                                                                                                                                                                                                                                                                                             Cox D,
                                                                                                                                                                                                                                                                                                                                         1993-161126/20.
                                                                                                                                                                                                                                                                             (CIBA ) CIBA GEIGY
                                                                                                                                                                                                                                                                                                                                                        P-PSDB; AAR39643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TGFB3P x AAQ41604
                                                                                                                                                                                                                                                                                                             McMaster GK,
                                                Homo sapiens
                                                                                                                                                                                                                   03-NOV-1992;
                                                                                                                                                                                                                                               11-NOV-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                alignment_scores:
                                                                                                                                                                                     19-MAY-1993
                                                                                           mat_peptide
                                                                                                                                                       EP542679-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        alignment_block
                                                                              Key
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tgfb3p.rng

to: 345

from: 1

Align seg 1/1 to: AAQ41599

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The invention covers hybrid TGF-beta molecules consisting of parts of the human isoforms TGF-beta1, TGF-beta2 and TGF-beta3 (see AAQ11599, AAQ41600 and AAQ41601, respectively). The hinge points between parts derived from different parent isoforms are pref. between amino acids 44 and 45, 56 and 57, 79 and 80, 90 and 91, or 22 and 23. The hybrid molecules promote cell migration, inhibit the growth of A375 melanoma cells, accelerate the healing of partial-thickness burn wounds and full-thickness incisional wounds and increase formation of fibrous granular tissue. See e.g. AAQ41602-Q41607 for pref. hybrids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New hybrid transforming growth factor-beta molecules - comprise portions of mature TGF-beta isoforms; useful as wound healants, cardioprotective, antiinflammatory and immunosuppressive agents etc.
                                                                                                                                                                                                                                                                                                                                                                                               hTGF-betal; hybrid protein; wound healing; cancer treatment; bone repair; growth regulation; ss.
                   201 GCATAACCCGGGCGCCTCGGCGCGCCGTGCTGCTGCGTGCCGCGGGGCGTGG 250
                                                                                       251 AGCCGCTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAG 300
                                                                   luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
                                                                                                                                                                                                       seq_name: /SIDS1/gcgdata/geneseq/geneseqn/NA1993.DAT:AAQ41599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 345 BP; 68 A; 115 C; 102 G; 60 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                               Mature human Transforming Growth Factor-betal
                                                                                                                                     101 LeuSerAsnMetValValLysSerCysLysCysSer 112
                                                                                                                                                       301 CTGTCCAACATGATCGTGCGCTCCTGCAAGTGCAGC 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kuhla J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 4; Page 21-22; 48pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cerletti N,
                                                                                                                                                                                                                                                           BP
                                                                                                                                                                                                                                         seq_documentation_block:
ID AAQ41599 standard; cDNA; 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          92EP-0810845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          91EP-0810870
                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ø
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1..336
/*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (CIBA ) CIBA GEIGY AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               McMaster GK, Cox D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1993-161126/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P-PSDB; AAR39638
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        03-NOV-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11-NOV-1991;
                                                                                                                                                                                                                                                                                                                             26-AUG-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19-MAY-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EP542679-A
                                                                                                                                                                                                                                                                                           AAQ41599;
                                                                 84
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111

Length:

Gaps: 0 Percent Identity: 76.577

496.00 5.113 87.387

Quality:
Ratio:
Percent Similarity:

alignment\_scores:

alignment\_block: TGFB3P x AAQ41599

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TGF-betal is one example of a novel TGF-beta produced as a dimeric, biologically active protein using the method of the invention.

This coding sequence was isolated from the CI-215 human glioma cell line. It was incorporated into an appropriate vector to transform Saccharomyces cerevisiae or E.coli. Monomeric TGF-betal was purified, denatured and dissolved in 140ml 150m Tris/HCl pH8. 1M NaCl, 5mM EDTA, 2mM reduced glutathione, lnM oxidised glutathione and 33mM Chaps.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          рy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Prodn. of.Transforming Growth Factor type-beta-like proteins subjecting denatured monomeric form to refolding conditions
                                                                              84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
                                                                                                                             20
                                                                                                                                                                                                                                                        84
                            1 GCCCTGGACACCAACTATTGCTTCAGCTCCACGGAGAAGAACTGCTGCGT 50
                                                                                                                                                                                         LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
                                                            17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            В;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   seq_name: /SIDS1/gcgdata/geneseq/geneseqn/NA1991.DAT:AAQ11993
                                                                                                                                                                                                           34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr
                                                                                                                                                                                                                                                      67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Meyhack
1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TGF-betal; biologically active protein production; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cox D, Schmitz A,
                                                                                                                                                                                                                                                                                                                                                                                       LeuSerAsnMetValValLysSerCysLysCys 111
                                                                                                                                                                                                                                                                                                                                                                                                                   301 crgrccaacardarcgrgcgcrccrgcaagrgc 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 27; 35pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Transforming Growth Factor beta 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq_documentation_block:
ID AAQ11993 standard; cDNA; 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             90EP-0810922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             89GB-0027546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cerletti N, McMaster GK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (CIBA ) CIBA GEIGY AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1991-180005/25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P-PSDB; AAR12402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29-AUG-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27-NOV-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             06-DEC-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19-JUN-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EP433225-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAQ11993;
                                                                                                                                                                                         51
                                                                                                                                                                                                                                                                                                                                                                                     101
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After 72 hrs at 4 deg C, pH was adjusted to 2.5 and the mixture was conc. 10 times. The conc. soln was diluted to the original vol. with 10mM HCl and conc to a final vol of 10 ml. The supernatant from centrifugation at 5000g for 30 min contained disulphide-linked dimeric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Transforming growth factor; TGF; TGF-beta; TGF-5 beta; simian;
Simian virus 40; SV40; expression vector; Chinese Hamster ovary; CHO;
vascular endothelial cell; TGF-beta 1; TGF-beta 2; ss.
                                                                                                                                                                                                                                                                                                                           101 ACGAGCCCAAGGGCTACCATGCCAACTTCTGCCTCGGGCCCTGCCCTAC 150
                                                                                                                                                                                                                                                                                                                                                                 201 GCATAAGCCGGGCGCCTCGGCGCGCCGTGCTGCCTGCCGCAGGCGCTGG 250
                                                                                                                                                                                                                                                                       luProLeuThrileLeuTyrTyrValGlyArgThrProLysValGluGln 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                         34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
                                                                                                                                                                                                                1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17
                                                                                                                                                                                                                                                            17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
                                                                                                                                                                                                                                                                                                                                                    LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
                                                                                                                                                                                                                                                                                                                                                                                               67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /*tag= a
/note= "Signal peptide, pre-pro-protein"
356..1105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq_name: /SIDS1/gcgdata/geneseq/geneseqn/NA1992.DAT:AAQ29178
                                                                                                                                                                                                                            59 T; 0 other;
                                                                                                                                     Percent Identity: 75.893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length:
                                                                                                                           Gaps:
                                                                                                                                                                                           to: 339
                                                                    66 A; 113 C; 101 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /*tag= b
/note= "Pro-protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
269.,355
                                                                                                                                                                                          Align seg 1/1 to: AAQ11993 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_documentation_block:
ID AAQ29178 standard; DNA; 1565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1106..1438
/*tag= c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                              494.00
5.041
87.500
                                                                    Sequence 339 BP;
                                                                                                               Quality:
                                                                                                                           Ratio:
                                                                                                                                   Percent Similarity:
                                                                                                                                                                   TGFB3P x AAQ11993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      precursor_RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10-MAR-1993
                                                                                                   alignment_scores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGF-beta 1.
                                                                                                                                                          alignment_block
                                              TGF-beta1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAQ29178;
                                                                                                                                                                                                                                                                                                                                                    51
                                                                                                                                                                                                                                                                                                                                                                        151
                                                                                                                                                                                                                                                                                                                                                                                                                                                               251
                                                                                                                                                                                                                                                                                                                                                                                                                                          84
  888888
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The sequence given encodes the human transforming growth factor (TGF)-beta 1. This was used within the scope of the invention to compare to a similan TGF hybrid termed TGF-beta 1/Deta 2 (or TGF-5 beta) (see also AAQ29177). The chimeric DNA sequence could be placed under the control of Simian virus 40 (SV40) expression regulatory region within an expression vector and used to transfect Chimese Hamster ovary (CHO) cells. GIO transfectants can be seen to synthesise and secrete high levels of mature TGF-5 beta. TGF-5 beta induces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         effects on the proliferation of vascular endothelial cells equivalent
                                                                                                                                                                                                                                                                                                                                                                     Compsn. comprising new chimeric TGF-B (TGF-beta 1-beta 2) -
inhibits proliferation of vascular endothelial cells, useful for
treating cancer and to promote wound healing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1106 GCCTGGACACCAACTATTGCTTCAGAAATGTGCAGGATAATTGCTGCCT 1155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1565 BP; 300 A; 553 C; 439 G; 273 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length: 112
Gaps: 1
Percent Identity: 75.893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1400 CTGTCCAACATGATCGTGCGCTCCGTCAAGTGCAGC 1435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LeuSerAsnMetValValLysSerCysLysCysSer 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            to: 1565
                                                                                                                                                                                                                                                Purchio AF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Align seg 1/1 to: AAQ29178 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Fig 1; 45pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  to those produced by TGF-beta 1.
                                                                                                                                                                                                  8
                                                                                                                                                                                               (BRIM ) BRISTOL-MYERS SQUIBB
                                                                                                 92WO-US01993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               489.00
4.990
87.500
                                                                                                                                                                                                                                                Merwin J,
                                                                                                                                                                                                                                                                                                WPI; 1992-348938/42.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                       P-PSDB; AAR29657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                alignment_block:
TGFB3P x AAQ29178
                                                                                              13-MAR-1992;
                                                                                                                                               14-MAR-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             alignment_scores:
WO9216228-A
                                                01-OCT-1992
                                                                                                                                                                                                                                             Madisen L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        51
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09-OCT-1990

67

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TGF-beta may be used in vivo to prevent formation of synctia and inhibit HIV infection. TGF may also be used with other HIV treatments (AZT, soluble CD4 etc.).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Compsns. contg. transforming growth factor beta - used for inhibitions of HIV infection and replication in vivo.
seq_name: /SIDS1/gcgdata/geneseq/geneseqn/NA1990.DAT:AAQ03508
                                           LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1560 BP; 301 A; 547 C; 445 G; 267 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIV; vaccine; AZT; CD4; cytokines; growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps: 0
Percent Identity: 75.893
                                                                                                                                                                                                                                          LeuSerAsnMetValValLysSerCysLysCysSer 112
                                                                                                                                                                                                                                                                                                                                                                                                                        Simian Transforming growth factor - Betal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
267..1437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Purchio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Fig 1; 20pp; English.
                                                                                                                                                                                                                                                                                                                                BP
                                                                                                                                                                                                                                                                                                                seq_documentation_block:
ID AAQ03508 standard; DNA; 1560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    89EP-0115719.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (ONCO-) ONCOGEN LTD PARTNER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /*tag= a
1103..1437
/*tag= b
                                                                                                                                                                                                                                                                                                                                                                                        14-AUG-1990 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Brankovan V, Lioubin M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  487.00
5.021
86.607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1990-068723/10.
P-PSDB; AAR05663.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              alignment_block:
TGFB3P x AAQ03508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25-AUG-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25-AUG-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    factors; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      07-MAR-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alignment_scores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EP356935-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      HIV; AIDS;
                                                                                                                                                                                                                                                                                                                                                              AAQ03508;
               1195
                                                                                                                                                                                                                           101
                                            21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Key
                                                                                                                                                                                                                                                                                                                                                              The cDNA is prepd. from African green monkey cell line BSC-40 and is expressed in eukaryotic cells in plasmid psV3. There is 100% homology between mature simian and human TGF-beta 1. The plasmid also contains the SV40 promoter and a selection marker, esp. DHFR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     of simian transforming growth factor beta-1 - by culturing ected eucaryotic cells, and new precursor proteins, useful for
                                                                                                                                                                            Transforming growth factor-beta 1; tumour treatment; ss cDNA
                                                                                                                                             Coding sequence of simian transforming growth factor-beta 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1095 GCCCTGGACACCAACTACTGCTTCAGCTCCACGGAGAACTGCTGCGT 1144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
            seq_name: /SIDS1/gcgdata/geneseq/geneseqn/NA1988.DAT:AAN81084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1560 BP; 301 A; 547 C; 445 G; 267 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps: 0
Percent Identity: 75.893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Align seg 1/1 to: AAN81084 from: 1 to: 1560
                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Twardzik D;
                                                         ВР
                                      seq_documentation_block:
ID AAN81084 standard; cDNA; 1560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Prodn. of simian transforming
transfected eucaryotic cells,
treating tumours.
                                                                                                                                                                                                                                                                                                                                                                                                                     88EP-0108528
                                                                                                                                                                                                                                                                                                                                                                                                                                                   87US-0055662.
88US-0147842.
                                                                                                                                                                                                                                                  261..1433
/*tag= a
282..323
/*tag= b
1095..1433
/*tag= c
                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; ; pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               487.00
5.021
86.607
                                                                                                                                                                                                       Cercopithecus aethiops.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gentry L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1988-347488/49.
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P-PSDB; AAP80647

(ONCO-) ONCOGEN

Purchio AF,

25-JAN-1988;

29-MAY-1987

27-MAY-1988;

07-DEC-1988 EP293785-A.

sig\_peptide mat\_peptide

CDS Key

112

Length:

Ä

Quality:

alignment\_scores:

Ratio:

Percent Similarity:

TGFB3P x AAN81084

alignment\_block:

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Key
Prodn. of simian transforming growth factor beta-1 - by culturing transfected eucaryotic cells, and new precursor proteins, useful for treating tumours.
                                                                                                                                                                                                                                                                          Transforming growth factor-beta 1; tumour treatment; ss cDNA
               Coding sequence of human transforming growth factor-beta 1.
                                                                                                                      67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
                                                                                                                                                                                                    seq_name: /SIDS1/gcgdata/geneseq/geneseqn/NA1988.DAT:AAN81085
                                                                                                                                                                                  LeuSerAsnMetValValLysSerCysLysCysSer 112
    to: 1560
                                                                                                                                                                                                                                                                                                    Location/Qualifiers
267..1442
                                                                                                                                                                                                                                                                                                                                                                                                                              Twardzik D;
    to: AAQ03508 from: 1
                                                                                                                                                                                                                       BP
                                                                                                                                                                                                                 _documentation_block:
AAN81085 standard; DNA; 1569
                                                                                                                                                                                                                                                                                                                                                                                 88EP-0108528
                                                                                                                                                                                                                                                                                                                                                                                              87US-0055662
88US-0147842
                                                                                                                                                                                                                                                                                                                              /*tag= b
1104..1442
/*tag= c
                                                                                                                                                                                                                                                09-OCT-1990 (first entry)
                                                                                                                                                                                                                                                                                                                 /*tag= a
288..329
                                                                                                                                                                                                                                                                                                                                                                                                                              Purchio AF, Gentry L,
                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1988-347488/49
P-PSDB; AAP81362.
                                                                                                                                                                                                                                                                                                                                                                                                                 (ONCO-) ONCOGEN
                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                              29-MAY-1987;
25-JAN-1988;
                                                                                                                                                                                                                                                                                                                                                                                 27-MAY-1988;
                                                                                                                                                                                                                                                                                                                       sig_peptide
                                                                                                                                                                                                                                                                                                                                     mat_peptide
                                                                                                                                                                                                                                                                                                                                                                    07-DEC-1988
                                                                                                                                                                                                                                                                                                                                                        EP293785-A.
    Align seg 1/1
                                                       1145
                                                                                                                                                                           101
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HIV; AIDS; SIV; vaccine; AZT; CD4; cytokines; transforming growth factor; TGF-beta1; ds.
                              cDNA is human and mature human TGF-beta 1 has 100% homology with mature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1104 GCCTGGACACCAACTATTGCTTCAGCTCCACGGAGAACTGCTGCGT 1153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          84
                                                                                                                                                                                                                                                                                                              1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysWa 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_name: /SIDS1/gcgdata/geneseq/geneseqn/NA1990.DAT:AAQ03509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG
                                                                                 Sequence 1569 BP; 295 A; 563 C; 445 G; 266 T; 0 other
                                                                                                                                                                           Gaps: 0
Percent Identity: 75.893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1404 CTGTCCAACATGATCGTGCGCTCCTGAAAGTGCAGC 1439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              101 LeuSerAsnMetValValLysSerCysLysCysSer 112
                                                                                                                                                       Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human Transforming growth factor - Betal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
267..1437
                                                                                                                                                                                                                                                                             from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seq_documentation_block:
ID AAQ03509 standard; DNA; 1569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    89EP-0115719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /*tag= a
1103..1437
/*tag= b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14-AUG-1990 (first entry)
Disclosure; ; pp; English.
                                                                                                                                                                   5.021
86.607
                                                                                                                                                                                                                                                                             Align seg 1/1 to: AAN81085
                                                                                                                                                       Quality: 487.00
                                                 simian TGF-beta 1.
                                                                                                                                                                       Ratio:
Percent Similarity:
                                                                                                                                                                                                                         alignment_block:
TGFB3P x AAN81085
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25-AUG-1989;
                                                                                                                                       alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 07-MAR-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EP356935-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAQ03509;
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Guicherit O,
             Unidentified
                                                                                                                                                                                                     10-FEB-1999;
                                                                                                                                                          17-AUG-2000
                                                                              sig_peptide
                                                                                                    mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alignment_scores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      39
                                    Key
   TGF-beta may be used in vivo to prevent formation of synctia and inhibit HIV infection. TGF may also be used with other HIV treatments
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        transforming growth factor-beta; TGF-beta; pancreatic tissue growth; pancreatic duct tissue outgrowth; diabetes; ss.
                                                                                                   Compsns. contg. transforming growth factor beta - used for inhibitions of HIV infection and replication in vivo.
                                                                                                                                                                                                                                                                                                                                                              1204 ACGAGCCCAAGGCTACCATGCCAACTTCTGCCTCGGGCCCTGCCCCTAC 1253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
                                                                                                                                                                                                                                                                                                                                                   1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17
                                                                                                                                                                                                                                                                                                                                                                                               17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_name: /SIDS1/gcgdata/geneseq/geneseqn/NA2000.DAT:AAA63944
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cDNA encoding a pancreatic ductal trophic factor (PDTF).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pancreatic ductal trophic factor; PDTF; mesenchyme cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                           34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG
                                                                                                                                                                                                      other;
                                                                                                                                                                                                                                                          Gaps: 0
Percent Identity: 75.893
                                                                                                                                                                                                      0
                                                                                                                                                                                                     G; 265 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1404 CTGTCCAACATGATCGTGCGCTCCTGAAAGTGCAGC 1439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LeuSerAsnMetValValLysSerCysLysCysSer 112
                                                                                                                                                                                                                                                 Length:
                                                                                                                                                                                                                                                                                                                              to: 1569
                                              À;
                                                                                                                                                                                                    Sequence 1569 BP; 295 A; 565 C; 444
                                             Purchio
                                                                                                                                                                                                                                                                                                                              from: 1
                                                                                                                                                                             Disclosure; Fig 1; 20pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq_documentation_block:
ID AAA63944 standard; cDNA; 2754
 88US-0236698
                       (ONCO-) ONCOGEN LTD PARTNER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                             Brankovan V, Lioubin M,
                                                                                                                                                         (AZT, soluble CD4 etc.).
                                                                                                                                                                                                                                                          5.021
86.607
                                                                                                                                                                                                                                                                                                                             Align seg 1/1 to: AAQ03509
                                                                                                                                                                                                                                              487.00
                                                                WPI; 1990-068723/10.
P-PSDB; AAR05664.
                                                                                                                                                                                                                                              Quality:
                                                                                                                                                                                                                                                           Ratio:
                                                                                                                                                                                                                                                                    Percent Similarity
                                                                                                                                                                                                                                                                                          alignment_block:
TGFB3P x AAQ03509
25-AUG-1988;
                                                                                                                                                                                                                                     alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                04-DEC-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAA63944;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          101
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The present sequence encodes a pancreatic ductal trophic factor (PDTF) polypeptide. The polypeptide is expressed by e14.5 pancreatic mesenchyme cells (especially members of the TGF-beta (transforming growth factor-beta) super family), and is capable of stimulating growth and differentiation of pancreatic tissue. The polypeptides may be used for inducing outgrowths of pancreatic duct tissue, e.g. for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             outgrowths of pancreatic duct tissue, using pancreatic ductal factors expressed by e14.5 pancreatic mesenchyme cells, for th
                                                            pancreatic ductal trophic factor (PDTF)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1329 TATTGCTTTGGGAACAATGGGCCAAACTGCTGTGTGAAACCTCTTTACAT 1378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        72 aSerAlaSerProCysCysValProGlnAspLeuGluProLeuThrIleL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TyrCysPheArgAsnLeuGluGluAsnCysCysValArgProLeuTyrIl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     yrTyrAlaAsnPheCysSerGlyProCysProTyrLeuArgSerAlaAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            56 ThrThrHisSerThrValLeuGlyLeuTyrAsnThrLeuAsnProGluAl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2754 BP; 905 A; 525 C; 599 G; 725 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Identity: 71.963
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Align seg 1/1 to: AAA63944 from: 1 to: 2754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 73-75; 76pp; English.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                             Ξ
                                                                 ב
מ
                                                                                                                                                                                                                                                                                                                                                                                                                               Wang
                                                                                                                                                                                                                                                                                        10-FEB-2000; 2000WO-US03424
                                                                                                                                                                                                                                                                                                                                    99US-0119574
                                                                                                      /*tag= b
567..1649
/*tag= c
                                          /*tag= a
/product=
504..566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        439.00
4.933
83.178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            treatment of diabetes -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Inducing outgrowths of
                                                                                                                                                                                                                                                                                                                                                                                                                               Pang K,
                                                                                                                                                                                                                                                                                                                                                                                   (ONTO-) ONTOGENY INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2000-524488/47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P-PSDB; AAB08338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Similarity:
                                                                                                                                                                                                 WO200047243-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TGFB3P x AAA63944
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Quality:
                                                               Percent Similarity:
                                                  Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    misc_structure
                                                                                                               TGFB3P x AAQ11774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23-JUL-1991
                   alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO9105565-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mat_peptide
                                                                                             alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAQ11775;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        misc_RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     misc_RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This synthetic gene was designed based on reported sequence data, codons inferred from known amino acid sequences and observations of partial homology with known genes of the TGF-beta family. It was assembled from chemically synthesised oligonucleotides and can be expressed in prokaryotic host cells. The truncated 6 Cys TGF-beta protein is cleaved from the Fb-Fb domain at the hinge region to give
                                                                                                                                                                                                                                                                                                                                                                                                                                         /*tag= b
/product= fragment B of Staphylococcal Protein A
/note= "directly linked to a second Fb fragment"
376..552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ¥
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Recombinant truncated transforming growth factor-beta analogues capable of inducing an anti-proliferative effect in mammalian epithelial cells in vitro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product= truncated TGF-beta containing 6 x Cys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /*tag= c
/product= Fragment B of Staphylococcal Protein
              euTyrTyrValGlyArgThrProLysValGluGlnLeuSerAsnMetVal 105
                                                                                                                       seq_name: /SIDS1/gcgdata/geneseq/geneseqn/NA1991.DAT:AAQ11774
                                                                                                                                                                                                                                                                                                                                                                                               /*tag= a
/note= "modified trp-LE leader sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 852 BP; 216 A; 222 C; 225 G; 189 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the truncated product.
See also AAQ11775, AAR11942-7 and AAR11954
                                                                                                                                                                                                                                                                                                 Transforming Growth Factor beta; AIDS; ss
                                                                                                                                                                                                                                                                Encodes Fb-Fb-truncated (6 Cys)-TGF-beta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /*tag= d
/product= hinge region
565..843
                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 23; Fig 2; 42pp; English.
                                                        seq_documentation_block:
ID AAQ11774 standard; DNA; 852
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             90090SD-0M06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          89US-0422962
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (CREA-) CREATIVE BIOMOLECUL
                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                          181..375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        . 564
                                                                                                                                                                                                                                                                                                                                                                             1..180
/*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1991-148530/20.
P-PSDB; AAR11956.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     misc_structure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             truncated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18-OCT-1989;
                                                                                                                                                                                                                                  23-JUL-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18-OCT-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO9105565-A.
                                                                                                                                                                                                                                                                                                                                                                           sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              02-MAY-1991
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Cohen CM;

the

Synthetic

šey

misc\_RNA

misc\_RNA

AAQ11774;

/product= truncated TGF-beta containing 8 x Cys /note= "only contains 6 Cys residues; sequence disclosed in specification omits 50 bases" /\*tag= c /product= Fragment B of Staphylococcal Protein A 553..564 /\*tag= b
/product= fragment B of Staphylococcal Protein A
/note= "directly linked to a second Fb fragment" 86 uThrIleLeuTyrTyrValGlyArgThrProLysValGluGlnLeuSerA 103 seq\_name: /SIDS1/gcgdata/geneseq/geneseqn/NA1991.DAT:AAQ11775 1..180 /\*tag= a /note= "modified trp-LE leader sequence" Length: 93 Gaps: 0 Percent Identity: 76.344 Encodes Fb-Fb-truncated "(8 Cys)"-TGF-beta. to: 852 /\*tag= d /product= hinge region 565..843 Transforming Growth Factor beta; AIDS; Location/Qualifiers Align seg 1/1 to: AAQ11774 from: 1 BP seq\_documentation\_block:
ID AAQ11775 standard; DNA; 817 (first entry) /\*tag= e 181..375 412.00 5.024 88.172 376..552

Cohen CM;

tgfb3p.rng

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inhibit anchorage-dependent growth of a variety of human cancer cell lines, it is esp. useful in treatment of burns and the promotion of surface and internal wound healing. TGF-beta may be expressed from a transformed CHO cell line.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene product is known to stimulate cell proliferation and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28 uGlyTrpLysTrpValHisGluProLysGlyTyrTyrAlaAsnPheCysS
                                                                                                Transforming growth factor beta; cancer; wound healing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12 GluGluAsnCysCysValArgProLeuTyrIleAspPheArgGlnAspLe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  erGlyProCysProTyrLeuArgSerAlaAspThrThrHisSerThrVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 from transformed hosts - useful esp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 975 BP; 274 A; 184 C; 338 G; 179 T; 0
                                                                  Genomic sequence encoding TGF-beta exon
                                                                                                                        Location/Qualifiers
1..347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ......LeuGlyLeuTyrAsnThrLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Fig 2; 26pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Align seg 1/1 to: AAN60973 from: 1
                                                                                                                                                                                                                                                                                                                                         86EP-0302112
                                                                                                                                                                                                                                                                                                                                                                            85US-0715142
                                                                                                                                                                                                                                                                                                                                                                                            87US-0025423
                                 (first entry)
                                                                                                                                                                    /*tag= a
348..500
                                                                                                                                                                                                    /*tag= b
501..975
                                                                                                                                                                                                                                       /*tag= c
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4.847
81.667
                                                                                                                                                                                                                                                                                                                                                                                                                               (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1986-326875/50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGF-beta prodn. frow
wounds (J6 2/9/86).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    See also AAN60972
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TGFB3P x AAN60973
                                                                                                                                                                                                                                                                                                                                         21-MAR-1986;
                                                                                                                                                                                                                                                                                                                                                                                             13-MAR-1987;
                                 28-OCT-1991
                                                                                                                                                                                                                                                                                                                                                                            22-MAR-1985;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Derynck RMA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alignment_scores:
                                                                                                                                                                                                                                                                                                        10-DEC-1986
                                                                                                                                                                                                                                                                      EP200341-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alignment_block
AAN60973;
                                                                                                                                     Key
intron
                                                                                                                                                                                                                       intron
                                                                                                                                                                                       exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62
This synthetic gene was designed based on reported sequence data, codons inferred from known amino acid sequences and observations of partial homology with known genes of the TGF-beta family. It was assembled from chemically synthesised oligonuclectides and can be expressed in prokaryotic host cells. The sequence is that given in the specification, however, 50 bases should be inserted between nuclectides 600 and 601 of this sequence; the two "missing" Cys codons are presumably contained in the omitted sequence. The truncated TGF-beta protein is cleaved from the Fb-Fb domain at the see also AAQ11774, AAR11942-7 and AAR11954.
                                                                                                                                                                                                                    Recombinant truncated transforming growth factor-beta analogues capable of inducing an anti-proliferative effect in mammalian epithelial cells in vitro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                617 ...ccgracarcregrereregaracecagracrecaaggreeregerer 663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15 CysCysValArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrp.L 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31 ysTrpValHisGluProLysGlyTyrTyrAlaAsnPheCysSerGlyPro 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               81 lnAspLeuGluProLeuThrIleLeuTyrTyrValGlyArgThrProLys 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_name: /SIDS1/gcgdata/geneseq/geneseqn/NA1986.DAT:AAN60973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       615 GT.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          48 CysProTyrLeuArgSerAlaAspThrThrHisSerThrValLeuGlyLe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             uTyrAsnThrLeuAsnProGluAlaSerAlaSerProCysCysValProG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ValGluGlnLeuSerAsnMetValValLysSerCysLysCysSer 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps: 2
Percent Identity: 60.606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 817 BP; 207 A; 213 C; 219 G; 178 T; 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     to: 817
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Align seg 1/1 to: AAQ11775 from: 1
                                                                                                                                                                                                                                                                                      Claim 23; Fig 2B; 42pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_documentation_block:
ID AAN60973 standard; DNA; 975 BP.
XX
                               90MO-US06006
                                                               89US-0422962
                                                                                                (CREA-) CREATIVE BIOMOLECUL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4.321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                302,50
                                                                                                                                                                  WPI; 1991-148530/20.
                                                                                                                                                                                    P-PSDB; AAR11957
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ratio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGFB3P x AAQ11775
                             18-OCT-1990;
                                                               18-OCT-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alignment_block:
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for treating

other;

Gaps: 1 Percent Identity: 68.333

9

Length:

seq\_name: /SIDS1/gcgdata/geneseq/geneseqn/NA1990.DAT:AAQ02815 504 CGTCTGGCCACCGGGCTACGAGATGCGCTT 533 9

403

28

to: 975

64

86

45

503

tgfb3p.rng

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seq_name: /SIDS1/gcgdata/geneseq/geneseqn/NA1996.DAT:AAT15721
                                                           AAT15721;
                                                                                                                                                                                                             Key
                                    Nucleotide sequence encoding transforming growth factor beta-3 -used as a probe, or to produce TGF beta 3, for inhibition of growth of normal and neoplastic cells, eg A549.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This sequence encodes an exon of transforming growth factor-beta 1 (TGF-beta 1) polypeptide corresponding to AA's 288-338 of mature TGF-beta 1. The nucleic acid sequence encoding the second subtype of TGF-beta (TGF-beta 3) is useful as a probe or to produce TGF-beta 3 for both normal and neoplastic cell growth inhibition.
                                                                                                                    growth factor beta-3 (TGF beta 3); tumour cells; growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12 GluGluAsnCysCysValArgProLeuTyrIleAspPheArgGlnAspLe 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            uGlyTrpLysTrpValHisGluProLysGlyTyrTyrAlaAsnPheCysS 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         45 erGlyProCysProTyrLeuArgSerAlaAspThrThrHisSerThrVal 61
                                                                                              genomic fragment encoding a TGF-beta 1 exon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 975 BP; 274 A; 183 C; 339 G; 179 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps: 1
Percent Identity: 68.333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   to: 975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         504 CGTCTGGCCACCGGGCTACGAGATGCGCTT 533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .....LeuGlyLeuTyrAsnThrLeu 68
                                                                                                                                                       Location/Qualifiers
348..500
/*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Fig. 2; 61pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Align seg 1/1 to: AAQ02815 from: 1
        seq_documentation_block:
ID AAQ02815 standard; DNA; 975 BP.
                                                                                                                                                                                                                                                                                 88WO-U001945.
                                                                                                                                                                                                                                                          88WO-US01945
                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             237.50
4.847
81.667
                                                                                                                                                                                                                                                                                                                                 Dernyck RM, Goeddel DV;
                                                                                                                                                                                                                                                                                                        (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                        WPI; 1990-007474/01.
                                                                                                                                                                                                                                                                                                                                                                     P-PSDB; AAR04075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TGFB3P x AAQ02815
                                                                                                                  Transforming
                                                                                                                                                                                                                                                         08-JUN-1988;
                                                                                                                                                                                                                                                                                 08-JUN-1988;
                                                                                            Sequence of
                                                                   31-MAY-1989
                                                                                                                                                                                                        WO8912101-A
                                                                                                                                                                                                                                14 - DEC - 1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    alignment_scores
                                                                                                                                inhibition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              alignment_block
                                            AAQ02815;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28
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The transforming growth factor (TGF) beta 1 exon was identified using the "long probe" strategy used previously for TGF-alpha. Long oligonucleotides (T1572-23) designed on the basis of the partial protein sequence were used as hybridisation probes for the exon in a human genomic DNA library. The TGF beta 1 exon was then used as a probe for the isolation of TGF beta 1 cDNA (see AAT15270). DNA encoding TGF beta 1 is useful for the recombinant production of the protein, which is useful in, e.g. wound healing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New recombinant human transforming growth factor-beta prods. - produced using Chinese hamster ovary cells, for use in diagnostic applications
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (Revised entry submitted to correct sequence analysis breakdown.)
                                                                                                                                                                                                                                                                                                                                                                                                                                to 302"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /*tag= a
/note= "encodes TGF beta 1 residues 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12 GluGluAsnCysCysValArgProLeuTyrIleAspPheArgGlnAspLe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 975 BP; 274 A; 184 C; 338 G; 179 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps: 1
Percent Identity: 68.333
                                                                                                                                                                                          Partial pre-transforming growth factor beta 1 DNA
                                                                                                                                                                                                                                      transforming growth factor beta 1; wound healing; recombinant production; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        to: 975
                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
347..500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 2; Fig 2; 26pp; English.
seq_documentation_block:
ID AAT15721 standard; DNA; 975 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    87US-0025423.
85US-0715142.
89US-0389929.
92US-0845893.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        85US-0715142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                93US-0147364
                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ď,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4.847
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           237.50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Align seg 1/1 to: AAT15721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Goeddel
                                                                                                                         (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1996-076891/08.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P-PSDB; AAR90828
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ratio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Derynck RMA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      using Chinese
or in therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TGFB3P x AAT15721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22-MAR-1985;
04-AUG-1989;
04-MAR-1992;
05-NOV-1993;
                                                                                                                 24-JUL-1997
25-JAN-1980
                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22-MAR-1985;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US5482851-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09-JAN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13-MAR-1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    alignment_block
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clones.
                                                                                                                                                                                                                                                                                                          62
222XX
                                                                                                                                                                                                                                                                                                                                                                                                       This nucleotide sequence comprises a fragment of the human transforming growth factor-beta 1 (TGF-beta 1) gene incorporating an exon and flanking intron sequences. It was isolated from a human genomic library using probes based on a partial protein sequence of TGH-beta 1. The exon encodes amino acids 288-338 (see AAW78788) of TGF-beta 1. Restriction fragments of the isolated exon were used as probes for the isolation of TGF-beta 1 cDNAs (see AAV5293). The invention relates to the recombinant production of TGF-beta Nucleic acids encoding TGF-beta have been isolated and cloned into vectors which are replicated in bacteria and expressed in eukaryotic cells. TGF-beta recovered from transformed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA encoding transforming growth factor-beta precursor sequence - useful for analysis to perform manipulations to increase yield of recombinant production of the protein
      Human transforming growth factor-beta.gene exon fragment.
                                                                                                                                  seq_name: /SIDS1/gcgdata/geneseq/geneseqn/NA1998.DAT:AAV52936
                                                                                                                                                                                                                                                      Transforming growth factor-beta 1; TGF-beta 1; human; ss
                                                45 erGlyProCysProTyrLeuArgSerAlaAspThrThrHisSerThrVal
                                                                                                             504 CGTCTGGCCACCGGGCTACGAGATGCGCTT 533
                                                                                          ......LeuGlyLeuTyrAsnThrLeu 68
                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 2; Fig 2; 26pp; English.
                                                                                                                                                                   ВР
                                                                                                                                                                                                                                                                                                                                                                                                                                                        85US-0715142.
89US-0389929.
92US-0845893.
93US-0147364.
                                                                                                                                                       seq_documentation_block:
ID AAV52936 standard; DNA; 975
                                                                                                                                                                                                                                                                                                                                                                                                                            85US-0715142
                                                                                                                                                                                                                                                                                                                                                                                                                                               87US-0025423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95US-0454468
                                                                                                                                                                                                                                                                                                                           347..500
/*tag= b
501..976
/*tag= c
                                                                                                                                                                                                            21-DEC-1998 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Derynck RMA, Goeddel DV;
                                                                                                                                                                                                                                                                                                          1..346
/*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1998-494840/42.
P-PSDB; AAW78788.
                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                 US5801231-A.
                                                                                                                                                                                                                                                                                                                                                                                                                           22-MAR-1985;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         22-MAR-1985;
04-AUG-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                               13-MAR-1987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              04-MAR-1992;
05-NOV-1993;
                                                                                                                                                                                                                                                                                                                                                                                                      01-SEP-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-MAY-1995
                                                                                                                                                                                       AAV52936;
                                                                                                                                                                                                                                                                                                          intron
                                                                                                                                                                                                                                                                                                                                                   intron
                                                                                                                                                                                                                                                                                                                               exon
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cells is used in known therapeutic applications. TGF-beta nucleic acids are also useful in diagnosis and identification of TGF-beta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGF-beta-1; TGF-beta-2; transforming growth factor beta-1; transforming growth factor beta-3; recombinant; wound healing;
                                                                                                                                                                                                                                                                                                                                                                                                                                  28
                                                                                                                                                                                                                                                                                                                                                                                                           28 uGlyTrpLysTrpValHisGluProLysGlyTyrTyrAlaAsnPheCysS 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        45 erGlyProCysProTyrLeuArgSerAlaAspThrThrHisSerThrVal 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq_name: /SIDS1/gcgdata/geneseq/geneseqn/NA1994.DAT:AAQ56924
                                                                                                                                                                                                                                                                                                                                 12 GluGluAsnCysCysValArgProLeuTyrIleAspPheArgGlnAspLe
                                                                        BP; 274 A; 184 C; 338 G; 179 T; 0 other;
                                                                                                                                                   Length: 60
Gaps: 1
Percent Identity: 68.333
                                                                                                                                                                                                                                                                                          Align seg 1/1 to: AAV52936 from: 1 to: 975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /codon_start= 348..350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ......LeuGlyLeuTyrAsnThrLeu 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
1..975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       504 CGTCTGGCCACCGGGCTACGAGATGCGCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     85US-0715142.
87US-0025423.
89US-0389929.
92US-0845893.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_documentation_block:
ID AAQ56924 standard; DNA; 975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                85US-0715142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ಹ
                                                                                                                                                 237.50
4.847
81.667
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human pre-TGF-beta-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1994-056343/07.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P-PSDB; AAQ56924
                                                                                                                                                                         Ratio:
Percent Similarity:
                                                                                                                                                         Quality:
                                                                                                                                                                                                                                alignment_block:
TGFB3P x AAV52936
                                                                        Sequence 975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     09-JUL-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22-MAR-1985;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22-MAR-1985;
13-MAR-1987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           04-AUG-1989;
04-MAR-1992;
                                                                                                                                   alignment_scores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US5284763-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          vulnerary.
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A X X X
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gene therapy; growth differentiation factor-8; GDF-8; AIDS; cachexia; neurodegenerative disease; amyotrophic lateral sclerosis; obesity; muscular dystrophy; musculodegenerative disease; tissue repair; muscle wasting disease; neuromuscular disorder; spinal cord injury; traumatic injury; congestive obstructive pulmonary disease; ss.
                                                                 cDNA sequences were determined for human pre-TGF-beta-1 (AAQ56923), pig TGF-beta-3 (AAQ56925) and human TGF-beta-3 (AAQ56926), and the corresponding amino acid sequences were determined (AAR46227-29, respectively). A genomic fragment corresponding to a human TGF-beta-1 exon (AAQ56924) was also isolated and its amino acid sequence determined (AAR46230). The sequences have been used in the construction of vectors for the expression of recombinant TGF-
Nucleic acid sequences encoding transforming growth factor-beta diagnostic probes, and for use in therapeutics
                                                                                                                                                                                                                                                                                                                                                                                            454 TCGGGCCCTGGCCCTACATTTGGAGCCTGGACACGCAGTACAGCTA 503
                                                                                                                                                                                                                                                                                                                                                                                                                                   45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seq_name: /SIDS1/gcgdata/geneseq/geneseqn/NA2001.DAT:AAF63556
                                                                                                                                                                                                                                                                                                                                                                            12 GluGluAsnCysCysValArgProLeuTyrIleAspPheArgGlnAspLe
                                                                                                                                                                                                                                                                                                                                                                                                                                   28 uGlyTrpLysTrpValHisGluProLysGlyTyrTyrAlaAsnPheCysS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        45 erGlyProCysProTyrLeuArgSerAlaAspThrThrHisSerThrVal
                                                                                                                                                                                              Sequence 975 BP; 274 A; 181 C; 341 G; 179 T; 0 other;
                                                                                                                                                                                                                                                   Length: 60
Gaps: 1
Percent Identity: 66.667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (UYJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
                                                                                                                                                                                                                                                                                                                                                  975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        504 CGTCTGGCCACCGGGCTACGAGATGCGCTT 533
                                                                                                                                                                                                                                                                                                                                                  ;;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ......LeuGlyLeuTyrAsnThrLeu 68
                                                                                                                                                                                                                                                                                                                                                 Align seg 1/1 to: AAQ56924 from: 1
                                      Disclosure; Fig 2; 25pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Zebrafish GDF-8 coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq_documentation_block:
ID AAF63556 standard; cDNA; 1125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2000WO-US22884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99US-0378238
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                                                                                                                                                                                                                                                 226.50
4.719
80.000
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                                                                                                                                                                                                                                                    Quality:
                                                                                                                                                                                                                                                                 Ratio:
                                                                                                                                                                                                                                                                           Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200112777-A2
                                                                                                                                                                                                                                                                                                                    TGFB3P x AAQ56924
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11-MAY-2001
                                                                                                                                                                                                                                      alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22-FEB-2001
                                                                                                                                                                                                                                                                                                         alignment_block
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAF63556
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The present invention relates to growth differentiation factor-8 (GDF-8) coding sequences and proteins. The present sequence is a coding sequence for GDF-8, which was isolated in the present invention. GDF-8 is useful for treating neurodegenerative diseases (e.g. amyotrophic lateral sclerosis and muscular dystrophy), musculodegenerative diseases or in proliferation of rauma, obesity and disorders related to abnormal proliferation of adipocytes. GDF-8 is also useful for treating muscle adipose tissues and in gene therapy for the treatment of cell proliferative or immunological diseases mediated by GDF-8 is also useful for adition, GDF-8 is also useful for treatment of cell proliferative or immunological diseases mediated by GDF-8 in addition, GDF-8 is also useful for treating muscle wasting disease, neuromuscular disorder, spinal cond injury, traumatic injury, congestive obstructive
                                                                                                       New substantially purified growth differentiation factor-8 polypeptide, useful for treating muscle wasting disease, obesity, muscular dystrophy, neuromuscular disorder, acquired immunodeficiency syndrome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   87 hrIleLeuTyrTyrValGlyArgThrProLysVal...GluGlnLeuSer 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           811 TGCGATGAGAATTCCTCAGAGTCTCGCTGCTGCAGGTACCCTCTCACTGT 860
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            958 TATCCCCACACCCAT...........CTGGTGAACAAGGCCAGTCC 992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    54 AlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnThrLeuAsnPr 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             70 oGluAlaSerAlaSerProCysCysValProGlnAspLeuGluProLeuT 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                seq_name: /SIDS1/gcgdata/geneseq/geneseqn/NA2001.DAT:AAF63558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            39 yrTyrAlaAsnPheCysSerGlyProCysPro.....TyrLeuArgSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7 CysPheArgAsnLeuGluGluAsn...CysCysValArgProLeuTyrIl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22 eAspPheArgGlnAspLeuGlyTrpLysTrpValHisGluProLysGlyT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1125 BP; 310 A; 285 C; 294 G; 236 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length: 110
Gaps: 5
Percent Identity: 40.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pulmonary disease (COPD), AIDS or cachexia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Align seg 1/1 to: AAF63556 from: 1 to: 1125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1093 rcgarggragragaccgcrgrgcrca 1122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                103 AsnMetValValLysSerCysLysCysSer 112
                                                                                                                                                                                                                                                                                         Claim 39; Fig 2; 124pp; English.
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ID AAF63558 standard; cDNA; 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  217.00
3.056
64.545
WPI; 2001-211209/21
                                        P-PSDB; AAB73196.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ratio:
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                                                                                                                                                                                                                       and cachexia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alignment_scores:
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....TCCATG

ValValLysSerCysLysCysSer 112

BP.

(first entry)

... ValGlyArgThrProLysValGluGlnLeuSerAsnMet

92

... CACCTGGTGAACAAGGCTAACCCTCGCGGCACCGGGGGCCCTGCTG LeuGlyLeuTyrAsnThrLeuAsnProGluAlaSerAlaSerProCysCy

62

sValProGlnAspLeuGluProLeuThrIleLeuTyrTyr......

78

tgfb3p.rng

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Gene therapy, growth differentiation factor-8; GDF-8; AIDS, cachexine neurodegenerative disease; amyotrophic lateral sclerosis; obesity; muscular dystrophy; musculodegenerative disease; tissue repair; muscle wasting disease; neuromuscular disorder; spinal cord injury; traumatic injury; congestive obstructive pulmonary disease; ss.
                                                                                                              seq_name: /SIDS1/gcgdata/geneseq/geneseqn/NA2001.DAT:AAF63557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (UYJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Salmon GDF-8 allele 1 coding sequence.
                                                                                                                                                                                                                   354 AGCAGATCATCTACGGCAAGATCCCC.
                                                                                                                                                                                                                                                                                                       386 GIGGIGGACCGCTGCGGCTGCTCG
                                                                                                                                                                                                                                                                                                                                                                                          seq_documentation_block:
ID AAF63557 standard; cDNA; 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17-AUG-2000; 2000WO-US22884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oncorhynchus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200112777-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11-MAY-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAF63557;
                                          257
                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention relates to growth differentiation factor-8 (GDF-8) coding sequences and proteins. The present sequence is a coding sequence for GDF-8, which was isolated in the present invention. GDF-8 is useful for treating neurodegenerative diseases (e.g. amyotrophic lateral sclerosis and muscular dystrophy), musculodegenerative diseases or in tissue repair due to trauma, obesity and disorders related to abnormal proliferation of adipocytes. GDF-8 is also useful for treating malignancies of the various organ systems, particularly cells in muscle or adipose tissues and in gene therapy for the treatment of cell proliferative or immunological diseases mediated by GDF-8. In addition, GDF-8 is also useful for treating muscle wasting disease, neuromuscular disorder, spinal cord injury, traumatic injury, congestive obstructive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New substantially purified growth differentiation factor-8 polypeptide, useful for treating muscle wasting disease, obesity, muscular dystrophy, neuromuscular disorder, acquired immunodeficiency syndrome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    spinal cord injury, traumatic injury, congestive obstructive disease (COPD), AIDS or cachexia.
                                                                              Gene therapy; growth differentiation factor-8; GDF-8; AIDS; cachexis neurodegenerative disease; amyotrophic lateral sclerosis; obesity; muscular dystrophy; musculeogenerative disease; tissue repair; muscle wasting disease; neuromuscular disorder; spinal cord injury; traumatic injury; congestive obstructive pulmonary disease; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 412 BP; 91 A; 134 C; 112 G; 75 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                     (UYJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE
                                        Salmon GDF-8 allele 2 coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 39; Fig 2; 124pp; English.
                                                                                                                                                                                                                                                                                                                                                 2000WO-US22884.
                                                                                                                                                                                                                                                                                                                                                                                            99US-0378238
(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  McPherron AC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-211209/21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P-PSDB; AAB73198
                                                                                                                                                                                                                 Oncorhynchus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Quality:
                                                                                                                                                                                                                                                            WO200112777-A2
                                                                                                                                                                                                                                                                                                                                                 17-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                            19-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and cachexia
11-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             alignment_scores
                                                                                                                                                                                                                                                                                                       22-FEB-2001
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The present invention relates to growth differentiation factor-8 (GDF-8) coding sequences and proteins. The present sequence is a coding sequence for GDF-8, which was isolated in the present invention. GDF-8 is useful for treating neurodegenerative diseases (e.g. amyotrophic lateral sclerosis and muscular dystrophy), musculodegenerative diseases or in tissue repair due to trauma, obesity and disorders related to abnormal proliferation of adipocytes. GDF-8 is also useful for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             malignancies of the various organ systems, particularly cells in muscle or adipose tissues and in gene therapy for the treatment of cell proliferative or immunological diseases mediated by GDF-8. In addition, GDF-8 is also useful for treating muscle wasting disease, neuromuscular disorder, spinal cord injury, traumatic injury, congestive obstructive pulmonary disease (COPD), AIDS or cachexia.
                                                                                                                                                                                                                                            New substantially purified growth differentiation factor-8 polypeptide, useful for treating muscle wasting disease, obesity, muscular dystrophy, neuromuscular disorder, acquired immunodeficiency syndrome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 39; Fig 2; 124pp; English.
S, McPherron AC;
                                                                                              WPI; 2001-211209/21
                                                                                                                                                             P-PSDB; AAB73197.
                                                                                                                                                                                                                                                                                                                                                                                                                    and cachexia
Lee
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116 GAGTCCCGCTGCCGGTACCCCCTCACGGTGGACTTT...GAAGACTT 162

GluGluAsnCysCysValArgProLeuTyrIleAspPheArgGlnAspLe

to: 412

from: 1

Align seg 1/1 to: AAF63558

12

TGFB3P x AAF63558

alignment\_block:

Percent Identity: 38.889

3.331 60.185

Percent Similarity:

Gaps:

uGlyTrpLysTrpValHisGluProLysGlyTyrTyrAlaAsnPheCysS 45

28

45

163 TGGCTGGGACTGGATTATTGCCCCCAAGCGCTACAAGGCCAACTACTGCT erGlyProCysProTyrLeuArgSerAlaAspThrThrHisSerThrVal 213 CTGGTGAGTGCGAGTACATGCACTGCAGAAGTACCCCCACACCC..... 256

61

99US-0378238

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Growth differentiation factor-8; GDF-8; baboon; transgenic animal; transforming growth factor-beta; muscle; meat; inhibitor; obesity; neuromuscular disease; muscular dystrophy; cachexia; cancer; AIDS;
                                                                                                                    CTGGTGAGTGTGCAGTACATGCACCTGCAGAAGTACCCCCCACACC..... 320
                                                                                                                                                                                                                                         CACCCCCACCAAGATGTCCCCCATCAACATGCTCTACTTCAACCGCAAAG 417
                                                                                                                                                  45
                                                                                                                                                                                                                              78
                                                                                                                                                                                        61
                                                                                                                                                                                                                                                                                                                                                                                          seq_name: /SIDS1/gcgdata/geneseq/geneseqn/NA1998.DAT:AAV45817
                                                                                                                                                                                                                                                                                                                        418 AGCAGATCATCTACGGCAAGATCCCC.....TCCATG
                                                                                                        12 GluGluAsnCysCysValArgProLeuTyrIleAspPheArgGlnAspLe
                                                                                                                                                uGlyTrpLysTrpValHisGluProLysGlyTyrTyrAlaAsnPheCysS
                                                                                                                                                                                       erGlyProCysProTyrLeuArgSerAlaAspThrThrHisSerThrVal
                                                                                                                                                                                                                             62 LeuGlyLeuTyrAsnThrLeuAsnProGluAlaSerAlaSerProCysCy
                                                                                                                                                                                                                                                                                                             .........ValGlyArgThrProLysValGluGlnLeuSerAsnMet
                                                                                                                                                                                                                                                                     sValProGlnAspLeuGluProLeuThrIleLeuTyr.......
                              Gaps: 4
Percent Identity: 38.889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Baboon growth differentiation factor-8 cDNA.
                   Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (UYJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
                                                                                      to: 476
                                                                                      to: AAF63557 from: 1
                                                                                                                                                                                                                                                                                                                                                  105 ValValLysSerCysLysCysSer 112
                                                                                                                                                                                                                                                                                                                                                                      GIGGIGGACCGITGCGGAIGCTCG 473
                                                                                                                                                                                                                                                                                                                                                                                                                         ВР
                                                                                                                                                                                                                                                                                                                                                                                                             seq_documentation_block:
ID AAV45817 standard; cDNA; 1128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97US-0862445.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98WO-US02479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97US-0795071
97US-0847910
                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                216.50
3.331
60.185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               McPherron AC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1998-437444/37.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P-PSDB; AAW69886.
                   Quality:
                          Ratio:
Percent Similarity:
                                                       alignment_block:
TGFB3P x AAF63557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO9833887-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                              07-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                05-FEB-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            05-FEB-1997;
28-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-MAY-1997;
        alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              06-AUG-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   therapy; ss
                                                                                    Align seg 1/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Papio sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lee S,
                                                                                                                                                                                                                                                 321
                                                                                                                                                                                                                                                                                                                                                                      450
                                                                                                                                                28
                                                                                                                                                                                       45
                                                                                                                                                                                                          277
                                                                                                                                                                                                                                                                     78
                                                                                                                                                                                                                                                                                        368
                                                                                                                                                                                                                                                                                                            92
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Transgenic animals with gene for growth differentiation factor 9 of disrupted - have increased muscle and reduced cholesterol contents, also use of GDP-8 inhibitors for treating cancer, obesity, an enrommacoular disease an enrommacoular disease content of the c

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93 lyArgThrProLysVal...GluGlnLeuSerAsnMetValValLysSer 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                          93
                                                                                                                                                                                                                                                                                                                                                                      60 ThrValLeuGlyLeuTyrAsnThrLeuAsnProGluAlaSerAlaSerPr 76
                                                                                                                                                                                          28 uGlyTrpLysTrpValHisGluProLysGlyTyrTyrAlaAsnPheCysS
                                                                                                        12 GluGluAsnCysCysValArgProLeuTyrIleAspPheArgGlnAspLe
                                                                                                                                                                                                                                                                                   erGlyProCysPro....TyrLeuArgSerAlaAspThrThrHisSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                        76 oCysCysValProGlnAspLeuGluProLeuThrIleLeuTyrTyrValG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1014 TIGCIGTACTCCCACAAAGATGTCTCCCAATTAATATGCTATATTTAATG
                                                                  to: 1128
                                                              Align seg 1/1 to: AAV45817 from: 1
alignment_block:
TGFB3P x AAV45817
                                                                                                                                                                                                                                                                                   45
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GluGluAsnCysCysValArgProLeuTyrIleAspPheArgGlnAspLe 28

to: 1128

to: AAZ06453 from: 1

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Align seg 1/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Differentiation Factor-8 (GDF-8). Skeletal muscle cDNA libraries from this species were screened with the murine GDF-8 probe, in order to isolate the GDF-8. The absolute conservation of the C-terminal region between species as evolutionarily far apart as humans and chickens, baboons and turkeys, suggests that this region will be highly conserved in many other species as well.

GDF-8 has been shown to result in increased bone and muscle mass (such as ribs) when expressed in reduced amounts. GDF-8 minus transgenic animals and forms of animal feed that can inhibit/reduce production of GDF-8 are of commercial interest.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  of muscle, bone or adipose tissue. A GDF-8 monocloral antibody, GDF-8 antisense molecule or dominant negative polypeptide could be used with foetal or adult muscle cells, bone cells or progenitor cells. These agents can be administered to a partient suffering from a disorder such as muscle wasting disease, neuro muscular disorder, muscle atrophy,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           degenerative diseases, obesity or other adipocyte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New differentiation factor useful for treating neurodegenerative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         growth differentiation factor; tissue growth; muscle growth; cell differentiation; animal feed; muscle disorder; bone degeneration; nerve degeneration; GBF-8; development; transforming growth factor beta; TGF-beta; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This is the cDNA nucleotide sequence of the Baboon Growth
                                                                                                                                            seq_name: /SIDS1/gcgdata/geneseq/geneseqn/NA1999.DAT:AA206453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1128 BP; 371 A; 225 C; 238 G; 294 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cDNA of Baboon Growth Differentiation Factor-8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (UYJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 9; Fig 14a; 138pp; English
                                                                                                                                                                                                           seq_documentation_block:
ID AAZ06453 standard; cDNA; 1128 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99WO-US02511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98US-0124180
98US-0019070
                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                  1114 TGCGGGTGCTCA 1125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     McPherron AC;
109 CysLysCysSer 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1999-494289/41.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P-PSDB; AAY33843
                                                                                                                                                                                                                                                                                                                                                                                                08-DEC-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO9940181-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             05-FEB-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        05-FEB-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12-AUG-1999
                                                                                                                                                                                                                                                                                                                          AAZ06453;
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Gaps: 4 Percent Identity: 40.385

208.50 3.159 63.462

Quality: Ratio:

alignment\_scores:

Percent Similarity: alignment\_block: TGFB3P x AA206453

Length:

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GDF-8; growth differentiation factor receptor; GDF-11; therapy; human; veterinary; medicine; treatment; muscle tissue disease; wasting disease; neuromuscular disorder; muscular atrophy; spinal cord injury; aging; fat; traumatic injury; acquired immune deficiency syndrome; cachexia; baboon; congenital obstructive pulmonary disease; transgenic animal; transgene; food animal; cholesterol; muscle mass; diagnostic; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Recombinant cells that express growth-differentiation factor receptors - and related antibodies, nucleic acids, vector,
                                                                                                                                                                                                                           ......CTGGTACACCAAGCAAACCCCAGAGGTTCAGCAGGCCC 1013
                                              832 GAATCGCGATGCTGTCGTTACCCTCTAACTGTGGATTTT...GAAGCTCT 878
                                                                                                                    929 CTGCAGAGTGTGAATTTGTATTTTTACAAAATATCCTCATACTCAT... 975
                             45
                                                                                                                                                                                                            93
                                                                                                                                                                                                                                                                                                                                                                                         seq_name: /SIDS1/gcgdata/geneseq/geneseqn/NA1999.DAT:AAZ09366
                              uGlyTrpLysTrpValHisGluProLysGlyTyrTyrAlaAsnPheCysS
                                                                                                                                                                                                          oCysCysValProGlnAspLeuGluProLeuThrIleLeuTyrTyrValG
                                                                                         erGlyProCysPro.....TyrLeuArgSerAlaAspThrThrHisSer
                                                                                                                                                60 ThrValLeuGlyLeuTyrAsnThrLeuAsnProGluAlaSerAlaSerPr
                                                                                                                                                                                                                                                                    93 lyArgThrProLysVal...GluGlnLeuSerAsnMetValValLysSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (UYJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "GDF-8"
                                                                                                                                                                                                                                                                                                                                                                                                                                      BP
                                                                                                                                                                                                                                                                                                                                                                                                                      seq_documentation_block:
ID AA209366 standard; cDNA; 1128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98WO-US15598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           97US-0054461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /*tag= a
                                                                                                                                                                                                                                                                                                                                                            1114 TGCGGGTGCTCA 1125
                                                                                                                                                                                                                                                                                                                               CysLysCysSer 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     McPherron A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1999-153789/13.
P-PSDB; AAY31190.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Baboon GDF-8 cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO9906559-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29-OCT-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11-FEB-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAZ09366;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sb.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Papio
                                                                                                                                                                                                                                                                                                  1064
                                                                                                                                                                                                                                                                                                                               109
                             28
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                                                                                                                                                                              916
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Tue Oct 30 12:56:48 2001

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c (ant)agonists, potentially useful therapeutically in human or veterinary medicine. Antibodies derived from the products of the invention are used to treat muscle tissue diseases (particularly wasting diseases, or treat muscle tissue diseases (particularly wasting diseases, neuromuscular disorders, muscular atrophy and aging, e.g. spinal cord and traumatic injury, congenital obstructive pulmonary diseases, acquired immune deficiency syndrome and cachexia). Transgenic, non-human animals immune deficiency syndrome and cachexia). Transgenic, non-human animals that express the products of the invention from a transgene present in germ and somatic cells, specifically where GDF 8 receptor is expressed, may be food animals and have decreased fat and cholesterol contents and increased muscle mass. Peptides derived from the products of the invention and GDF-receptor binding and blocking agents, are reagents and diagnostic agents for studying muscle wasting diseases and for development of therapeutic agents. This sequence encodes the baboon (Papio Sp.) GDF-8 protein which is used in the method of the invention.
                                                                                                                                                                                      growth-differentiation factor-8 (GDF-8) receptor polypeptide or GDF-11 receptor polypeptide. The GDF receptors are used to identify specific
                                                                                                                                                        novel recombinant cell lines that express
transformed cells, peptide fragments and transgenic animals, for treatment and diagnosis of muscle tissue diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1128 BP; 372 A; 224 C; 237 G; 295 T; 0 other;
                                                                                           Examples; Fig 2A; 89pp; English.
                                                                                                                                                               invention describes
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Length: Gaps: Quality: Ratio Percent Similarity alignment\_scores:

alignment block

TGFB3P x AAZ09366

Align seg 1/1

12 GluGluAsnCysCysValArgProLeuTyrIleAspPheArgGlnAspLe

58 879

erGlyProCysPro.....TyrLeuArgSerAlaAspThrThrHisSer 59 45

76 oCysCysValProGlnAspLeuGluProLeuThrIleLeuTyrTyrValG 93

93 lyArgThrProLysVal...GluGlnLeuSerAsnMetValValLysSer 108

CysLysCysSer 112 109

seq\_name: /SIDS1/gcgdata/geneseq/geneseqn/NA1999.DAT:AAX16675

AAX16675;

29-APR-1999

Percent Identity: 40.385 208.50 3.159 63.462

to: 1128 from: 1 to: AAZ09366

928 uGlyTrpLysTrpValHisGluProLysGlyTyrTyrAlaAsnPheCysS 45

TGGATGGGATTGGATTATCGCTCCTAAAAGATATAAGGCCAATTACTGCT

|||||| ||||| ctggagagtgtattttacaaaatatcctcatactcat... 975 929

|||||||||:::||| 1014 TIGCIGTACICCCCACAAAGAIGICTCCCAAITAAIAAIGCIAIAIIITAAIG 1063

1064 GCAAAGAACAAATAATATGGGAAAATTCCAGCCATGGTAGTAGACCGC 1113

1114 TGCGGGTGCTCA 1125

seq\_documentation\_block:
ID AAX16675 standard; DNA; 1554

ВP

(first entry)

Kenopus WA545 protein encoding DNA.

Xenopus; WA545 protein; TGF-beta; transforming growth factor beta; proliferation; differentiation; mesodermal tissue; neural; muscle; bone; cartilage; connective tissue; wound healing; gene therapy; ss 

Xenopus sp

Location/Qualifiers 55..1119 Key

"WA545 protein" /product= "\ 55..774 /\*+\*\* ag= b 5..1116 /\*tag= 775..11] sig\_peptide

WO9902678-A1

mat\_peptide

/\*tag=

21-JAN-1999

98WO-US08334, 24-APR-1998; 97US-0890918. 10-JUL-1997; (GEMY ) GENETICS INST INC. (WHED ) WHITEHEAD INST BIOMEDICAL RES.

Lavallie ER,

Sun B;

Sive H,

Racie LA,

WPI; 1999-120879/10.

P-PSDB; AAW94656

Lansforming growth factor-beta superfamily, used to induce tissue formation and in wound healing

Claim 1; Page 51-52; 73pp; English.

The present sequence encodes the Xenopus WA545 protein. WA545 proteins have the ability to induce, enhance and/or inhibit the formation, growth, proliferation, differentiation, maintenance of mesodermal establishment, proliferation, differentiation, maintenance of mesodermal clissue, including neurons and/or related neural cells and tissues such as brain cells, Schwann cells, glial cells and astrocytes, as well as muscle, nerve, epidermis and/or other connective tissue defects, as well as periodontal disease and healing of various epidermis, nerve, including spinal cord, muscle, including cardiac, striated or smooth muscle, and other tissues and wounds, and other organs such as liver, pancreas, spleen brain, lung, cardiac and kidney tissue. They can also be used to treat or prevent such conditions as osteoarthritis, osteoprosis, and other abnormalities of bone, cartilage, muscle, nerve, epidermis or other connective tissue, organs such as liver, pancreas, spleen, lung, cardiac and kidney and other tissues. They can also be used for wound healing, reduction of fibrosis and reduction of scar tissue formation. They can also be used to induce bone and/or cartilage or other connective tissue formation, and in wound healing and tissue repair and for augmenting the activity of bone morphogenetic proteins. They can also be used for treating cell populations, such as embryonic cells and incleam and for gene therapy and long and for gene therapy applications

Sequence 1554 BP; 503 A; 340 C; 309 G; 402 T; 0 other;

alignment\_scores:

Length: 104 Gaps: 5 Percent Identity: 42.308 2.930 68.269 208.00 Quality: Ratio: Percent Similarity:

alignment\_block:

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seq_name: /SIDS1/gcgdata/geneseq/geneseqn/NA1998.DAT:AAV69286
   erythroid; ovarian follicular maturation; hormone; neuronal survival; spermatogenesis; bone; insulin; cardiac morphogenesis; osteoporosis; osteomalacia; erythropoiesis; heemophilia; cystic fibrosis; immunoassay; menstrual disorder; transgenic; modulator; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Liver activin; beta c; beta e; cell differentiation; haematopoiesis;
                                                                                                                                                                                                                                             1052 ACAACAATGACAATGTGGTACTGAGGCACTATGAAGATATGGTAGTGGAT 1101
                                                                                                                                                                                                92 alGlyArgThrProLysVal...GluGlnLeuSerAsnMetValValLys 107
                                                        908 AGTGCCCCTATCCACTGACGGAATGCTAAGGGGC.....ACAAATCAT 951
                                                                                                                GAACTGGGTCATTGCACCCCGTGGTTACATGGCAAACTACTGCCATGGAG 907
                                                                                                                                     47 roCysProTyr.....LeuArgSerAlaAspThrThrHis 58
                                                                                                                                                                                   SerThrValLeuGlyLeuTyrAsnThrLeuAsnProGluAlaSerAlaSe 75
                                                                                                                                                                                                                                75 rProCysCysValProGlnAspLeuGluProLeuThrIleLeuTyrTyrV 92
                                                                                         31 s...TrpValHisGluProLysGlyTyrTyrAlaAsnPheCysSerGlyP 47
                                                                                                                                                                                                                                                                                                                                                                        seq_name: /SIDS1/gcgdata/geneseq/geneseqn/NA1998.DAT:AAV38238
                                              15 CysCysValArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "activin beta e polypeptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Murine liver activin beta e polypeptide encoding cDNA
                        to: 1554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                       from: 1
                                                                                                                                                                                                                                                                                                                                                                                            _documentation_block:
AAV38238 standard; cDNA; 2125 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              97WO-US20882
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279..1265
                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
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/product=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          216..278
                       Align seg 1/1 to: AAX16675
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                                                                                                                                                                                                                                                                                                                                               1102 GAGTGTGGTTGC 1113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (UNMI ) UNIV MICHIGAN
                                                                                                                                                                                                                                                                                                                          108 SerCysLysCys 111
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TGFB3P x AAX16675
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This cDNA encodes a murine liver activin beta e polypeptide. Sequences derived from a beta c cDNA clone is used for screening and cloning the activin beta e gene. Disorders of cell growth or differentiation (or susceptibility to them) are diagnosed by measuring liver activin gene activity or by detecting a mutation in the liver activin gene. Disorders of haematopolesis, erythroid differentiation, ovarian follicular maturation, hormone secretion, neuronal survival, spermatogenesis, bone formation, insulin secretion or cardiac morphogenesis are some conditions that can be diagnosed using the liver activin. Cell growth and compound or agent that upregulates the compound's expression. Antagonists can be used to treat liver diseases while agonists can be used to creat liver diseases while agonists can be used to creat liver diseases while agonists can be used to creat liver diseases while dayonists.

Increase growth and regeneration of liver tissue. The liver activin compound may also induce bone growth (e.g. for treating osteoporosis, or osteomalacia) or haematopolesis, particularly erythropolesis, e.g. for treating haemophilia, cystic fibrosis or menstrual disorders. Antibodies are useful in immunoassays, to generate anti-fidictypic antibodies (which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      bind to liver activin receptors) and to inhibit liver activin. Also, transpenie animals contrading liver activin gene can be used to produce the liver activin (in correctly processed and modified forms) proteins, or the transgenic animals, are useful for screening for liver activin
                                       for
New isolated nucleic acid encoding sub-units of liver activin - useful for regulating growth and differentiation of cells, e.g. treating liver, bone and haematopoietic disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1000
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Gaps: 6
Percent Identity: 42.453
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                                                                                                                                       Claim 2; Fig 2; 141pp; English
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tgfb3p.rng

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erythroid; ovarian follicular maturation; hormone; neuronal survival; spermatogenesis; bone; insulin; cardiac morphogenesis; osteoporosis; osteomalacia; erythropoiesis; heamophilia; cystic fibrosis; immunoassay; menstrual disorder; transgenic; modulator; ss.
                                                                          activin; beta c; beta e; cell differentiation; haematopolesis;
                                                                                                                                                                                                                                              /number= 1
/note= "activin beta c partial intron (12-kb)"
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/note= "activin beta e promoter region"
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/note= "activin beta e exon
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/note= "contains introns"
8249..8546
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                                                           Sequence of mouse activin genetic loci.
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1463..1994
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/note= "activin
seq_documentation_block:
ID AAV69286 standard; DNA; 10708
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P-PSDB; AAW60617, AAW60618.
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relates to murine beta c and beta e polypeptides and the genes encoding them. Disorders of cell growth or differentiation (or susceptibility to them) are diagnosed by measuring liver activin gene activity or by detecting a mutation in the liver activin gene. Disorders of heematopoiesis, erythroid differentiation, ovarian follicular maturation, hormone secretion, neuronal survival, spermatogenesis, bone formation, insulin secretion or cardiac morphogenesis are some conditions that can be diagnosed using the liver activin. Cell growth and differentiation can be stimulated by treatment with an liver activin compound or agent that upregulates the compound's expression. Antagonists can be used to treat liver diseases while agonists can be used to increase growth and capentation of liver tissue. The liver activin compound may also induce bone growth (e.g. for treating osteoporosis or osteomalacia) or heematopoiesis, particularly erythropoiesis, e.g. for treating cueful in immunoassas, to generate anti-idiotypic antibodies which bind to liver activin receptors) and to inhibit liver activin. Also, transgenic animals containing liver activin gene can be used to produce the liver activin (in correctly processed and modified forms) proteins, or the transgenic animals, are useful for screening for liver activin
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        Disclosure; Fig 4D-G; 141pp; English.
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TGFB3P x AAV69286
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9222 TGTTGTAGGGGAGCCACTATGTAGACTTC...CAGGAGCTGGGGTGGCG 9268

s...TrpValHisGluProLysGlyTyrTyrAlaAsnPheCysSerGlyP 47

31

New isolated nucleic acid encoding sub-units of liver activin - useful for regulating growth and differentiation of cells, e.g. for treating liver, bone and haematopoietic disorders

47 roCys...ProTyrLeuArgSer.....AlaAspThrThrHis

59 SerThrValLeuGlyLeuTyrAsnThrLeuAsnProGluAlaSerAlaSe 75

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28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      78
    This cDNA clone codes for ovine growth differentiation factor-8 (GDF-8) (see AAW69892), a novel member of the transforming growth factor-beta superfamily that appears to relate to various cell.

C proliferative disorders, especially those involving muscle, nerve and adipose tissue. It was isolated from a skeletal muscle cDNA library. The invention provides novel mammalian and avian GDF-8 c proteins (see AAW6983-92). Transgenic non-human animals are claimed in which GDF-8 expression is disrupted or interfered with. Also claimed are: (1) chicken or turkey eggs or meat, beef, milk, pork and lamb from these animals; (2) a method for increasing muscle comess in animals by administering an antibody (Ab) that binds to GDF-8; (3) inhibiting the action of GDF-8 by treating foetal or adult muscle or progenitor cells with a GDF-8 inhibitor; and (4) isolated nucleic acid encoding a GDF-8 protein truncated by loss of the C-terminal active fragment. The transgenic animals have increased muscle mass and for poultry reduced cholesterol contents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Transgenic animals with gene for growth differentiation factor-8 disrupted - have increased muscle and reduced cholesterol contents, also use of GDF-8 inhibitors for treating cancer, obesity,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Growth differentiation factor-8; GDF-8; sheep; transgenic animal; transforming growth factor-beta; muscle; meat; inhibitor; obesity; neuromuscular disease; muscular dystrophy; cachexia; cancer; AIDS;
                                                                                              91 ..TyrValGlyArgThrProLysValGluGlnLeuSerAsnMetValVal 106
                                                                    90
                                                                                                                                                                                                                                                                                                                                           seq_name: /SIDS1/gcgdata/geneseq/geneseqn/NA1998.DAT:AAV45823
  9369 TCTGCCGTCTTTAGCCTCCTCAAAGCCAACAACCCTTGGCCTGCGGGTTC
                                                               75 rProCysCysValProGlnAspLeuGluProLeuThrIleLeuTyr....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sheep growth differentiation factor-8 cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (UXJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 9; Fig 14f; 125pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                               BP
                                                                                                                                                                                                                                                                                                                                                                                        seq_documentation_block:
ID AAV45823 standard; cDNA; 1128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      97US-0862445.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97US-0795071.
97US-0847910.
                                                                                                                                                                                                                                                                                           9516 GAGGCCTGTGGCTGCAGC 9533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98WO-US02479
                                                                                                                                                                                                                                                   107 LysSerCysLysCysSer 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
neuromuscular disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           McPherron AC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1998-437444/37.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P-PSDB; AAW69892.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO9833887-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     07-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         05-FEB-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         05-FEB-1997;
28-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          06-AUG-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ovis aries.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAV45823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lee S,
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Method (3) is used to treat muscle wasting or neuromuscular diseases, muscular atrophy and aging, particularly muscular dystrophy, spinal cord or traumatic injuries, congestive or obstructive lung disease, AIDS and cachexia. Method (4) is used to treat cancer of muscle, connective tissue and bone, or obesity. Also (not claimed) GDF-8 can be used to maintain myoblasts intended for transplanting or to improve efficiency of fusion. Detection may be performed with nucleic acid probes or primers. GDF-8, or sequences encoding it, can also be used to treat cell proliferative disorders associated with underexpression of GDF-8, or expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Growth differentiation factor-8; GDF-8; rat; transgenic animal; transforming growth factor-beta; muscle; meat; inhibitor; obesity; neuromuscular disease; muscular dystrophy; cachexia; cancer; AIDS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1070 AACAAATAATATATGGGAAGATTCCAGGCATGGTAGTAGATCGCTGTGGG 1119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           95 hrProLysVal...GluGlnLeuSerAsnMetValValLysSerCysLys 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |||::::::||||||| | |||||| :::||||||| :::
832 GAATCTCGATGCTGTTACCCTCTAACTGTGGATTTT...GAAGCTTT 878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        972
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        45
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12 GluGluAsnCysCysValArgProLeuTyrIleAspPheArgGlnAspLe 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_name: /SIDS1/gcgdata/geneseq/geneseqn/NA1998.DAT:AAV45820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         erGlyProCysProTyrLeuArgSerAlaAspThrThrHisSerThrVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        uGlyTrpLysTrpValHisGluProLysGlyTyrTyrAlaAsnPheCysS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    879 TGGATGGGATTATTGCACCTAAAAGATATAAGGCCAATTACTGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     929 CTGGAGAATGTGAATTTTTTTTTTTGCAAAAGTATCCTCATACC.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62 LeuGlyLeuTyrAsnThrLeuAsnProGluAlaSerAlaSerProCysCy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sValProGlnAspLeuGluProLeuThrIleLeuTyrTyrValGlyArgT
                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1128 BP; 366 A; 234 C; 241 G; 287 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length: 102
Gaps: 3
Percent Identity: 39.216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rat growth differentiation factor-8 cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Align seg 1/1 to: AAV45823 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      вР
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               207.50
3.192
63.725
                                                                                                                                                                                                                                                                                                                             of a mutant protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1120 TGCTCA 1125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        111 Cysser 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TGFB3P x AAV45823
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO9833887-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                07-DEC-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alignment_block
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAV45820;
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68

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Transgenic animals with gene for growth differentiation factor-8 disrupted - have increased muscle and reduced cholesterol contents, also use of GDF-8 inhibitors for treating cancer, obesity,
                                                   (UYJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE
                                                                                                                                 Example 9; Fig 14d; 125pp; English
                        97US-0862445.
97US-0795071.
97US-0847910.
            98WO-US02479
                                                                                                                     neuromuscular disease
                                                                McPherron AC
                                                                             WPI; 1998-437444/37.
                                                                                   P-PSDB; AAW69889
                               05-FEB-1997;
28-APR-1997;
            05-FEB-1998;
                         23-MAY-1997;
06-AUG-1998
                                                                s,
                                                                 Lee
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This cDNA clone codes for rat growth differentiation factor-8 (GDF-8) (see AAW69889), a novel member of the transforming growth factor-beta superfamily that appears to relate to various cell proliferative disorders, especially those involving muscle, nerve and adipose tissue. It was isolated from a skeletal muscle convalutary. The invention provides novel mammalian and avian GDF-8 proteins (see AAW6988-92). Transgenic non-human animals are claimed in which GDF-8 expression is disrupted or interfered with. Also claimed are: (1) chicken or turkey eggs or meat, beef, milk, pork and lamb from these animals; (2) a method for increasing muscle mass in animals by administering an antibody (Ab) that binds to GDF-8: (3) inhibiting the action of GDF-8 by treating foetal or adult muscle or progenitor cells with a GDF-8 by treating foetal or isolated nucleic acid encoding a GDF-8 protein truncated by loss of the C-terminal active fragment. The transgenic animals have increased muscle mass and for poultry reduced cholesterol contents. Method (3) is used to treat muscle wasting or neuromuscular dystrophy, spinal cord or traumatic injuries, congestive or obstructive lung disease, AIDS and cachexia. Method (4) is used to treat muscle wasting on or obestive. An example of the farmance of muscle, connective tissue and bone, or obestive. for transplanting or to improve efficiency of fusion. Detection may be performed with nucleic acid probes or primers. GDF-8, or sequences encoding it, can also be used to treat cell proliferative disorders associated with underexpression of GDF-8, or expression of a mutant protein.

Sequence 1131 BP; 348 A; 250 C; 266 G; 267 T; 0 other;

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Percent Identity: 39.423
          Length:
                      Gaps:
       207.50
3.097
64.423
           Quality:
                    Ratio:
Percent Similarity:
alignment_scores:
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alignment\_block: TGFB3P x AAV45820

Align seg 1/1 to: AAV45820 from: 1 to: 1131

erGlyProCysPro......TyrLeuArgSerAlaAspThrThrHisSer 59 45

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Process for Refolding Recombinantly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_name: /cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-486-057B-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq_documentation_block:
; Sequence 3, Application US/08486057B
; Patent No. 5650494
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      McMaster, Gary K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cox, David
Schmitz, Albert
Meyhack, Bernd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT
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                                                                                                                                        -MODEL-frame+_p2n.model -DEV=xlh
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-QGAPOF=4.500 -QGAPORT=0.050 -XGAPOF=10.000 -XGAPEXT=0.500
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-DELOP=6.000 -DELEXT=7.000 -STAFT=1 -MAPRIX=bloaum62
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                                                                      About: Results were produced by the GenCore software, version 4.5, Copyright (c) 1993-2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                             -USER=DUFFY097_@CGN1_1_70 -NCPU=6 -ICPU=3 -LONGLOG
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Database: Issued_Patents_NA:*
Database sequences: 324599
Database length: 9465562
Search time (sec): 35.810000
                                     Date: Oct 30, 2001 9:12 AM
                                                                                                                                                                                                                                                                                                                                                                                   Search information block:
                                                                                                                             Command line parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                       length: 113
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1.8e-16 1
16 1393
16 1393
16 1340
-16 1196
16 687 1
16 1633
16 1633
2923
2923
2923 t
                                                                 076-5+ 206.00 429.87 2.5e-16 2923
25-5968-5 + 204.50 445.07 3.6e-17 55
25-5968-11 + 204.50 427.44 3.4e-16 2
27-8608-11 + 204.50 427.44 3.4e-16 2
25-5968-13 + 204.50 427.47 3.4e-16 2
25-5968-13 + 204.50 427.17 3.5e-16 2
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                                                                                                          2.6/ptodata/2/ina/5A_COMB.seq.US-08-555-596B-5 + 204.50 445.07 3.6e-1
2.6/ptodata/2/ina/5A_COMB.seq.US-09-177-860A-5 + 204.50 445.07 3.6e-1
2.6/ptodata/2/ina/6A_COMB.seq.US-09-177-860A-11 + 204.50 427.44 3.4e-1
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2.6/ptodata/2/ina/6A_COMB.seq.US-08-755-596B-13 + 204.50 427.17 3.5e-1
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2.6/ptodata/2/ina/5A_COMB.seq.US-08-755-671-3 + 203.00 437.64 9.2e-17
2.6/ptodata/2/ina/5A_COMB.seq.US-08-755-772-1 + 203.00 437.64 9.2e-17
2.6/ptodata/2/ina/5A_COMB.seq.US-08-447-907A-1 + 203.00 437.64 9.2e-17
2.6/ptodata/2/ina/5A_COMB.seq.US-08-447-907A-1 + 203.00 437.64 9.2e-17
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2.6/ptodata/2/ina/5A_COMB.seq.US-08-477-907A-10 + 203.00 432.34 1.8e-1
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422.72 6.
413.95 1.
413.95 1.
413.95 1.
420.22 8.(
0. 413.33 2.
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1 + 203.00 431.31

-3 + 202.00 431.31

-4 + 201.50 429.60

2 + 200.50 432.50

42 + 200.00 422.72

42 + 200.00 422.72

42 + 200.00 422.72

42 + 200.00 413.33

2 + 200.00 413.33

-24 + 195.00 413.33

-24 + 195.00 413.33

-24 + 195.00 413.33

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/ina/PCTUS_COMB.seq:PCT-US93-08868-24
/ina/PCTUS_COMB.seq:PCT-US93-08885-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ## Optodata/2/ina/5B_COMB.seq:US-08-765-875-14-6/ptodata/2/ina/6A_COMB.seq:US-08-765-875-14-6/ptodata/2/ina/6A_COMB.seq:US-08-765-875-14-6/ptodata/2/ina/6A_COMB.seq:US-08-795-671-1+6/ptodata/2/ina/6A_COMB.seq:US-08-891-789B-1+6/ptodata/2/ina/5A_COMB.seq:US-08-455-550-2+6/ptodata/2/ina/5A_COMB.seq:US-08-459-810-242+6/ptodata/2/ina/5A_COMB.seq:US-08-459-810-32+6/ptodata/2/ina/5A_COMB.seq:US-08-197-792-32+6/ptodata/2/ina/5A_COMB.seq:US-08-197-792-32+6/ptodata/2/ina/5A_COMB.seq:US-08-459-810-32+6/ptodata/2/ina/5A_COMB.seq:US-08-459-214-32+6/ptodata/2/ina/5A_COMB.seq:US-08-459-214-32+6/ptodata/2/ina/5A_COMB.seq:US-08-459-214-32+6/ptodata/2/ina/5A_COMB.seq:US-08-459-214-32+6/ptodata/2/ina/5A_COMB.seq:US-08-459-224+6/ptodata/2/ina/5A_COMB.seq:US-08-459-234+6/ptodata/2/ina/5A_COMB.seq:US-08-415-343A-24+6/ptodata/2/ina/5A_COMB.seq:US-08-412-673-24+6/ptodata/2/ina/5A_COMB.seq:US-08-412-673-34+6/ptodata/2/ina/5A_COMB.seq:US-08-412-673-34+6/ptodata/2/ina/5A_COMB.seq:US-08-412-673-34+6/ptodata/2/ina/5A_COMB.seq:US-08-412-673-34+6/ptodata/2/ina/5A_COMB.seq:US-08-412-673-34+6/ptodata/2/ina/5A_COMB.seq:US-08-412-673-34+6/ptodata/2/ina/5A_COMB.seq:US-08-412-673-34+6/ptodata/2/ina/5A_COMB.seq:US-08-412-673-34+6/ptodata/2/ina/5A_COMB.seq:US-08-412-673-34+6/ptodata/2/ina/5A_COMB.seq:US-08-412-673-34+6/ptodata/2/ina/5A_COMB.seq:US-08-412-673-34+6/ptodata/2/ina/5A_COMB.seq:US-08-412-673-34+6/ptodata/2/ina/5A_COMB.seq:US-08-412-673-34+6/ptodata/2/ina/5A_COMB.seq:US-08-412-673-34+6/ptodata/2/ina/5A_COMB.seq:US-08-412-953A-24+6/ptodata/2/ina/5A_COMB.seq:US-08-412-953A-24+6/ptodata/2/ina/5A_COMB.seq:US-08-412-953A-24+6/ptodata/2/ina/5A_COMB.seq:US-08-412-953A-24+6/ptodata/2/ina/5A_COMB.seq:US-08-412-953A-24+6/ptodata/2/ina/5A_COMB.seq:US-08-412-953A-24+6/ptodata/2/ina/5A_COMB.seq:US-08-412-953A-24+6/ptodata/2/ina/5A_COMB.seq:US-08-412-953A-24+6/ptodata/2/ina/5A_COMB.seq:US-08-412-953A-24+6/ptodata/2/ina/5A_COMB.seq:US-08-412-953A-24+6/ptodata/2/ina/5A_COMB.seq:US-08-412-953A-24+6/ptodata/2/ina/5A_COMB.seq:US-08-412-953A-24+6/ptodata/2/i
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2/ina/5B_COMB.seq:US-08-461:
2/ina/5B_COMB.seq:US-08-912:
2/ina/6A_COMB.seq:US-08-278:
2/ina/6A_COMB.seq:US-08-445:
2/ina/6A_COMB.seq:US-08-480-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /ina/5A_COMB.seq:US-07-71
/ina/5A_COMB.seq:US-08-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMB.seq:US-08-27
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151 CTCCGCAGTGCAGACACACCCACAGCACGGTGCTGGGACTGTACAACAC 200 201 TCTGAACCCTGAAGCATCTGCCTCGCCTTGCTGCGTGCCCCAGGACCTGG 250 APPLICANT: Nimni, Marcel E.
APPLICANT: Hall, Frederick L.
APPLICANT: Tuan, Tal-Lan
APPLICANT: Tuan, Tal-Lan
APPLICANT: Wu, Lingtao
APPLICANT: Cheung, David T.
TITLE OF INVENTION: Transforming Growth Factor B Fusion
TITLE OF INVENTION: and
TITLE OF INVENTION: Their Use in Wound Healing
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS: seq\_name: /cgn2\_6/ptodata/2/ina/5A\_COMB.seq:US-08-470-837-33 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG Gaps: 0 Percent Identity: 100.000 ADDRESSEE: Merchant & Gould STREET: 11150 Santa Monica Boulevard, Suite 400 SYSTEM: PC-DOS/MS-DOS PatentIn Release #1.0, Version #1.30 34,051 R: 30630-1US01 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,837 NAME: Sharp, Janice A.
REGISTRATION NUMBER: 34,051
REFERENCE/DOCKET NUMBER: 36
TELECOMMUNICATION INFORMATION: TELEFAX: 310-445-9031 INFORMATION FOR SEQ ID NO: 33: ATTORNEY/AGENT INFORMATION: 310-445-1140 339 base pairs SEQUENCE CHARACTERISTICS: 310-445-9031 Quality: 633.00 Ratio: 5.652 Percent Similarity: 100.000 mat\_peptide FILING DATE: CLASSIFICATION: 424 TYPE: nucleic acid STRANDEDNESS: doub MOLECULE TYPE: CDNA FEATURE: CITY: Los Angeles STATE: California OPERATING SYSTEM: SOFTWARE: PatentI 1..336 linear TELEPHONE: NAME/KEY: TOPOLOGY: LOCATION: NAME/KEY: alignment\_scores: ; LOCATION: US-08-470-837-33 29

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84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
                                                                                                                                                                                                         1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17
                                                                                                                    17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 3, Application US/08789588
Patent No. 5922846
GENERAL INFORMATION:
APPLICANT: Cerletti, Nico
APPLICANT: Cox, David
APPLICANT: Schmitz, Albert
APPLICANT: Schmitz, Albert
APPLICANT: Methack, Bernd
TITLE OF INVENTION: Process for Refolding Recombinantly
TITLE OF INVENTION: Produced TGF-beta-like Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_name: /cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-789-588-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF EXCURDES: 43
CORRESPONDENCES: 43
CORRESPONDENCES: 43
ADDRESSES: Henry P. No. 5922846ak
STREET: 520 White Plains Road, P.O. Box 2005
CITY: Tarrytown
STATE: New York
COUNTRY: U.S.A.
ZIP: 10591-9005
COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/789,588
                                                               to: 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                101 LeuSerAsnMetValValLysSerCysLysCysSer 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  301 CTCTCCAACATGGTGGTGAAGTCTTGTAAATGTAGC 336
                                                           Align seg 1/1 to: US-08-470-837-33 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/486,057
FILING DATE: 07-UUN-1995
APPLICATION NUMBER: US 08/201,703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             UMBER: US 08/201,703
25-FEB-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 25-FEB-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/960,309
FILING DATE: 13-OCT-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
                   TGFB3P x US-08-470-837-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq_documentation_block
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alignment_block
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No. 6057430el process for the production of biologically active dimeric protein 84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100 34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50 67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84 seg\_name: /cgn2\_6/ptodata/2/ina/6A\_COMB.seq:US-09-123-233-5 Quality: 633.00 Length: 112 Ratio: 5.652 Gaps: 0 Percent Similarity: 100.000 Percent Identity: 100.000 Align seg 1/1 to: US-08-789-588-3 from: 1 to: 339 ATOMICATION NUMBER: GB 8927546.5
FILING DATE: 06-DEC-1989
ATTOMEN'S CONTROLL OF CONTROL OF C 101 LeuSerAsnMetValValLysSerCysLysCysSer 112 APPLICATION NUMBER: US 07/621,502 FILING DATE: 03-DEC-1990 us/09123233 LENGTH: 339 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLLGY: linear
MOLECULE TYPE: DNA (genomic) FILING DATE: 03-DEC-1 PRIOR APPLICATION DATA: Sequence 5, Application Patent No. 6057430 GENERAL INFORMATION: APPLICANT: TITLE OF INVENTION: TITLE OF INVENTION: NUMBER OF SEQUENCES: alignment\_block: TGFB3P x US-08-789-588-3 \_documentation\_block: ; NAME/KEY: ; LOCATION: US-08-789-588-3 alignment\_scores:

30 Rockefeller Plaza

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    Sequence 1, Application PC/TUS9104541
    GENERAL INFORMATION:
    APPLICANT: Oncogene Science Inc.
    TITLE OF INVENTION: TISSUE DERIVED TUMOR GROWTH INHIBITORS:
    NUMBER OF SEQUENCES: 2
    CORRESPONDENCE S:
    ADDRESSE: Cooper & Dunham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq_name: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:PCT-US91-04541-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GCTTTGGACACCAATTACTGCTTCCGCAACTTGGAGGAGAACTGCTGTGT 50
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/123,233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percent Identity: 100.000
                                                                                                                                                                                                                                                                                                                                  IMMEDIATE SOURCE:
CLONE: E. coli LC137/pPLMu.hTGF-beta3 (DSM 5658)
                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: 1..336
COTHER INFORMATION: /product= "human TGF-beta3"
US-09-123-233-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Align seg 1/1 to: US-09-123-233-5 from: 1 to: 339
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps:
                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: CDNA to mRNA
                                                                                                                                                                 CLASSIFICATION: 530
INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
LENGTH: 339 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Quality: 633.00
Ratio: 5.652
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              alignment_block:
TGFB3P x US-09-123-233-5
                                                                                                                                                                                                                                                                                              linear
                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: CDS
                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                                                                                         TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        alignment_scores
                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
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34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
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Percent Identity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Transforming Growth Factor-Beta 3
                                                                                                                                                                                                                                                            1919/22669-F-PCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length:
                                                                                                                                                            APPLICATION NUMBER: PCT/US91/04541
FILING DATE: 19910625
                                                                                                             OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.24
CURRENT APPLICATION DATA:
                                                                                                                                                                                                       ATTORNEY AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE, DOCKET NUMBER: 1919,
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEX: 42253 COOP UI
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2529 base pairs
                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: RIOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; NAME/KEY: mat_peptide
; LOCATION: 263..1498
; OTHER INFORMATION:
PCT-US91-04541.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ratio: 5.652
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Quality: 633.00
                                                                                                                                                                                                                                                                                                                                                                                           TYPE: NUCLEIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TGFB3P x PCT-US91-04541-1
                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: CDNA HYPOTHETICAL: N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: 263..14 OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                           linear
                New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ANTI-SENSE: N
FRAGMENT TYPE: N-
ORIGINAL SOURCE:
ORGANISM: Trans
New York
                                                                                                                                                                                            CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: CDS
LOCATION: 263
                                 USA
                                            10112
                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY:
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                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alignment_block
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seq_documentation_block:
;Patent No. 5262319
; Patent No. 5262319
; Petent No. 5262319
; PETER T.;HALEY, JOHN D.
; PETER T.;HALEY, JOHN D.
; TITLE OF INVENTION: METHOD FOR OBSTAINING BONE MARROW FREE
;OF TUMOR CELLS USING TRANSFORMING GROWTH FACTOR B3
; NUMBER OF SEQUENCES: 9
; UNMBER OF SEQUENCES: 9
; UNMBER OF SEQUENCES: 9
; TILING DATE: 25-JUN-1990
; FILING DATE: 25-JUN-1990
; FILING DATE: 17-MAY-1989
; APPLICATION NUMBER: 183,410
; FILING DATE: 20-OCT-1986
; APPLICATION NUMBER: 111,022
; FILING DATE: 20-OCT-1986
; APPLICATION NUMBER: 922,121
; FILING DATE: 07-APR-1986
; APPLICATION NUMBER: 922,033
; FILING DATE: 07-APR-1986
; FILING DATE: 07-APR-1986
; FILING DATE: 07-APR-1986
; FILING DATE: 07-APR-1986
; FILING DATE: 19-APR-1985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1363 TCTGAACCCTGAAGCATCTGCCTCGCCTTGCTGCGTGCCCCAGGACCTGG 1412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1312
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               67
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67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG
                                            1363 TCTGAACCCTGAAGCATCTGCCTCGCCTTGCTGCGTGCCCCAGGACCTGG
                                                                                                                    1413 AGCCCCTGACCATCCTGTACTATGTTGGGAGGACCCCCAAAGTGGAGCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1263 ATGAACCTAAGGGCTACTATGCCAACTTCTGCTCAGGCCCTTGCCCATAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG
                                                                                                                                                                                                                                                                                           seq_name: /cgn2_6/ptodata/2/ina/backfiles1.seq:5262319-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps: 0
Percent Identity: 100.000
                                                                                                                                                                                                                                         1463 CTCTCCAACATGGTGGTGAAGTCTTGTAAATGTAGC 1498
                                                                                                                                                                                          101 LeuSerAsnMetValValLysSerCysLysCysSer 112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ratio: 5.652
Percent Similarity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alignment_block:
TGFB3P x 5262319-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 2529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO:1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21
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84 luProLeuThrIleLeuTyrTyrValGlyArqThrProLysValGluGln 100

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1413 AGCCCCTGACCATCCTGTACTATGTTGGGAGGACCCCCAAAGTGGAGGAGCAG 1462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1259 ATGAACCTAAGGCTACTATGCCAACTTCTGCTCAGGCCCTTGCCCGTAC 1308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1409 AGCCCCTGACCATCCTGTACTACGTCGGGAGGACCGCCAAGGTGGAGCAG 1458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
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                                                                                                                                                    17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq_name: /cgn2_6/ptodata/2/ina/backfiles1.seq:5168051-10
                                                                                                                    seq_name: /cgn2_6/ptodata/2/ina/backfiles1.seq:5168051-9
                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps: 0
Percent Identity: 98.214
                                                                                  1463 CTCTCCAACATGTGGTGTAAGTCTTGTAAATGTAGC 1498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1459 CICICITAACAIGGIGGIGGAAGICCIGCAAGIGCAGC 1494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              101 LeuSerAsnMetValValLysSerCysLysCysSer 112
                                                                                                                                                                                                                                                                                                                                                                                                   Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Align seg 1/1 to: 5168051-9 from: 1 to: 2671
                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/389,929
FILING DATE: 04-AUG-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/07/389,929
FILING DATE: 04-AUG-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                 621.00
5.595
99.107
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Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
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TGFB3P x 5168051-9
                                                                                                                                                                                                                                                                                                              LENGTH: 2671
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                                                                                                                                                                                                                                                                                                                                                                                    alignment_scores:
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                                                                                                                                                                                                                                                                                                SEQ ID NO:9
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No. 6057430el process for the production of biologically active dimeric protein
                                                                                                                                                                                                                                                                                                                                                                       luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
                                                                                                                                                                                                                34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
                                                                                                                                                                                            1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17
                                                                                                                                                                                                                                                                        17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
                                                                                                                                                                                                                                                                                                                                                                                                                             51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TCTGAACCCTGAAGCATCTGCCTCGCCTTGCTGCATGCCCCAGGACCTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO) CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/123,233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq_name: /cgn2_6/ptodata/2/ina/6A_COMB.seq:US-09-123-233-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLONE: E. coli LC137/pPLMu.TGF-betal(44/45)beta3 FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "recombinant hybrid DNA of
DESCRIPTION: TGF-betal and TGF-beta3 DNA"
                                                         Percent Identity: 98.214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             to: 2173
                                       Gaps:
                   Length:
                                                                                                                                                      Align seg 1/1 to: 5168051-10 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 7, Application US/09123233
Patent No. 6057430
GENERAL INFORMATION:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 530
INFORMATION FOR SEQ ID NO: 7
SEQUENCE CHARACTERISTICS:
LENGTH: 336 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: NO.
TITLE OF INVENTION: DIOJ
NUMBER OF SEQUENCES: 14
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
                                       5.405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: mat_peptide LOCATION: 1..132
                 600.00
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                   Quality:
Ratio:
                                                       Percent Similarity:
                                                                                                                   TGFB3P x 5168051-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
alignment_scores
                                                                                                 alignment_block
                                                                                                                                                                                                                                                                                                             328
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TITLE OF INVENTION: No. 6057430el process for the production of TITLE OF INVENTION: biologically active dimeric protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           201 TCTGAACCCTGAAGCATCTGCCTCGCCTTGCTGCGTGCCCAGGACCTGG 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        84 luProLeuThrileLeuTyrTyrValGlyArgThrProLysValGluGln 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     251 AGCCCCTGACCATCCTGTACTATGTTGGGAGGACCCCCAAAGTGGAGCAG 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 14
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
APPLICATION NUMBER: US/09/123,233
                                                                                                                                                                                     /product= "hybrid TGF-beta named TGF-betal-3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq_name: /cgn2_6/ptodata/2/ina/6A_COMB.seq:US-09-123-233-9
     amino
                                                                                                                                                                                                                                                                                                        Length: 112
Gaps: 0
Percent Identity: 92.857
                                                                                                                                                                                                                                                                                                                                                                                                                                          from: 1 to: 336
/product= "N-terminal 44 acids of human TGF-betal'
                                                                                             /product= "C-terminal 68 acids of human TGF-beta3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    101 LeuSerAsnMetValValLysSerCysLysCysSer 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       301 CTCTCCAACATGGTGGTGAAGTCTTGTAAATGTAGC 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Align seg 1/1 to: US-09-123-233-7
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                                                        mat_peptide
                                                                                                                                                                                                                                                                                                      595.00
5.459
97.321
                                                                                                                            FEATURE:

NAME/KEY: CDS

LOCATION: 1..336

OTHER INFORMATION:

US-09-123-233-7
                                                      NAME/KEY: mat_peptic
LOCATION: 133..336
OTHER INFORMATION: ,
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                  alignment_block:
TGFB3P x US-09-123-233-7
                                                                                                                                                                                                                                                                                                    Quality:
Ratio:
Percent Similarity:
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                                                                                                                                                                                                                                                                                    alignment_scores
                                      FEATURE:
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biologically active dimeric protein
TITLE OF INVENTION: biologically active dimeric proteinumber OF SEQUENCES: 14
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GCTTTGGACACCAATTACTGCTTCCGCAACTTGGAGGAGAACTGCTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: 1.336
COTHER INFORMATION: /product= "hybrid TGF-beta3-2"
US-09-123-233-11
                                                                                                                                                                                                                                                                                                                                                                                    CLONE: E. coli LC137/pPLMu.TGF-beta3(44/45)beta2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps: 0
Percent Identity: 88.393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Align seg 1/1 to: US-09-123-233-11 from: 1 to: 336
                                                                                                                                                                                                                                     LENGTH: 336 base pairs

TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "recombinant hybrid DNA
DESCRIPTION: coding for hybrid TGF-beta3-2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product= "N-terminal 44 acids of human TGF-beta3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product= "C-terminal 68 acids of human TGF-beta2'
                                                                                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/123, 233
                                                                                                                                                                                                       11:
                                                                                                                                                                                  CLASSIFICATION: 530
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: mat_peptide LOCATION: 1..132
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95.536
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OTHER INFORMATION:
OTHER INFORMATION:
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OTHER INFORMATION:
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Ratio:
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                                                                                                                                                                  FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             101 ACGAACCCAAAGGGTACAATGCCAACTTCTGCTCAGGCCCTTGCCCATAC 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq_name: /cgn2_6/ptodata/2/ina/6A_COMB.seq:US-09-123-233-11
                                                                                                                                                                                               NAME/KEY: mat_peptide
LOCATION: 1..132
OTHER INFORMATION: /product= "N-terminal 44 amino
OTHER INFORMATION: acids of human TGF-beta2"
FEATURE:
                                                                                                                                                                                                                                                                                                                                amino
                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: 1..336
CTHER INFORMATION: /product= "hybrid TGF-beta2-3"
US-09-123-233-9
                                                                                                                                      IMMEDIATE SOURCE:
CLONE: E. coli LC137/pPLMu.TGF-beta2(44/45)beta3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Identity: 91.071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Align seg 1/1 to: US-09-123-233-9 from: 1 to: 336
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DESCRIPTION: /desc = "recombinant hybrid DNA
DESCRIPTION: coding for hybrid TGF-beta2-3"
                                                                                                                                                                                                                                                                                                                            /product= "C-terminal 68 acids of human TGF-beta3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 11, Application US/09123233; Patent No. 6057430; GENERAL INFORMATION:
             LENGTH: 336 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                         NAME/KEY: mat_peptide
LOCATION: 133..336
OTHER INFORMATION: /pr
OTHER INFORMATION: aci
 SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5.373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               591.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alignment_block:
TGFB3P x US-09-123-233-9
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TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                seq_documentation_block
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ratio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY:
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amino

Length:

amino

FEATURE:

20

201

29

51

84

84 luProLeuThrileLeuTyrTyrValGlyArgThrProLysValGluGln 100 17 largProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34 34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50 67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84 1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17 APPLICANT: Namni, Marcel E.
APPLICANT: Hall, Frederick L.
APPLICANT: Tuan, Tai-Lan
APPLICANT: Tuan, Tai-Lan
APPLICANT: Wu, Lingtao
APPLICANT: Cheung, David T.
ITTLE OF INVENTION: Transforming Growth Factor B Fusion
TITLE OF INVENTION: and
TITLE OF INVENTION: Their Use in Wound Healing
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS: seq\_name: /cgn2\_6/ptodata/2/ina/5A\_COMB.seq:US-08-470-837-31 E: Merchant & Gould 11150 Santa Monica Boulevard, Suite 400 to: 339 PatentIn Release #1.0, Version #1.30 LeuSerAsnMetValValLysSerCysLysCysSer 112 from: 1 30630-1US01 APPLICATION NUMBER: US/08/470,837 PC-DOS/MS-DOS to: US-08-486-057B-2 COUNTRIE .....
ZIP: 90025-3395
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible 34,051 REFERENCE/DOCKET NUMBER: 3C TELECOMMUNICATION INFORMATION: INFORMATION FOR SEQ ID NO: 31: ATTORNEY/AGENT INFORMATION:
NAME: Sharp, Janice A.
REGISTRATION NUMBER: 34,0 LENGTH: 339 base pairs TYPE: nucleic acid SEQUENCE CHARACTERISTICS: CURRENT APPLICATION DATA: 310-445-9031 CLASSIFICATION: 424 CITY: Los Angeles STATE: California OPERATING SYSTEM: FILING DATE: ADDRESSEE: SOFTWARE: COUNTRY: Align seg 1/1 STREET: 101

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84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
                                                                                                                                                                                                                                                                                                                                                                             1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Cerletti, Nico
APPLICANT: McMaster, Gary K.
APPLICANT: Cox, David
APPLICANT: Cox, David
APPLICANT: Schmitz, Albert
APPLICANT: Meyhack, Bernd
TITLE OF INVENTION: Produced TGF-beta-like Proteins
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq_name: /cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-789-588-2
                                                                                                                                                                                                          535.00 Length: 112
5.095 Gaps: 0
93.750 Percent Identity: 79.464
                                                                                                                                                                                                                                                                                                                            Align seg 1/1 to: US-08-470-837-31 from: 1 to: 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Henry P. No. 5922846ak
STREET: 520 White Plains Road, P.O. Box 2005
CITY: Tarrytown
STATE: New York
COUNTRY: U.S.A.
ZIP: 10591-9005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_documentation_block:
    Sequence 2, Application US/08789588
    Patent No. 5922846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                         NAME/KEY: mat_peptide LOCATION: 1
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                                                                             alignment_block:
TGFB3P x US-08-470-837-31
          MOLECULE TYPE: CDNA FEATURE:
                                                                             1..336
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                                                               NAME/KEY: CDS
                                                                                                                                                                                                                                          Percent Similarity
                                                                             LOCATION:
FEATURE:
                                                                                                                                                                                               alignment_scores:
                                                                                                                                              US-08-470-837-33
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84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
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                                    Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Align seg 1/1 to: US-08-789-588-2 from: 1 to: 339
                                                                                                                                                                                                                                                                                                                                                                             PRIOR AFFLEX.

APPLICATION NUMBER: GB 0>2...

FILING DATE: 06-DEC-1989

ATTORNEY/AGENT INFORMATION:

NAME: NO. 5922846k, Henry P.

REGISTRATION NUMBER: 33200

REGISTRATION INFORMATION:

FELECOMMUNICATION INFORMATION:

TELECHONE: (908) 277-5110

TELEPAX: (908) 277-5110

TELEPAX: (908) 277-5310

TELEPAX: (908) 277-4366

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 339 base pairs

TENGTH: 330 base pairs

TENGTH: 330 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps:
                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/960,309
FILING DATE: 13-0CT-1992
PROOR APPLICATION DATA:
APPLICATION NUMBER: US 07/621,502
FILING DATE: 03-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 8927546.5
                                                                                                                   CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/486,057
FILING DATE: 07-40N-1995
APPLICATION NUMBER: US 08/201,703
FILING DATE: 25-PEB-1994
                                       SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/789,588
IBM PC compatible YSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: DNA (genomic)
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5.095
93.750
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TGFB3P x US-08-789-588-2
                   OPERATING SYSTEM:
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US-08-789-588-2
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Quality:
Ratio:
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                                                                                                      FILING DATE
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251 AACCTCTAACCATTCTCTACTACATTGGCAAAACACCCAAGATTGAACAG 300
                                                                                                                                                                                                                                                       No. 6057430el process for the production of biologically active dimeric protein
251 AACCTCTAACCATTCTCTACTACATTGGCAAAACACCCAAGATTGAACAG 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20
                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO) CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/123,233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh
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IMMEDIATE SOURCE:
CLONE: E. coli LC137/PPLMu.hTGF-beta2 (DSM5657)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Identity: 79.464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; NAME/KEY: CDS
; LOCATION: 1..336
; O'HENFORMATION: /product= "human TGF-beta2":
US-09-123-233-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Align seg 1/1 to: US-09-123-233-3 from: 1 to: 339
                                     101 LeuSerAsnMetValValLysSerCysLysCysSer 112
                                                         Length:
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                                                                                                                                                                                                                                                   TITLE OF INVENTION: No. 6057430el pr
TITLE OF INVENTION: biologically act
NUMBER OF SEQUENCES: 14
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
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Patent No. 6057430
GENERAL INFORMATION:
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FILLING DATE:
CLASSIFICATION: 530
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 339 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 535.00
5.095
93.750
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TGFB3P x US-09-123-233-3
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1088 GCTTTGGAFGCGGCCTATTGCTTTAGAAATGTGCAGGATAATTGCTGCCT 1137
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Percent Identity: 79.464
                                                                                                                                                                      APPLICANT: Mu-ED LEE
APPLICANT: Mark A. Perrella
TITLE OF INVENTION: FACTOR- INHIBITS
TITLE OF INVENTION: FACTOR- INHIBITS
TITLE OF INVENTION: SYNTHASE GENE
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
101 LeuSerAsnMetValValLysSerCysLysCysSer 112
                      COUNTRY: U.S.A.

ZIP: 02110-2804

COMPUTER READBLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

COMPUTER: IBM PS/2 Model 50Z or 55SX

OPERATING SYSTEM: MS-DOS (Version 5.0)

SOFTWARE: WordPerfect (Version 5.1)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US94/03705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AFFILING DATE:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Janis K. Fraser
REGISTRATION NUMBER: Reg. No. 34,819
                                                                                                                     REFERENCE/DOCKET NUMBER: 0
TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5 April 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEX: 200154
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1695
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5.095
93.750
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                         Massachusetts
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TGFB3P x PCT-US94-03705-4
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STREET: 22.
-mv: Boston
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Quality:
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PCT-US94-03705-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX:
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Tue Oct ,30 12:56:49 2001

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Page 11

1657 CATAAATCCAGAAGCATCTGCTTCTCCTTGCTGCGTGTCCCAAGATTTAG 1706

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1238 TIATGGAGTTCAGACACTCAGCACGCAGGGTCCTGAGCTTATATAATAC 1287
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;Patent No. 5221620
;Patent No. 5221620
;APPLICANT: PURCHIO,ANTHONY F.:MADISEN, LINDA;WEBB, NANCY ITTLE OF INVENTION: CLONING AND EXPRESSION OF TRANSFORMING;GNOWTH FACTOR BETA-2
;RUMBER OF SEQUENCES: 16
;CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17
34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr
                                                                                 51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh
                                                                                                                                                                   67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG
                                                                                                                                                                                                                                                                                                                                                                                                                           seq_name: /cgn2_6/ptodata/2/ina/backfiles1.seq:5221620-1
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Percent Identity: 79.464
                                                                                                                                                                                                                                                                                                                                     Length:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US,07/446,020
FILING DATE: 05-DEC-1989
FRIOR APPLICATION DATA:
APPLICATION NUMBER: 285,140
FILING DATE: 16-DEC-1988
APPLICATION NUMBER: 234,065
FILING DATE: 18-AUG-1988
APPLICATION NUMBER: 148,267
FILING DATE: 25-JAN-1988
APPLICATION NUMBER: 106,752
FILING DATE: 06-OCT-1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            from: 1
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5.095
93.750
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84

67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG

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seq_documentation_block:
;Patent No. 5221620
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; APPLICANT: PURCHIO, ANTHONY F.; MADISEN, LINDA; WEBB, NANCY TITLE OF INVENTION: CLONING AND EXPRESSION OF TRANSFORMING; GROWTH FACTOR BETA-2
; GROWTH FACTOR BETA-2
; UNUMBER OF SEQUENCES: 16
; UNUMBER OF SEQUENCES: 16
; FILING DATE: 05-DEC-1989
; PRIOR APPLICATION NUMBER: 285,140
; FILING DATE: 16-DEC-1988
; APPLICATION NUMBER: 234,065
; FILING DATE: 18-MG-1988
; APPLICATION NUMBER: 134,267
; FILING DATE: 25-JAN-1988
; FILING DATE: 25-JAN-1988
; FILING DATE: 25-JAN-1988
; FILING DATE: 25-JAN-1988
; FILING DATE: 06-OCT-1987
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1095 GCTTTGGATCCGGCCTATTGCTTTAGAAATGTGCAGCATAATTGCTGCCT 1144
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84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
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Percent Identity: 79.464
                                                                                                         101 LeuSerAsnMetValValLysSerCysLysCysSer 112
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5.115
92.857
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ratio:
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TGFB3P x 5221620-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 2207
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO:3
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## Sequence 1, Application US/08486057B
## Sequence 1, Applicant: McMaster, Gary K.
## APPLICANT: Oox, David
## APPLICANT: Schmitz, Albert
## APPLICANT: Schmitz, Albert
## APPLICANT: Meyhack, Bernd
## TITLE OF INVENTION: Process for Refolding Recombinantly
## TITLE OF INVENTION: Produced TGF-beta-like Proteins
## ADPLICANT: ADPLI
         84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
                                                                                                                                                                                                                                                                                                                                                              seq_name: /cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-486-057B-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                101 LeuSerAsnMetValValLysSerCysLysCysSer 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4-17861/+/Cont3
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....ск: US/08/486,057B
07-JUN-1995
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PRIOR APPLICATION DATA.
APPLICATION NUMBER: US 08/201,703
FILING DATE: 25-FEB-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/960,309
FILING DATE: 13-OCT-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/621,502
FILING DATE: 03-DEC-1990
PRIOR APPLICATION NUMBER: US 07/621,502
FILING DATE: 06-DEC-1999
ATTORNEY/AGENT INFORMATION:
NAME: NO. 5650494ak, Henry P.
RESISTRATION NUMBER: 33200
RESISTRATION NUMBER: 33200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 520 White Plains Road, P.O. CITY: Tarrytown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: DNA (genomic)
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INFORMATION FOR SEQ ID NO: 1
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LENGTH: 339 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 07 CLASSIFICATION:
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LOCATION:
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                                                                                                                                                                                  APPLICANT: PURCHIO, ANTHONY F.
APPLICANT: MADISEN, LINDA
APPLICANT: MADISEN, LINDA
APPLICANT: MEMENIN, JUNE RAE
TITLE OF INVENTION: TGF-bJ/b2: A NOVEL CHIMERIC TRANSFORMING
TITLE OF INVENTION: GROWTH FACTOR-BETA
GORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1154 ACGTCCGCTTTACATTGATTTCAAGAGGGATCTAGGCTGGAAGTGGATCC 1203
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17
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seq_name: /cgn2_6/ptodata/2/ina/5A_COMB.seq:US-07-669-171-3
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                                                                                                                                                                                                                                                                                                                                                                 STREET: 1155 AVENUE OF THE AMERICAS CITY: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/669,171
FTT-ING DATE: 19910314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                             eq_documentation_block:
Sequence 3. Application US/07669171
Patent No. 5304541
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-909
TELEFAX: 212-869-9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1569 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: SINGle
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MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: MISROCK, S. LESLIE
REGISTRATION NUMBER: 18,8
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Quality: 513.00
Ratio: 5.079
nilarity: 90.179
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MEDIUM TYPE: Floppy
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CLASSIFICATION: 435
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TGFB3P x US-07-669-171-3
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Percent Similarity:
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alignment\_scores:

US-07-669-171-3

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"Squence 29, Application US/08470837

Squence 29, Application US/08470837

Patent No. 5800811

GENERAL INFORMATION:

APPLICANT: Nimni, Marcel E.

APPLICANT: Tuan, Tai-Lan

APPLICANT: Tuan, Tai-Lan

APPLICANT: Wu, Lingtao

TITLE OF INVENTION: Transforming Growth Factor B Fusion

TITLE OF INVENTION: Their Use in Wound Healing

TITLE OF INVENTION: Their Use in Wound Healing

NUMBER OF SEQUENCES: 34

CORRESPONDENCE ADDRESS:

ADDRESSE: Merchant & Gould

STREET: 11150 Santa Monica Boulevard, Suite 400

CITY: Los Angeles

COUNTRY: USA

710.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            201 GCATAACCGGGGGGCCCTCGGCGGGCGCGTGCTGCGTGCCGCAGGCGCTGG 250
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                                                                                                                                                                                                                                                                                                                                                                                                          51 GCGCCAGCTGTACATTGACTTCCGCAAGGACCTCGGCTGGAAGTGGATCC 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
                                                                                                                                                                                                                                                                                                1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               seq_name: /cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-470-837-29
                                                                                                                                      Percent Identity: 76.786
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,837
                                                                                                                                                                                                                                                       from: 1 to: 339
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OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                     Align seg 1/1 to: US-08-486-057B-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 90025-3395
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                                                            5.102
87.500
                                                                                         500.00
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                                                                                                                                                                                 alignment_block:
TGFB3P x US-08-486-057B-1
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                                                                  alignment_scores:
Quality:
                                                                                                            Ratio:
Percent Similarity:
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US-08-486-057B-1
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84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 AlaLeuAspThrasnTyrCysPheArgAsnLeuGluGluAsnCysCysVa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 GCCCTGGACACCAACTATTGCTTCAGCTCCACGGAGAAGAACTGCTGCGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr
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Percent Identity: 76.786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             from: 1 to: 339
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               34,051
FR: 30630-1US01
NAME: Sharp, Janice A.
REGISTRATION NUMBER: 34,051
REFERENCE/DOCKET NUMBER: 30631
TELECOMMUNICATION INFORMATION:
TELEPHONE: 310-445-1140
INFORMATION FOR SEO ID NO: 29:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Align seg 1/1 to: US-08-470-837-29
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; Sequence I, Application US/08789588
; Setent No. 5922846
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cerletti, Nico
McMaster, Gary K.
Cox, David
Schmitz, Albert
                                                                                                                             LENGTH: 339 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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                                                                                                                                                                                                                                                                                                                                                                                                                          500.00
5.102
87.500
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TGFB3P x US-08-470-837-29
                                                                                                                                                                                 TOPOLOGY: linear MOLECULE TYPE: CDNA
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                                                                                                                                                                                                                              NAME/KEY: CDS
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Ratio:
Percent Similarity:
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                                                                                                                                                                                                                                                                               NAME/KEY:
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US-08-470-837-29
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APPLICANT:
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APPLICANT:
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17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
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Ratio:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HYPOTHETICAL:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Meyhack, Bernd
TITLE OF INVENTION: Process for Refolding Recombinantly
TITLE OF INVENTION: Produced TGF-beta-like Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps: 0
Percent Identity: 76.786
                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/789,588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Align seg 1/1 to: US-08-789-588-1 from: 1 to: 339
                                                                                                ADDRESSEE: Henry P. No. 5922846ak
STREET: 520 White Plains Road, P.O. Box 2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 08/201,703
FILING DATE: 25-FEB-1994
PRIOR APPLICATION NUMBER: US 07/960,309
FILING DATE: 13-OCT-1992
PRIOR APPLICATION NUMBER: US 07/960,309
FILING DATE: 13-OCT-1992
PRIOR APPLICATION NUMBER: US 07/621,502
FILING DATE: 03-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 8927546.5
FILING DATE: 06-DEC-1999
ATTORNEY/AGENT INFORMATION:
NAME: NO. 59228464k, Henry P.
REGISTRATION NUMBER: 33200
REFERENCE/DOCKET NUMBER: 4'-17861/+/Cont3
TELECOMMUNICATION INFORMATION:
TELEFRAX: (908) 277-4306
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LEMETH: DUCTH: 333 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/486,057
FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIble
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 500.00
5.102
87.500
                                                             NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               alignment_block:
TGFB3P x US-08-789-588-1
                                                                                                                                                                                                                                                                                  OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1.339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1.,339
                                                                                                                                                                 New York
                                                                                                                                                                                    COUNTRY: U.S.A.
ZIP: 10591-9005
                                                                                                                                           CITY: Tarrytown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: CDS
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Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; LOCATION:
US-08-789-588-1
                                                                                                                                                                                  COUNTRY:
                                                                                                                                                             STATE:
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No. 6057430el process for the production of biologically active dimeric protein
                                                                                                                                                               84 luProLeuThrileLeuTyrTyrValGlyArgThrProLysValGluGln 100
                                                                51 GCGCCAGCTGTACATTGACTTCCGCAAGGACCTCGGCTGGAAGTGGATCC 100
                                                                                                                                                                                                                         67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
                                                                                                                                 51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCySCysVa 17
                                              34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PatentIn Release #1.0, Version #1.30 (EPO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seq_name: /cgn2_6/ptodata/2/ina/6A_COMB.seq:US-09-123-233-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IMMEDIATE SOURCE:
    CLONE: E. coli LC137/pPLMu.hTGF-betal (DSM 5656)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   500.00 Length: 112
5.102 Gaps: 0
87.500 Percent Identity: 76.786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: 1..336
OTHER INFORMATION: /product= "human TGF-betal"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Align seg 1/1 to: US-09-123-233-1 from: 1 to: 339
                                                                                                                                                                                                                                                                                                                                                                                                           101 LeuSerAsnMetValValLysSerCysLysCysSer 112
                                                                                                                                                                                                                                                                                                                                                                                                                                    301 CTGTCCAACATGATCGTGCGCTCCTGCAAGTGCAGC 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/123,233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: CDNA to mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 530
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 339 base pairs TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: NO.
TITLE OF INVENTION: biol
NUMBER OF SEQUENCES: 14
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         double
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TGFB3P x US-09-123-233-1
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Length:

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Quality:
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APPLICANT: MADISEN, LINDA
APPLICANT: MADISEN, LINDA
APPLICANT: MENNIN, JUNE RAE
TITLE OF INVENTION: TGF-b1/b2: A NOVEL CHIMERIC TRANSFORMING
TITLE OF INVENTION: GROWTH FACTOR-BETA
NUMBER OF SEQUENCES: 3
ADDRESSEE: PENNIE & EDMONDS
STREET: 1155 AVENUE OF THE AMERICAS
CITY: NEW YORK
                                                                                                                                                                                                                                                               34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr
                                                                                                                                                                                                                                                                                                                                                                                                             seq_name: /cgn2_6/ptodata/2/ina/5A_COMB.seq:US-07-669-171-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTE TOOLS
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/669,171
FILING DATE: 19910314
                                                                                                                                                                                                                                                                                                                                      101 LeuSerAsnMetValValLysSerCysLysCysSer 112
                                                                                                                                                                                                                                                                                                                                                            5624-159-999
                                                                                                                                                                                                                                                                                                                                                                                                                                              seq_documentation_block:
; Sequence 1, Application US/07669171
; Patent No. 5304541
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: MISROCK, S. LESLIE
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 5624
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 212-869-9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1560 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: NUCLEIC ACID
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          261..1430
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 19 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; NAME/KEY:
; LOCATION:
US-07-669-171-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE:
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alignment\_scores:

1676 GCCCTGGACACCAACTATTGCTTCAGCTCCACGGAGAAGAACACCTGCGT 1,725 1245 ATTTGGAGCCTGGACACGCAGTACAGCAAGGTCCTGGCCCTGTACAACCA 1294 84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100 1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17 17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34 51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67 APPLICANT: DERYNCK, RIK M.A.; GOEDDEL, DAVID V.
TITLE OF INVENTION: NUCLEIC ACID ENCODING TGF-B ITS USES
UNMBER OF SEQUENCES: 21
CURRENT APPLICATION DATA: 67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr seq\_name: /cgn2\_6/ptodata/2/ina/backfiles1.seq:5168051-1 Gaps: 0 Percent Identity: 76.786 Length: 112 Gaps: 0 Percent Identity: 76.786 Align seg 1/1 to: US-07-669-171-1 from: 1 to: 1560 101 LeuSerAsnMetValValLysSerCysLysCysSer 112 Align seg 1/1 to: 5168051-1 from: 1 to: 2537 APPLICATION NUMBER: US/07/389,929 FILING DATE: 04-AUG-1989 500.00 5.102 87.500 500.00 5.102 87.500 TGFB3P x US-07-669-171-1 seq\_documentation\_block:
;Patent No. 5168051 Percent Similarity: Ratio: Quality: Ratio: Percent Similarity: alignment\_block: TGFB3P x 5168051-1 LENGTH: 2537 alignment\_scores: alignment\_block: SEQ ID NO:1:

to: 2745

from: 1

tqfb3p.rni

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seq_name: /cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-274-215A-11
   to: PCT-US94-03705-3
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4.724
81.667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            alignment_block:
TGFB3P x 5168051-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               alignment_scores:
   Align seg 1/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; SEQ ID NO:3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          101
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                                                                                                                                                   seq_name: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:PCT-US94-03705-3
51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
                                                                       67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps: 0
Percent Identity: 76.786
                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Mu-En Lee
APPLICANT: Mark A. Perrella
TITLE OF INVENTION: TRANSFORMIG GROWTH
TITLE OF INVENTION: FACTOR- INHIBITS
TITLE OF INVENTION: SYNTHASE GRNE
TITLE OF INVENTION: SYNTHASE GRNE
TITLE OF INVENTION: TRANSCRIPTION
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                   101 LeuSerAsnMetValValLysSerCysLysCysSer 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: 1BM PS/2 Model 502 or 553X
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOSTWARE: WORDPERFECT (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/03705
FILING DATE: 5 APril 1994
CLASSIFTCATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Janis K. Fraser
REGISTRATION NUMBER: Reg. NO. 34,819
REFERENCE/DOCKET NUMBER: 05433/007001
                                                                                                                                                                                                                                                                                                                                                                Sequence 3, Application PC/TUS9403705
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Fish & Richardson STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (617) 542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (617) 542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (617) 542-890
TELEX: 200154
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5.102
87.500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Boston
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     500.00
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TGFB3P x PCT-US94-03705-3
                                                                                                                                                                                                                                                                                                                                                seg_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: U.S.A. ZIP: 02110-2804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TOPOLOGY:
PCT-US94-03705-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alignment_scores;
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51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67 ::: ||| |||||||||||| 1829 ATTTGGAGCCTGGACAGTACAGCAAGGTCCTGGCCTGTACAACCA 1878
                                                                                                404 CGGCTGGAAGTGGATCCACGAGCCCAAGGGCTACCATGCCACCTTCTGCC 453
                                                                        17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
                                                                                                                                                    34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28 uGlyTrpLysTrpValHisGluProLysGlyTyrTyrAlaAsnPheCysS 45
                                                                                                                                                                                                                                                                                                             67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq_documentation_block:
;Patent No. 5168051
; APPLICANT: DERYNCK, RIK M.A.;GOEDDEL, DAVID V.
; TITLE OF INVENTION: NUCLEIC ACID ENCODING TGF-B ITS USES:
NUMBER OF SEQUENCES: 21
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/389,929
1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                seq_name: /cgn2_6/ptodata/2/ina/backfiles1.seq:5168051-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length: 60
Gaps: 1
Percent Identity: 66.667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LeuSerAsnMetValValLysSerCysLysCysSer 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Align seg 1/1 to: 5168051-3 from: 1 to: 975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  504 CGTCTGGCCACCGGCTACGAGATGCGCTT 533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ......LeuGlyLeuTyrAsnThrLeu 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 04-AUG-1989
) NO:3:
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alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31 s...TrpValHisGluProLysGlyTyrTyrAlaAsnPheCysSerGlyP 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      47 roCys...ProTyrLeuArgSer.....AlaAspThrThrHis 58
         Sequence 11, Application US/08274215A
Sequence 11, Application US/08274215A
Sequent No. 5831054
GENERAL INFORMATION:
APPLICANT: Esquela, Aurora F.
ITLEO PO INVENTION: GROWTH DIFFERENTIATION FACTOR-12
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSE: Fish & Richardson, P.C.
STREET: 4.25 Executive Square, Suite 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SerThrValLeuGlyLeuTyrAsnThrLeuAsnProGluAlaSerAlaSe 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15 CysCysValArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLy 31
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Percent Identity: 41.509
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                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSED for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/274,215A
FILING DATE: 13-JUL-1994
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       07265/040001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Haile, Ph.D., Lisa A. REGISTRATION NUMBER: 38,347 REFERENCE/DOCKET NUMBER: 07. TELECOMMUNICATION INFORMATION: 619-678-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPAX: 619-68-5099
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 360 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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2.784
69.811
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MEDIUM TYPE: Diskett
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TGFB3P x US-08-274-215A-11
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seq_documentation_block:
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Ratio:
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                                                                                                                                                                                                                                                COUNTRY: US
                                                                                                                                                                                                                                  CA
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US-08-274-215A-11
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                                                                                                                                                                                                           CITY: I
STATE:
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293 ATCATAATGGCAATGTGGTCAAGACGGAT...GTGCCAGATATGGTGGTG 339
                    91 ..TyrValGlyArgThrProLysValGluGlnLeuSerAsnMetValVal 106
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75 rProCysCysValProGlnAspLeuGluProLeuThrIleLeuTyr.... : |||||||||||||
                                                                                                                                                                                                                                                                    seq_documentation_block:
Sequence 11, Application US/08765662
Patent No. 5929213
GENERAL INFORMATION:
GAPPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEI
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-12
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 4225 Executive Square, Suite 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              bercent Identity: 41.509
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TELECOMUNICATION INFORMATION:
TELEPHONE: 619-678-5070
TELEPAX: 619-678-5099
                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Fish & Richardson
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/765,662
FILING DATE: 28-APR-1997
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/08745
FILING DATE: 12-UL-1995
ATTORIEV AGENT INFORMATION:
NAME: Haile, Ph.D., Lisa A
REGISTRATION NUMBER: 38, 3477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                          107 LysSerCysLysCysSer 112
                                                                                                                                                                               340 GAGGCCTGTGGCTGCAGC 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 360 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEX:
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          206.00
2.784
69.811
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LOCATION: 1...357
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ORIGINAL SOURCE:
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Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: CA
COUNTRY: US
ZIP: 92037
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TOPOLOGY: linear MOLECULE TYPE: CDNA
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                                                                                                                                                                                                                                        Percent Similarity:
                                                                                                                                                                                                                       Ratio:
                                                                                                                                                                              alignment_scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            293 ATCATAATGGCAATGTGGTCAAGACGGAT...GTGCCAGATATGGTGGTG 339
                                                                                                                                                                                                                                                        47 roCys...ProTyrLeuArgSer.......AlaAspThrThrHis 58
                                                                                                                                                                                                                                                                                                                                                                                                                           75 rProCysCysValProGlnAspLeuGluProLeuThrIleLeuTyr.... 90
                                                                                  15 CysCysValArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLy 31
                                                                                                          31 s...TrpValHisGluProLysGlyTyrTyrAlaAsnPheCysSerGlyP 47
                                                                                                                                                                                                                                                                                                                                          SerThrValLeuGlyLeuTyrAsnThrLeuAsnProGluAlaSerAlaSe 75
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 11, Application US/09184933
Patent No. 6130050
GENERAL INFORMATION:
CENTRAL INFORMATION:
APPLICANT: Esquela, Aurora F.
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-12
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
                                         Align seg 1/1 to: US-08-765-662-11 from: 1 to: 360
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SOFTWARE: FastSTO for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/184,933
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STREET: 4225 Executive Square, Suite 1400
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APPLICATION NUMBER: 08/274,215
FILING DATE: 13-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Halle, Ph.D., Lisa A.
REGISTRATION NUMBER: 38,347
REFRENCE/POCKET NUMBER: 07265/040001
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPRAK: 619-678-5070
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INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 360 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows9
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340 GAGGCCTGTGGCTGCAGC 357
TGFB3P x US-08-765-662-11
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seq\_name: /cgn2\_6/ptodata/2/ina/PCTUS\_COMB.seq:PCT-US95-08745-11 143 AGTGCCCTCCCCACCTGGCTGGCAGCCCAGGCATTGCTGCCTCTTTCCAT 192 ..TyrValGlyArgThrProLysValGluGlnLeuSerAsnMetValVal 106 47 roCys...ProTyrLeuArgSer......AlaAspThrThrHis 58 SerThrValLeuGlyLeuTyrAsnThrLeuAsnProGluAlaSerAlaSe 75 75 rProCysCysValProGlnAspLeuGluProLeuThrIleLeuTyr.... Percent Identity: 41.509 ADDRESSEE: Fish Fichardson STREET: 4225 Executive Square, Suite 1400 CITY: La Jolla STATE: CA Length: Align seg 1/1 to: US-09-184-933-11 from: 1 SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/08745
FILLING DATE: 12-JUL-1995 APPLICATION NUMBER: PCT/US95/ FILING DATE: 12-JUL-1995 CLASSIFICATION: ATTORNEY/AGENT INFORMATION: NAME: Halle, Ph.D., LISA A REGISTRATION NUMBER: 38,347 NAME/KEY: Coding Sequence; LOCATION: 1...357 US-09-184-933-11 COMPUTER: IBM Compatible OPERATING SYSTEM: DOS 107 LysSerCysLysCysSer 112 340 GAGGCCTGTGGCTGCAGC 357 ZIP: 92037 COMPUTER READABLE FORM: MEDIUM TYPE: Diskette 2.784 69.811 206.00 NUMBER OF SEQUENCES: 1 CORRESPONDENCE ADDRESS: TGFB3P x US-09-184-933-11

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143 AGTGCCCTCCCCACCTGGCTGGCAGCCAGGCATTGCTGCTTTCCAT 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .. TyrValGlyArgThrProLysValGluGlnLeuSerAsnMetValVal 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         47 roCys...ProTyrLeuArgSer.......AlaAspThrThrHis 58
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APPLICANT: Rosen, Vicki A.
APPLICANT: Wang, Elizabeth A.
APPLICANT: Wozney, John M.
TITLE OF INVENTION: Methods for Producing BMP-7 Proteins NUMBER OF SEQUENCES: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15 CysCysValArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLy 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31 s...TrpValHisGluProLysGlyTyrTyrAlaAsnPheCysSerGlyP 47
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps: 6
Percent Identity: 41.509
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    07265/042WO1 (FD-3830)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length:
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; Sequence 5, Application US/07764731B
; Patent No. 5366875
REFERENCE/DOCKET NUMBER: 07
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-678-5070
                                                                                                INFORMATION FOR SEQ ID NO: 11: SEQUENCE CHARACTERISTICS: LENGTH: 360 base pairs TYPE: nucleic acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                            ) NAME/KEY: Coding Sequence

) LOCATION: 1...357

) OTHER INFORMATION:

PCT-US95-08745-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               107 LysSerCysLysCysSer 112
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2.784
69.811
                                                             TELEFAX: 619-678-5099
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGFB3P x PCT-US95-08745-11
                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                              ANTI-SENSE: NO
FRAGMENT TYPE:
ORIGINAL SOURCE:
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Quality:
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36 roLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyrLeuArg
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ADDRESSEE: Legal Affairs, Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
CITY: Cambridge
                                                                                                                         COMPUTER: FLOPPY disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/764,731B
FILING DATE: 19910924
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: KAPINGS, Ellen J.
REGISTRATION NUMBER: 32,245
REFERENCE/DOCKET NUMBER: G15159B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps: 4
Percent Identity: 37.168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LIBRARY: U2-05 human osteosarcoma cDNA library CLONE: U2-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Homo sapiens
CELL LINE: U2-OS Osteosarcoma
                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION TELEPHONE: 617-876-1170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: circular
MOLECULE TYPE: CDNA tO MRNA
HYPOTHETICAL: NO
FRAGMENT TYPE: C-terminal
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 617-876-5851
INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
LENGTH: 400 base pairs
TYPE: NUCLEIC ACLD
STRANDEDNESS: double
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1..400
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2.822
64.602
                                                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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TGFB3P x US-07-764-731B-5
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Percent Similarity:
                                                                          USA
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                                                                                             02140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alignment_scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
US-07-764-731B-5
                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE
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ADDRESSEE: Genetics Institute, Inc - Legal Affairs STREET: 87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/360,914B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US 08/163,877
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/163,
FILING DATE: December 7, 1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLUM TYPE: Floppy disk COMPUTER: IBM PC COMPATIBLE OPERATING CVCM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      32,618
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TELEPHONE: 617 498-8260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFRX: 617 876 5851
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Lazar, Steven R.
REGISTRATION NUMBER: 32,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 406 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Cambridge
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
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                         :::|||
205 AACGCACACATGAATGCAACCACGCGATTGTGCAGACCTTGGTTCA 254
                                                                                                       ||::: ::::::::|||||||::
305 TAAATGCCATCTCGGTTCTTTACTTTGATGACAACTCCAATGTCATTCTG 354
53 SerAlaAsp.....ThrThrHisSerThrValLeuGlyLeuTyrAs 66
                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: McCoy, John
APPLICANT: McCoy, John
APPLICANT: Molfman, Neil
TITLE OF INVENTION: MITANTS OF BONE MORPHOGENIC PROTEINS
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSE: Genetics Institute, Inc - Legal Affairs
STREET: 87 cambridgePark Drive
                                                                                                                                                              83 euGluProLeuThrIleLeuTyrTyrValGlyArgThrProLysVal... 98
                                                                                66 nThrLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspL
                                                                                                                                                                                                                                                                                                                                 seq_name: /cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-163-877-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps: 4
Percent Identity: 37.168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/163,877
                                                                                                                                                                                                                                               99 GluGlnLeuSerAsnMetValValLysSerCysLysCys 111
                                                                                                                                                                                                                                                                                         355 AAAAAATACAGGAATATGGTTGTAAGAGCTTGTGGATGC 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
ATTORNEY_AGENT INFORMATION:
NAME: Lazar, Steven R.
REGISTRATION NUMBER: 32.618
REFERENCE/DOCKET NUMBER: GI 5219
TELECHONE: 617 876-1170 x 8260
TELEFAX: 617 876-5851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GI 5219
                                                                                                                                                                                                                                                                                                                                                                     eq_documentation_block:
Sequence 7, Application US/08163877
Patent No. 5399677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: DNA (genomic) ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 406 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    206.00
2.822
64.602
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TGFB3P x US-08-163-877-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM:
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Ratio:
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US-08-163-877-7
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to: 406 from: 1 Align seg 1/1 to: US-08-163-877-7

:::||| :::||205 AACGCACATGAATGCAACCAAGCGATTGTGCAGACCTTGGTTCA 254 58 TCAGATTACAACAGCAGTGAATTGAAAACAGCCTGCAGGAAGCATGAGCT 107 20 uTyrIleAspPheArgGlnAspLeuGlyTrpLys...TrpValHisGluP 36 53 SerAlaAsp.....ThrThrHisSerThrValLeuGlyLeuTyrAs 66 36 roLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyrLeuArg 52 66 nThrLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspL 83 4 ThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysValArgProLe 20 83 euGluProLeuThrIleLeuTyrTyrValGlyArgThrProLysVal... 98 seq\_name: /cgn2\_6/ptodata/2/ina/5A\_COMB.seq:US-08-360-914B-7 99 GluGlnLeuSerAsnMetValValLysSerCysLysCys 111 355 AAAAAATACAGGAATATGGTTGTAAGAGCTTGTGGATGC 393

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seq_documentation_block:

Sequence 7, Application US/08741589A

Fatent No. 580416

GENERAL INFORMATION:

TITLE OF INVENTION:

MUMBER OF SEQUENCES: 13

CORRESPONDENCE NORESS:

ADDRESSE: Genetics Institute, Inc - Legal Affairs

STREET: 87 Cambridge

COUNTRY: Massachusetts

COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           58 TCAGATTACAACAGCAGTGAATTGAAAACAGCCTGCAGGAAGCATGAGCT 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                20 uTyrIleAspPheArgGlnAspLeuGlyTrpLys...TrpValHisGluP 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             53 SerAlaAsp.....ThrThrHisSerThrValLeuGlyLeuTyrAs 66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           83 euGluProLeuThrIleLeuTyrTyrValGlyArgThrProLysVal... 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_name: /cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-741-589A-7
                                                                                                                                                                                                                                                                                                                                                                           4 ThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysValArgProLe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       36 roLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyrLeuArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Quality: 206.00 Length: 113
Ratio: 2.822 Gaps: 4
Percent Similarity: 64.602 Percent Identity: 37.168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/741,589A
                                                                                                                                                                                                                                                                                                                                    from: 1 to: 406
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           355 AAAAAATACAGGAATATGGTTGTAAGAGGTTGTGGATGC 393
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/163,877
FILING DATE: December 7, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 02140
COMPUTER REACABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                  Align seg 1/1 to: US-08-360-914B-7
                                                                                                                                                                                                                                                                alignment_block:
TGFB3P x US-08-360-914B-7
                                                                  1..396
    9-dwq
ORGANISM:
FEATURE:
                                         ; NAME/KEY:
; LOCATION:
US-08-360-914B-7
                                                                                                                                                      alignment_scores:
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58 TCAGATTACAACAGCAGTGAATTGAAAACAGCCTGCAGGAAGCATGAGCT 107 seq\_name: /cgn2\_6/ptodata/2/ina/PCTUS\_COMB.seq:PCT-US94-13181-7 seq\_documentation\_block:
; Sequence 7, Application PC/TUS9413181
; GENERAL INFORMATION:
; APPLICANT: GENETICS INSTITUTE, INC.
; TITLE OF INVENTION: MUTANTS OF BONE MORPHOGENIC PROTEINS
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc - Legal Affairs
; STREET: 87 CambridgePark Drive :::||| 205 AACGCACACATGAATGCAACCAACCAGGGATTGTGCAGACCTTGGTTCA 254 53 SerAlaAsp.....ThrThrHisSerThrValLeuGlyLeuTyrAs 66 66 nThrLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspL 83 4 ThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysValArgProLe 20 20 uTyrIleAspPheArgGlnAspLeuGlyTrpLys...TrpValHisGluP 36 83 euGluProLeuThrIleLeuTyrTyrValGlyArgThrProLysVal... 98 36 roLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyrLeuArg Gaps: 4
Percent Identity: 37.168 Align seg 1/1 to: US-08-741-589A-7 from: 1 to: 406 99 GluGlnLeuSerAsnMetValValLysSerCysLysCys 111 355 AAAAAATACAGGAATATGGTTGTAAGAGCTTGTGGATGC 393 Length: GI 5219B-DIV NAME: Lazar, Steven R.
REGISTRATION NUMBER: 32,618
REFERENCE/DOCKET NUMBER: GI 5
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617 498-8260
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 406 base pairs
TYPE: nucleic acid
STRANDEDNESS: double ATTORNEY/AGENT INFORMATION: 206.00 2.822 64.602 STREET: 87 Cambridger CITY: Cambridge STATE: Massachusetts alignment\_block: TGFB3P x US-08-741-589A-7 TOPOLOGY: linear MOLECULE TYPE: DNA ORIGINAL SOURCE: 1..396 ORGANISM: bmp-6 Quality: Percent Similarity: NAME/KEY: alignment\_scores: LOCATION: US-08-741-589A-7 FEATURE

APPLICANT: Rosen, Vicki A.
APPLICANT: Wang, Elizabeth A.
APPLICANT: Wozney, John M.
TITLE OF INVENTION: Methods for Producing BMP-7 Proteins
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS: Percent Identity: 37.168 CORRENT 150 FC COMPOSITORS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/764,731B
FILING DATE: 19910924
CLASSIFICATION: 435 ...urkESSEE: Legal Affairs, Genetics Institute, STREET: 87 CambridgePark Drive CITY: Cambridge Align seg 1/1 to: US-07-764-731B-3 from: 1 to: 894 Bovine bone cDNA library seq\_documentation\_block:
; Sequence 3, Application US/07764731B
; Patent No. 5366875 NAME: Kapinos, Ellen J.
REGISTRATION NUMBER: 32,245
REFERENCE/DOCKET NUMBER: GIS.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-876-1170
TELEFAX: 617-876-5851 Fetal long bone COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible 32,245 TOPOLOGY: circular MOLECULE TYPE: CDNA to MRNA HYPOTHETICAL: NO ATTORNEY/AGENT INFORMATION: TELEFAX: 617-876-5851 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTER.ESTICS: LENGTH: 894 base pairs TYPE: NUCLEIC ACID STRANDEDNESS: double C-terminal mat\_peptide 250..666 206.00 2.822 64.602 ORGANISM: Bos taurus TISSUE TYPE: Fetal lo alignment\_block: TGFB3P x US-07-764-731B-3 1..669 GENERAL INFORMATION: POSITION IN GENOME: IMMEDIATE SOURCE: FRAGMENT TYPE: CORIGINAL SOURCE: NAME/KEY: CDS Quality: USA Percent Similarity: HEL16

to: 5187076-3 from: 1 to: 894

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Align seg 1/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq_documentation_block:
;Patent No. 5187076
; Patent No. 5187076
; Patent No. 5187076
; Carent World W.;Wang, ELIZABETH A.;ROSEN,VICKI A.;
;CELESTE, ANTHONY J.
;TITLE OF INVENTION: DNA SEQUENCES ENCODING BMP-6 PROTEINS
;NUMBER OF SEQUENCES: 16
;CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/490,033
FILING DATE: 07 MAR-1990
;PRIOR APPLICATION NUMBER: 370,544
FILING DATE: 23-JUN-1989
;APPLICATION NUMBER: 347,559
;FILING DATE: 28-MAR-1989
;FILING DATE: 28-MAR-1989
;FILING DATE: 28-MAR-1989
                             ||::: :::::::::|||||||::
575 TGAACGCCATCTCGGTGCTCTACTTCGACGACGAATGTCATCCTG 624
                                                                                  20 uTyrIleAspPheArgGlnAspLeuGlyTrpLys...TrpValHisGluP 36
                                                                                                                                                                                                                                                                                                                                                                                                    525 CCTCATGAACCCCGAGTACGTCCCCAAACCGTGCTGCGCGCCCCACGAAAC 574
4 ThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysValArgProLe 20
                                                                                                                                                                              roLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyrLeuArg 52
                                                                                                                                                                                                                                                                     SerAlaAsp.....ThrThrHisSerThrValLeuGlyLeuTyrAs 66
                                                                                                                                                                                                                                                                                                                                                          nThrLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspL 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                 euGluProLeuThrIleLeuTyrTyrValGlyArgThrProLysVal... 98
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  625 AAGAAGTACCGGAACATGGTCGTACGAGCGTGTGGGTGC 663
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 179,100
FILING DATE: 08-APR-1988
APPLICATION NUMBER: 179,101
FILING DATE: 08-APR-1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 179,197
FILING DATE: 08-APR-1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 943,322 FILING DATE: 17-DEC-1986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 880,776 FILING DATE: 01-JUL-1986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 28,285
FILING DATE: 20-MAR-1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 31,346
FILING DATE: 26-MAR-1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2.822
64.602
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Ratio:
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TGFB3P x 5187076-3
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APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-12 NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 4225 Executive Square, Suite 1400
                                        328 TCAGACTACAACAGCAGCGAGCTGAAGACGGCCTGCCGGAAGCATGAGCT 377
                                                                                    525 CCTCATGAACCCCGAGTACGTCCCCAAACCGTGCTGCGCGCCCCACGAAAC 574
                                                                                                                                                                                                                                                                                                                                                                         66 nThrLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspL 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq_name: /cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-765-662-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 ThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysValArgProLe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     83 euGluProLeuThrIleLeuTyrTyrValGlyArgThrProLysVal...
                                                                                                                                                                                                                                                                                SerAlaAsp.....ThrThrHisSerThrValLeuGlyLeuTyrAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07265/042WO1 (FD-3830)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        625 AAGAAGTACCGGAACATGGTCGTACGAGCGTGTGGGTGC 663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99 GluGlnLeuSerAsnMetValValLysSerCysLysCys 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 28-APR-1997
CLASSIFICATION: 536
PRIOR APPLICATION DAMBER: PCT/US95/08745
FILING DATE: 12-JUL-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/765,662 FILING DATE: 28-APR-1997 CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq_documentation_block:
; Sequence 13, Application US/08765662
Sequence 13, Application
; Setten No. 5929213
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION: TELEPHONE: 619-678-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Haile, Ph.D., Lisa A REGISTRATION NUMBER: 38,347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 2419 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO:
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STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             USA
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                                                                                                                                                                                                                                                                                23
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CLASSIFICATION:

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seq_documentation_block:
    Sequence 13, Application PC/TUS9508745
    GENERAL INFORMATION:
    APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-12 NUMBER OF SEQUENCES: 14
    CORRESPONDENCE ADDRESS:
    CORRESPONDENCE ADDRESS:
    ADDRESSEE: Fish & Richardson STREET: 4225 Executive Square, Suite 1400
    CITY: La Jolla
                                                                                                                                                                                                                                                                                                                                                                                                                                   seq_name: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:PCT-US95-08745-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         91 ..TyrvalGlyArgThrProLysValGluGlnLeuSerAsnMetValVal 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31 s...TrpValHisGluProLysGlyTyrTyrAlaAsnPheCysSerGlyP 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              47 roCys...ProTyrLeuArgSer.....AlaAspThrThrHis 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SerThrValLeuGlyLeuTyrAsnThrLeuAsnProGluAlaSerAlaSe 75
                                                                                                                                                                                                                                                                                                                                                                                                               15 CysCysValArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLy
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Percent Identity: 41.509
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SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/08745
FILING DATE: 12-JUL-1995
                                                                                                                                                                                                                                                                                                                                                                           Align seg 1/1 to: US-08-765-662-13
                                                                                      FEATURE:
NAME/KEY: Coding Sequence
LOCATION: 218...1267
OTHER INFORMATION:
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                                                                                                                                                                                                                                           206.00
2.784
69.811
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MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                     alignment_block:
TGFB3P x US-08-765-662-13
             HYPOTHETICAL: NO ANTI-SENSE: NO FRAGMENT TYPE: ORIGINAL SOURCE:
                                                                                                                                                                                                                                           Quality:
Ratio:
                                                                                                                                                                                                                                                                              Percent Similarity:
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MOLECULE TYPE:
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                                                                                                                                                                                                                          alignment_scores:
                                                                                                                                                                  US-08-765-662-13
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91 ..TyrvalGlyArgThrProLysValGluGlnLeuSerAsnMetValVal 106 15 CysCysValArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLy 31 47 roCys...ProTyrLeuArgSer.....AlaAspThrThrHis 58 31 s...TrpValHisGluProLysGlyTyrTyrAlaAsnPheCysSerGlyP 47 SerThrValLeuGlyLeuTyrAsnThrLeuAsnProGluAlaSerAlaSe 75 75 rProCysCysValProGlnAspLeuGluProLeuThrIleLeuTyr.... seq\_name: /cgn2\_6/ptodata/2/ina/5A\_COMB.seq:US-08-377-292-6 Align seg 1/1 to: PCT-US95-08745-13 from: 1 to: 2419 Length: 106 Gaps: 6 Percent Identity: 41.509 07265/042WO1 (FD-3830) ATTORNEZ/AGENT INFORMATION: NAME: Haile, Ph.D., Lisa A REGISTRATION NUMBER: 38,347 REFERENCE/DOCKET NUMBER: 07
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-678-5070
TELEFAX: 619-678-5099 NAME/KEY: Coding Sequence 1250 GAGGCCTGTGGCTGCAGC 1267 INFORMATION FOR SEQ ID NO: 1 SEQUENCE CHARACTERISTICS: LENGTH: 2419 base pairs 107 LysSerCysLysCysSer 112 2.784 69.811 TYPE: nucleic acid STRANDEDNESS: single 206.00 alignment\_block: TGFB3P x PCT-US95-08745-13 linear ; LOCATION: 218...3; OTHER INFORMATION: PCT-US95-08745-13 TOPOLOGY: linear MOLECULE TYPE: CDN FRAGMENT TYPE: ORIGINAL SOURCE: HYPOTHETICAL: NAMI-SENSE: NO Quality: Ratio: Percent Similarity: alignment\_scores: TELEX:

4 ThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysValArgProLe 20

20 uTyrlleAspPheArgGlnAspLeuGlyTrpLys...TrpValHisGluP 36

53 SerAlaAsp.....ThrThrHisSerThrValLeuGlyLeuTyrAs 66

66 nThrLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspL 83

euGluProLeuThrIleLeuTyrTyrValGlyArgThrProLysVal... 98 83

99 GluGlnLeuSerAsnMetValValLysSerCysLysCys 111

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Recombinant Bone Morphogenetic Protein
Heterodimers, Compositions and Methods of Use.
                                                                                             Sequence 7. Application US/07989847

Sequence 7. Application US/07989847

Patent No. 586564

GENERAL INFORMATION:

APPLICANT: Israel, David

APPLICANT: Wolfman, Neil M.

TITLE OF INVENTION: Recombinant Bone Morphogenetic Prot

TITLE OF INVENTION: Heterodimers, Compositions and Meth

NUMBER OF SEQUENCES: 30

CORRESPONDENCE ADDRESS:

ADDRESSEE: Legal Affairs, Genetics Institute, Inc.
                                            seq_name: /cgn2_6/ptodata/2/ina/5B_COMB.seq:US-07-989-847-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LIBRARY: Stratagene catalog #936203 Human placenta
LIBRARY: cDNA library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percent Identity: 37.168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/989,847
1657 AAAAAATACAGGAATATGGTTGTAAGAGCTTGTGGATGC 1695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: REPLEND., ELLEN J.
REGISTRATION NUMBER: 32,245
REFERENCE/DOCKET NUMBER: GI-5192B
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-876-1170
TELEPHONE: 617-876-5851
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 2923 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human placenta
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MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
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1282..1698
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MEDIUM TYPE: Tape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Quality: 206.00
Ratio: 2.822
nilarity: 64.602
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TGFB3P x US-07-989-847-7
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POSITION IN GENOME:
                                                                                        seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
ZIP: 02140-2387
                                                                                                                                                                                                                                                                                                                                                               Cambridge
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE
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; LOCATION:
US-07-989-847-7
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ORIGINAL SOURCE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Israel, David
APPLICANT: Israel, David
Wolfman, Neil M.
TITLE OF INVENTION: Recombinant Bone Morphogenetic Protein
Heterodimers, Compositions and Methods of Use.
                                                                          ADDRESSEE: Legal Affairs, Genetics Institute, Inc. STREET: 87 CambridgePark Drive CITY: Cambridge
                                                                                                                                 20 uTyrIleAspPheArgGlnAspLeuGlyTrpLys...TrpValHisGluP 36
                                                                                                                                                                                                                                                                                                                                                                              66 nThrLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspL 83
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA
ZIP: 02140-2387
COMPUTER READABLE FORM:
MEDIUM TYPE: TEMP COMPUTER: IBM PC COMPUTER: IBM PC COMPUTER: TEMP COMPUTER: Patentin Release #1.0, Version #1.25
                                              4 ThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysValArgProLe
                                                                                                                                                                                                                                                                                                53 SerAlaAsp.....ThrThrHisSerThrValLeuGlyLeuTyrAs
                                                                                                                                                                                                                 36 roLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyrLeuArg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1657 AAAAAATACAGGAATATGGTTGTAAGAGCTTGTGGATGC 1695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GluGlnLeuSerAsnMetValValLysSerCysLysCys 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Kapinos, Ellen J.
REGISTRATION NUMBER: 32,245
REFERENCE/DOCKET NUMBER: GI-5192B-CON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,411
FILING DATE: 06-Jun-1995
CLASSIFICATION: <Unknown>
          to: US-07-989-847-7 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-498-8622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 7, Application US/08469411
Patent No. 6190880
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 2923 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: circular MOLECULE TYPE: CDNA to mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 617-876-5851
INFORMATION FOR SEQ ID NO: 7:
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STRANDEDNESS: double
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            Align seg 1/1
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; Patent No. 5187076
; APPLICANT: WOZNEY, JOHN M.; WANG, ELIZABETH A.; ROSEN, VICKI A.;
; CELESTE, ANTHONY J.
; TITLE OF INVENTION: DNA SEQUENCES ENCODING BMP-6 PROTEINS
                                                                    LIBRARY: Stratagene catalog #936203 Human placenta cDNA library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1360 TCAGATTACAACAGCAGTGAATTGAAAACAGCCTGCAGGAAGCATGAGCT 1409
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1607 TABAATGCCATCTCGGTTCTTTACTTTGATGACAACTCCAATGTCATTCTG 1656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1507 AACGCACACATGAATGCAACCAACCACGCGATTGTGCAGACCTTGGTTCA 1556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1557 CCTTATGAACCCCGAGTATGTCCCCAAACCGTGCTGTGCGCCAACTAAGC 1606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20 uTyrIleAspPheArgGlnAspLeuGlyTrpLys...TrpValHisGluP 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        53 SerAlaAsp......ThrThrHisSerThrValLeuGlyLeuTyrAs 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 ThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysValArgProLe 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nThrLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspL 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              36 roLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyrLeuArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           euGluProLeuThrIleLeuTyrTyrValGlyArgThrProLysVal...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seq_name: /cgn2_6/ptodata/2/ina/backfiles1.seq:5187076-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2.82 Gaps: 4
64.602 Percent Identity: 37.168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Align seg 1/1 to: US-08-469-411-7 from: 1 to: 2923
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1657 AAAAAATACAGGAATATGGTTGTAAGAGCTTGTGGATGC 1695
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                                                                                                                                                                                                                                                                                                                                                                      LOCATION: 1..2923
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-08-469-411-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 16
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/490,033
FILING DATE: 07-MAR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 370,544
                    TISSUE TYPE: Human placenta IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                          mat_peptide
1282..1698
ORGANISM: Homo sapiens
                                                                                                                                                                                                                        CDS
160..1701
                                                                                                                                                                                                                                                                                                                                                                   mRNA
                                                                                                                    CLONE: BMP6C35
POSITION IN GENOME:
UNITS: bp
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                                                                                                                                                                                                                                          LOCATION:
                                                                                                                                                                                                                                                                                             NAME/KEY:
                                                                                                                                                                                                                      NAME/KEY:
                                                                                                                                                                                                                                                                                                                      LOCATION:
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Percent Similarity:
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Quality:
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1457 CCAAGGGCTATGCTGCCAATTACTGTGAAGAATGCTCCTTCCCACTC 1506
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1607 TABARTGCCATCTCGGTTCTTTACTTTGATGACAACTCCAATGTCATTCTG 1656
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20 uTyrIleAspPheArgGlnAspLeuGlyTrpLys...TrpValHisGluP 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          36 roLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyrLeuArg 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    53 SerAlaAsp.....ThrThrHisSerThrValLeuGlyLeuTyrAs 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 66 nThrLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspL 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seg_name: /cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-525-596B-5
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APPLICANT: Huynh, Thanh
APPLICANT: Lee, Se-Jin
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-8
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps: 4
Percent Identity: 37.168
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Sequence 5, Application US/08525596B
Patent No. 5827733
                 APPLICATION NUMBER: 347,559
FILING DATE: 04-MAY-1989
PPLILORATION NUMBER: 329,610
FILING DATE: 28-MAR-1989
APPLICATION NUMBER: 179,100
FILING DATE: 08-APR-1988
APPLICATION NUMBER: 179,101
FILING DATE: 08-APR-1988
APPLICATION NUMBER: 179,197
FILING DATE: 08-APR-1988
APPLICATION NUMBER: 28,285
FILING DATE: 20-MAR-1987
APPLICATION NUMBER: 31,346
FILING DATE: 20-MAR-1987
APPLICATION NUMBER: 943,322
FILING DATE: 17-DEC-1986
APPLICATION NUMBER: 943,322
FILING DATE: 17-DEC-1986
APPLICATION NUMBER: 880,776
FILING DATE: 01-JUL-1986
FILING DATE: 23-JUN-1989
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2.822
64.602
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Ratio:
Percent Similarity:
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TGFB3P x 5187076-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 2923
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO:5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5187076-5
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93 lyArgThrProLysVal...GluGlnLeuSerAsnMetValValLysSer 108 28 uGlyTrpLysTrpValHisGluProLysGlyTyrTyrAlaAsnPheCysS 45 :||||||| |||||||:::||||| 60 ThrValLeuGlyLeuTyrAsnThrLeuAsnProGluAlaSerAlaSerPr 76 76 oCysCysValProGlnAspLeuGluProLeuThrIleLeuTyrTyrValG 93 12 GluGluAsnCysCysValArgProLeuTyrIleAspPheArgGlnAspLe 45 erGlyProCysPro.....TyrLeuArgSerAlaAspThrThrHisSer Percent Identity: 39.423 Align seg 1/1 to: US-08-525-596B-5 from: 1 to: 550 MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSED for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/525,596B
FILING DATE: 19-5EP-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/07762
FILING DATE: 08-JUL-1994
ATTORNEY-AGENT INPORMATION:
NAME: Wetherell, Jr., Ph.D, John R.
REGISTRATION NUMBER: 31,678
REGISTRATION NUMBER: 31,678
REGISTRATION INPORMATION:
TELEPHONE: 619-678-5070
TELEPHONE: 619-678-5070 5: Fish & Richardson P.C. 4225 Executive Square, Suite 1400 Length: Gaps: INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHRRACTERISTICS:
LENGTH: 550 base pairs
TYPE: nucleic acid
STRANDEDNESS: single 204.50 3.098 63.462 COMPUTER READABLE FORM: alignment\_block: TGFB3P x US-08-525-596B-5 CLONE: mouse GDF-8 linear La Jolla TOPOLOGY: line NAME/KEY: CDS ; LOCATION: 59.. US-08-525-596B-5 Quality: Percent Similarity: Ratio: ADDRESSEE: STREET: 4: alignment\_scores: CITY: La STATE: C COUNTRY:

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93 lyArgThrProLysVal...GluGlnLeuSerAsnMetValValLysSer 108
                                                                                                                                               |||| :::||||||| 287 ...........CTTGTGCACCAGAGCAAACCCCAGAGGCTCAGGAGGCCC 324
                                                                                                                                                                                                                                                                          60 ThrValLeuGlyLeuTyrAsnThrLeuAsnProGluAlaSerAlaSerPr 76
                                                                                                                                                                                                                                      76 oCysCysValProGlnAspLeuGluProLeuThrIleLeuTyrTyrValG 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               seq_name: /cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-525-596B-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence in Application US/08525596B
Patent No. 5827733
GENERAL INFORMATION:
APPLICANT: Lee, Se-Jin
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-8
NUMBER OF SEQUENCES:
CORRESPONDED ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 92037

ZIP: 92037

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: Diskette
COMPUTER: TBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSEO for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/525,596B
FILING DATE: 19-SEP-1995
CLASSIFICATION 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/07762
FILING APPLICATION NUMBER: PCT/US94/07762
ATTORNEY APPLICATION NUMBER: NG-JUL-1994
ATTORNEY APPLICATION NUMBER: NAME: Wetherell, Jr., Ph.D, John R.
REGISTRATION NUMBER: N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07265/075001
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-678-5079
TELEFAX: 619-678-5099
INFORMATION FOR SEQ ID NO: 11:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
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LENGTH: 2676 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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CLONE: Murine GDF-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   109 CysLysCysSer 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               425 TGTGGGTGCTCA 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: La Jolla
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Quality:
Ratio:
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US-08-525-596B-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                    eq_documentation_block:
Sequence 5, Application US/09177860A
Patent No. 6096506
GENERAL INFORMATION:
APPLICANT: Haynh, Thanh
APPLICANT: Haynh, Thanh
TITLE OF INVENTION: 32
CORRESPONDENCE: 3 32
CORRESPONDENCE ADDRESS:
ADDRESSE: Gray Cary Ware & Freidenrich LLP
STREET: 4365 Executive Drive, Suite 1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       143 GAATCCCGGTGCTGCCGCTACCCCTCACGGTCGATTT...GAAGCCTT 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28 uGlyTrpLysTrpValHisGluProLysGlyTyrTyrAlaAsnPheCysS 45
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                                                                                                                              seq_name: /cgn2_6/ptodata/2/ina/6A_COMB.seq:US-09-177-860A-5
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Percent Identity: 39.423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Align seg 1/1 to: US-09-177-860A-5 from: 1 to: 550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM: Windows95
SOFTWARE: FASSES for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/17,860A
FILING DATE: 23-OCT-1998
CLASSIFCATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/525,596
FILING DATE: 19-SEP-1995
ATTOMNEY/AGENT INFORMATION:
NAME: HAILE, Ph.D. Lisa A.
REGISTRATION NUMBER: 38,347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 07265/075003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 858-677-1456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 858-677-1465
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 550 base pairs
TYPE: nucleic acid
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3.098
63.462
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 92121
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        alignment_block:
TGFB3P x US-09-177-860A-5
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                                        109 CysLysCysSer 112
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   Quality:
    Ratio:
   Percent Similarity:
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US-09-177-860A-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
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STATE:
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1082 ........CTTGTGCACCAGAGCACAGAGCTCAGAGCCC 1119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1035 CAGGAGAGTGTGAATTTGTGTTTTACAAAAATATCCGCATACTCAT... 1081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    93 lyArgThrProLysVal...GluGlnLeuSerAsnMetValValLysSer 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        938 GAATCCCGGTGCTGCCGCTACCCCTCACGGTCGATTTT...GAAGCCTT 984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28 uGlyTrpLysTrpValHisGluProLysGlyTyrTyrAlaAsnPheCysS 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               erGlyProCysPro.....TyrLeuArgSerAlaAspThrThrHisSer 59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         76 oCysCysValProGlnAspLeuGluProLeuThrIleLeuTyrValG
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3 1/2 inch, 1.4 Mb storage
COMPUTER: COMPAQ, IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Percent Identity: 39.423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Align seg 1/1 to: US-09-177-860A-11 from: 1
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    Sequence 5, Application US/08891789B
    Patent No. 6103466
    GENERAL INFORMATION:
    APPLICANT: Grobet, Luc; Georges, Michel
    TITLE OF INVENTION: Double-Muscling in Land
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
CADRESSEE: Blake, Cassels & Graydon STREET: Box 25, Commerce Court West
                                                                                                                                                      Genomic DNA
   LENGTH: 2676 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                204.50
3.098
63.462
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                                                                                  single
                                                                                                                                                                                                                                                                                          ) NAME/KEY: CDS
; LOCATION: 104...1231
US-09-177-860A-11
                                                                                                                                                                                    IMMEDIATE SOURCE:
CLONE: Murine GDF-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               alignment_block:
TGFB3P x US-09-177-860A-11
                                             TYPE: nucleic acid
STRANDEDNESS: sing
TOPOLOGY: linear
MOLECULE TYPE: Genom:
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COUNTRY: Canada
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STATE: Ontario
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ratio:
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    Sequence 11, Application US/09177860A
    Sequence 11, Application US/09177860A
    Sequence 11, Application US/09177860A
    GERREAL INFORMATION:
    APPLICANT: Huynh, Thanh
    APPLICANT: Lee, Se-Jin
    TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR GROWTH DIFFERENTIATION FACTOR-8 AN NUMBER OF SEQUENCES: 32
    CORRESPONDENCE ADDRESS:
    ADDRESSEE: Gray Cary Ware & Freidenrich LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 :|||||| |||:::
985 TGGATGGACTGGATTATCGCACCAAAAGATATAAGGCCAATTACTGCT 1034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1082 ......CTTGTGCACCAAGCAAACCCCAGAGGCTCAGCAGGCCC 1119
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|120 TTGCTGCACTCCGACAAAATGTCTCCCATTAATATGCTATATTTTAATG 1169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    93 lyArgThrProLysVal...GluGlnLeuSerAsnMetValValLysSer 108
                                                                                                                                                                                                                                                                                                                        938 GAATCCCGGTGCTGCCGCTACCCCTCACGGTCGATTTT...GAAGCCTT 984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60 ThrValLeuGlyLeuTyrAsnThrLeuAsnProGluAlaSerAlaSerPr 76
                                                                                                                                                                                                                                                                                                                                                                                               28 uGlyTrpLysTrpValHisGluProLysGlyTyrTyrAlaAsnPheCysS 45
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                                                                                                                                                                                    to: 2676
Percent Identity: 39.423
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COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
CONFURANCE: FastSEQ for Windows Version 2.0
CURSENT APPLICATION DATA:
APPLICATION NUMBER: US/09/17,860A
FILING DATE: 23-OCT-1998
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/525,596
FILING DATE: 19-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: Halle, Ph.D, Lisa A.
REGISTRATION NUMBER: 38,347
COMPANDED TO THE STATEMENT OF THE ST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E: Gray Cary Ware & Freidenrich LLP 4365 Executive Drive, Suite 1600
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 858-677-1456
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Percent Similarity: 63.462
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                   alignment_block:
TGFB3P x US-08-525-596B-11
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CA
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COMPUTER READABLE FORM:

1035 CAGGAGAGTGTGAATTTGTGTTTTTACAAAAATATCCGCATACTCAT... 1081 1082 .....CTTGTGCACCAAGCAAACCCCAGAGGCTCAGCAGGCCC 1119 ||::: |170 GCAAAGAACAAATATATGGCAAATTCCAGCCATGGTAGTAGACCGC 1219 93 lyArgThrProLysVal...GluGlnLeuSerAsnMetValValLysSer 108 60 ThrValLeuGlyLeuTyrAsnThrLeuAsnProGluAlaSerAlaSerPr 76 12 GluGluAsnCysCysValArgProLeuTyrIleAspPheArgGlnAspLe 28 28 uGlyTrpLysTrpValHisGluProLysGlyTyrTyrAlaAsnPheCysS 45 erGlyProCysPro.....TyrLeuArgSerAlaAspThrThrHisSer 59 76 oCysCysValProGlnAspLeuGluProLeuThrIleLeuTyrTyrValG 93 seq\_name: /cgn2\_6/ptodata/2/ina/5A\_COMB.seq:US-08-525-596B-13 seq\_documentation\_block:
 Sequence 13, Application US/08525596B
 Patent No. 5827733
 GENERAL INFORMATION:
 APPLICANT: Huynh, Thanh
 APPLICANT: Lee, Se-Jin
 TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-8
 NUMBER OF SEQUENCES: 3
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Fish & Richardson P.C.
 STREET: 4225 Executive Square, Suite 1400
 CITY: La Jolla
 STATE: CA Percent Identity: 39.423 Align seg 1/1 to: US-08-891-789B-5 from: 1 to: 2676 Length: Gaps: REFERENCE/DOCKET NUMBER: 52836/00004
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 863-4344
TELEFAX: (416) 863-2653
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 2676 base pairs
TYPE: nucleic acid
STRANDEDNESS: SINGle US/08/891,789B FILING DATE: July 14, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Hunt, John C.
REGISTRATION NUMBER: 36,424 204.50 3.098 63.462 APPLICATION NUMBER: alignment\_block: TGFB3P x US-08-891-789B-5 1220 TGTGGGTGCTCA 1231 109 CysLysCysSer 112 linear Quality: Percent Similarity: Ratio: COUNTRY: US ZIP: 92037 ; TOPOLOGY: US-08-891-789B-5 alignment\_scores: 45

1034 .......CTGGTACACCAAGCAAACCCCAGAGGTTCAGCAGGCCC 1071 987 CTGGAGAGTGTGAATTTGTATTTTACAAAAATATCCTCATACTCAT... 1033 93 lyArgThrProLysVal...GluGlnLeuSerAsnMetValValLysSer 108 890 GAATCACGATGCTGTCGTTACCCTCTAACTGTGGATTTT...GAAGCTTT 936 937 TGGATGGGATTATCGCTCCTAAAAGATATAAGGCCAATTACTGCT 986 12 GluGluAsnCysCysValArgProLeuTyrIleAspPheArgGlnAspLe 28 28 uGlyTrpLysTrpValHisGluProLysGlyTyrTyrAlaAsnPheCysS 45 60 ThrValLeuGlyLeuTyrAsnThrLeuAsnProGluAlaSerAlaSerPr 76 45 erGlyProCysPro.....TyrLeuArgSerAlaAspThrThrHisSer 59 76 oCysCysValProGlnAspLeuGluProLeuThrlleLeuTyrTyrValG 93 Align seg 1/1 to: US-08-525-596B-13 from: 1 to: 2743 Percent Identity: 39.423 MEDIUM 11EE:
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSEQ for Windows Version 2.0
CURENT APPLICATION DATA:
APPLICATION NUMBER: US/08/525,596B
FILING DATE: 19-SEP-1995
CLASSIPICATION 514
PROOF APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/07762
FILING DATE: 08-UGL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Wetherell, Jr., Ph.D, John R.
REGISTRATION NUMBER: 31,678 REFERENCE/DOCKET NUMBER: 07265/075001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-678-5070
TELEPA: 619-678-5099
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS: MOLECULE TYPE: Genomic DNA LENGTH: 2743 base pairs 204.50 3.098 63.462 single 59...1183 alignment\_block: TGFB3P x US-08-525-596B-13 nucleic acid Human GDF-8 1172 reregerecrea 1183 109 CysLysCysSer 112 linear IMMEDIATE SOURCE: NAME/KEY: CDS Quality: Percent Similarity: Ratio: STRANDEDNESS: ; LOCATION: US-08-525-596B-13 alignment\_scores: TOPOLOGY:

seq\_name: /cgn2\_6/ptodata/2/ina/6A\_COMB.seq:US-09-177-860A-13

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.........CTGGTACACCAAACCCCAGAGGTTCAGCAGGCCC 1071
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1072 TIGCIGTACTCCCAAAAGAIGTCTCCAATTAATATATATTTTAAIG 1121
                                                                                                                                                     93 lyArgThrProLysVal...GluGlnLeuSerAsnMetValValLysSer 108
                                                                 76 oCysCysValProGlnAspLeuGluProLeuThrIleLeuTyrTyrValG
                                                                                                                                                                                                                                                                                                                                seq_name: /cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-765-875-3
                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: LEE, SE-JIN
APPLICANT: MCPHERRON, ALEXANDRA C.
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-11
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Identity: 36.667
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: SPENSLEY HORN JUBAS & LUBITZ
STREET: 1880 CENTURY PARK EAST, FIFTH FLOOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/706,958
FILING DATE:
APPLICATION NUMBER: US/08/272,763
FILING DATE: 08-UUL-1994
ATTORNEY/AGENT INFORWATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: TUMARKIN PH.D., LISA A. REGISTRATION NUMBER: P.38,347
REPERENCE/DOCKET NUMBER: PD3641
TELECOMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                         DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: 619/455-5100
TELEFAX: 619/455-5110
INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
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3.076
55.000
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STRANDEDNESS: single
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198..575
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                                                                                                                                                                                                                                                                                     1172 TGTGGGTGCTCA 1183
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STATE: CALIFORNIA
                                                                                                                                                                                                                                          109 CysLysCysSer 112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: DIMMEDIATE SOURCE:
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Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: U
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LOCATION:
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                                                                                                 APPLICANT: Huynh, Thanh
APPLICANT: Lee, Se-Jin
TILE OF INVENTION: ANTHODIES SPECIFIC FOR GROWTH DIFFERENTIATION FACTOR-8 AN
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSE: GATY CATY Ware & Freidenrich LLP
STREET: 4365 Executive Drive, Suite 1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      987 CTGGAGAGTGTGAATTTGTATTTTACAAAATATCCTCATACTCAT... 1033
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            45 erGlyProCysPro.....TyrLeuArgSerAlaAspThrThrHisSer 59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28 uGlyTrpLysTrpValHisGluProLysGlyTyrTyrAlaAsnPheCysS 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 60 ThrValLeuGlyLeuTyrAsnThrLeuAsnProGluAlaSerAlaSerPr 76
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Identity: 39.423
                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/177,860A
FILING DATE: 23-OCT-1998
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/525,596
FILING DATE: 19-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: Haile, Ph.D, Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 38,347
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPAX: 858-677-1456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps:
                                      Sequence 13, Application US/09177860A
Patent No. 6096506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 2743 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genomic DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Quality: 204.50
Ratio: 3.098
nilarity: 63.462
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59...1183
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TGFB3P x US-09-177-860A-13
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IMMEDIATE SOURCE:
CLONE: Human GDF-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
                  seq_documentation_block:
                                                                                 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                         92121
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; LOCATION:
US-09-177-860A-13
                                                                                                                                                                                                                                                                                     CA
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STATE:
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GlyArgThrProLysValGluGlnLeuSerAsnMetValValLysSerCy 109
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                                                                                                                                                                                         16 sValArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpV 33
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                                                                                                        .....GluGluAsnCysCy 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Se-Jin Lee and Alexandra McPherron
TITLE OF INVENTYON: GROWTH DIFFERENTIATION FACTOR-11
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OFTGATION SISTEM: TO LOUS/MS-LOUS
SOFTGATE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/795,671
FILING DATE: February 6, 1997
CLASSIFICATION: 800
ATTONNEY/AGENT INFORMATION:
NAME: HALLE, PH.D., LISA A.
REGISTRATION NUMBER: 38,347
REFERENCE/POCKET NUMBER: 38,347
TREECOMMULCATION INFORMATION:
TELEPHONE: 619/678-5070
                                                             Align seg 1/1 to: US-08-765-875-3 from: 1 to: 630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  eq_documentation_block:
Sequence 3, Application US/08795671
Patent No. 6008434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              534 GCCAAGATCCCT.....
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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alignment_block:
TGFB3P x US-08-765-875-3
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93 GlyArgThrProLysValGluGlnLeuSerAsnMetValValLysSerCy 109 534 GGCAAGAICCCI......GGCAIGGIGGIGGAICGAIG 565 393 TACATGTTCATGCAAAAGTATCCACACACC......CACTTGGTGCA 433 33 alHisGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysPro 49 16 sValArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpV 33 9 ArgAsnLeu.....GluGluAsnCysCy 16 50 TyrLeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAs 66 euGluProLeuThrIleLeuTyrTyr.....val 92 seq\_name: /cgn2\_6/ptodata/2/ina/5A\_COMB.seq:US-08-247-907A-1 Length: 120 Gaps: 5 Percent Identity: 36.667 Align seg 1/1 to: US-08-795-671-3 from: 1 to: 630 APPLICANT: WOZNEY, John
APPLICANT: CELESTE, Anthony J.
TITLE OF INVENTION: BMP-11 COMPOSITIONS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE GENETICS INSTITUTE, INC.
STREET: 87 CambridgePark Drive COUNTRA ZIP: 02140 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk TOPOLOGY: linear MOLECULE TYPE: DNA (genomic) 203.00 3.076 55.000 single IMMEDIATE SOURCE: CLONE: MOUSE GDF-11 CDS 198..575 alignment\_block: TGFB3P x US-08-795-671-3 566 TGGCTGCTCC 575 109 sLysCysSer 112 alignment\_scores: Quality: Ratio: Percent Similarity: STRANDEDNESS: ; NAME/KEY: ; LOCATION: US-08-795-671-3 STATE: FEATURE

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109 sLysCysSer 112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
NAME/KEY: misc_feature
LOCATION: 322..333
OTHER INFORMATION: /note= "putative 3' end of intron"
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/247,907A
FILING DATE: May 20, 1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: LAZAR, Steven R.
REGISTRATION NUMBER: 32,618
REGISTRATION NUMBER: 32,618
REGISTRATION NUMBER: 32,618
TELEPHONE: 617 876-1170
TELEPHONE: 617 876-1170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps: 5
Percent Identity: 36.667
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                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 789 base pairs TYPE: nucleic acid STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                              DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                               STRAIN: Bovine Activin WC
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3.076
55.000
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375..701
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TGFB3P x US-08-247-907A-1
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MOLECULE TYPE: D
ORIGINAL SOURCE:
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Percent Similarity:
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US-08-247-907A-1
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NAME/KEY: misc_feature
LOCATION: 322..323
OTHER INFORMATION: /note= "putative 3' end of intron"
                                       seq_name: /cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-452-772-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/452,772
FILING DATE: 30-MAY-1995
CLASSIFICATION 1530
PRIOR APPLICATION NUMBER: US 08/247,907
APPLICATION NUMBER: US 08/247,907
FILING DATE: 20-MAY-1994
ATONENY/AGERT INFORMATION:
NAME: LAZAR, Steven R.
REGISTRATION NUMBER: 32,618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Identity: 36.667
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: G15205-CIP
TELEPOMMUNICATION INFORMATION:
TELEPHONE: 617 876-1170
TELEPRAX: 617 876-5851
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 789 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                       APPLICANT: WOZNEY, John
APPLICANT: CELESTE, Anthony J.
TITLE OF INVENTION: BMP-11 COMPOSITIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    to: US-08-452-772-1 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: GENETICS INSTITUTE,
STREET: 87 CambridgePark Drive
                                                                           seq_documentation_block:
Sequence 1, Application US/08452772
Sequence 1, Application US/08452772
Setent No. 5700911
General Information:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN: Bovine Activin WC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       203.00
3.076
55.000
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375..701
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MEDIUM TYPE: Floppy
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TGFB3P x US-08-452-772-1
                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
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692 reserrect 701
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MOLECULE TYPE: D
ORIGINAL SOURCE:
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                                                                                                                                                                                                                                                                                                                                                 USA
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; LOCATION:
US-08-452-772-1
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                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Align seg 1/1
                                                                                                                                                                                                                                                                                                                            STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
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GluGluAsnCysCy 16    ::::::      AGTGAGTCCCGCTGTG 421 pleuGlyTrpLysTrpV 33 :::              TTTTGGCTGGACTGA 468 ysSerGlyProCysPro 49          GCTCCGGCCAGTGCGG 518 ValleuGlyLeuTyTAS 66		:T-US94-05288-1	id of intron"
AACATTCAAGTGAG AAGATTCAAGTGAG ATGGINASPLeuG]GAGGCTTTTGG AASNPHeCYSSETG     :::       CAACTACTGCTCGG		7/ina/PCTUS_COMB.seq:PC PC/TUS9405288 BMP-11 COMPOSITIONS 11 MW: yy disk compatible PC-DOS/MS-DOS RELease #1.0, Version RR-RELEASE #1.0, Version ATA:	"putative 3' end
ArgasnLeu	: : :		1: wc wc
9 ArgAsnLeu 	519 TACATGTTATG 66 nThrLeuAsnPr 560 ACAGGCTAACCC 83 euGluProLeuT ::::   ::: 610 TGTCCCCAATCA 93 GLyArgThrPro 93 GLyArgThrPro 109 sLySCysSer 1                       600 GGCAAGATCCCT 109 sLySCysSer 1		INFORMATION FOR SEON IN OCCENSION FOR SEON IN SEQUENCE CHARACTERISTICS: LENGTH: 789 base pairs Internation of STRANDEDNESS: double STRANDEDNESS: double STRANDEDNESS: double STRANDEDNESS: double STRANDES STRANDES BOS TAUTUS STRAIN: BOVINE ACTIVIN FEATURE: NAME/KEY: MISC_feature CATTON 324.704 FEATURE: NAME/KEY: MISC_feature CATTON 322.333 COTHER INFORMATION: /no FEATURE: NAME/KEY: MISC_feature CATTON 375.701
ल चंच	и и и и и и и и и и и и и и и и и и и	seq_name: seq_docum ; Sequency ; Sequency ; APPL ;	INFC

519 TACATGTTTATGCAAAAGTATCCGCACACC......CACTTGGTGCA 559 16 sValArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpV 33 9 ArgAsnLeu.....GluGluAsnCysCy 16 33 alHisGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysPro 49 50 TyrLeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAs 66 66 nThrLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspL 83 83 euGluProLeuThrIleLeuTyrTyr.....Val 92 seq\_name: /cgn2\_6/ptodata/2/ina/5A\_COMB.seq:US-08-247-907A-10 COMPUTER TEACHER
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPOTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/247,907A
FILING DATE: May 20, 1994
CLASSICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: LAZAR Steven R.
REGISTRATION NUMBER: 32,618
REGISTRATION NUMBER: 32,618
REFERENCE/DOCKET NUMBER: GI5205-A
TELECOMMUNICATION INFORMATION: alignment\_scores:
Quality: 203.00 . Length: 120
Ratio: 3.076 Gaps: 5
Percent Similarity: 55.000 Percent Identity: 36.667 Align seg 1/1 to: PCT-US94-05288-1 from: 1 to: 789 seq\_documentation\_block:
 Sequence 10, Application US/08247907A
 Sequence 10, Application US/08247907A
 Patent No. 5639638
 GENERAL INFORMATION:
 APPLICANT: WOZNEY, John
 APPLICANT: CELESTE, Anthony J.
 TITLE OF INVENTION: BMP-11 COMPOSITIONS
 NUMBER OF SEQUENCES: 12
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: GENETICS INSTITUTE, INC.
 STRRET: 87 CambridgePark Drive 660 GGCAAGATCCCT..... alignment\_block: TGFB3P x PCT-US94-05288-1 109 sLysCysSer 112 | |||||| 692 TGGCTGCTCC 701 COUNTRY: USA ZIP: 02140 Æ STATE: MA COUNTRY:

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......GGCATGGTGGTGGATCGCTG 1076
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Percent Identity: 36.667
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_documentation_block:
    Sequence 10, Application US/08452772
; Patent No. 5700911
; GENERAL INFORMATION:
    APPLICANT: WOZNEY, John
    APPLICANT: CELESTE, Anthony J.
    TITLE OF INVENTION: BMP-11 COMPOSITIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   83 euGluProLeuThrIleLeuTyrTyr.....
TELEPHONE: 617 876-1170
TELEFAX: 617 876-5851
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 1270 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                   TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                           ORGANISM: Human BMP-11
IMMEDIATE SOURCE:
CLONE: FB30.5
                                                                                                                                                                                                                                                                                                                          NAME/KEY: mat_peptide LOCATION: 760..1086
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Percent Similarity: 55.000
                                                                                                                                                                                                                                                                                                                                                                                                                                              203.00
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TGFB3P x US-08-247-907A-10
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LOCATION: 1..1086
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                                                                                                                                                                          ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                            Quality:
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US-08-247-907A-10
                                                                                                                                                                                                                                                                                                                                                                                                                            alignment_scores:
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| 904 TACATGTTCATGCAAAAATATCCGCATACC........CATTTGGTGCA 944
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                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPAtible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Identity: 36.667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Align seg 1/1 to: US-08-452-772-10 from: 1 to: 1270
                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/247,907
FILING DATE: 20-MAT-1994
ATTORNEY AGENT INFORMATION:
NAME: LAZAR, Steven R.
REGISTRATION NUMBER: 32,618
REFERNCE/DOCKET NUMBER: GI5205-CIP
TELECOMMUNICATION:
TELEPHONE: 617 876-1170
                                                                                                                                                                                                                                                                                                                                                                                                                                GI5205-CIP
                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/452,772
FILING DATE: 30-MAY-1995
CLASSIFICATION: 530
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENETICS INSTITUTE,
STREET: 87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 617 876-5851
INFORMATION FOR SEQ ID NO: 10
SEQUENCE CHARACTERISTICS:
LENGTH: 1270 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Human BMP-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mat_peptide
760..1086
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3.076
55.000
                                                                                                                                  ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 alignment_block:
TGFB3P x US-08-452-772-10
                                             ALL...
STREET: 8/ ...
TTV: Cambridge
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Ratio:
Percent Similarity:
                                                                                                                 USA
                                                                                                                                02140
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US-08-452-772-10
                                                                                                                 COUNTRY:
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tgfb3p.rni

ov ninkledaapirodinAlaSerAlaSerProCysCysValProGinaspi. 83 	
109 sLysCysSer 112 	
seq_name: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:PCT-US94-05288-10	
<pre>seq_documentation_block:</pre>	
APPLICANT: TITLE OF INVENTION: BMP-11 COMPOSITIONS NUMBER OF SEQUENCES: 11 COMPUTER READABLE FORM:	
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LICATION DATA: ON NUMBER: PCT/US94/0528	
CLASSIFICATION: INFORMATION FOR SEO. SEOTIEMES CHARACTERITY.	
LENGTH: 1270 base pairs TYPE: nucleic acid	
TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)	
ORGANISM: Human BMP-11 IMMEDIATE SOURCE: CLONE: F830.5	
<u> </u>	
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alignment_scores:     Quality: 203.00	
alignment_block: TGFB3P x PCT-US94-05288-10	
Align seg 1/1 to: PCT-US94-05288-10 from: 1 to: 1270	
9 ArgAsnLeuGludluAsnCysCy 16 	
16 sValargProLeuTyrIleaspPheArgGlnAspLeuGlyTrpLysTrpV 33	
33 alHisGluProLysGlyTyTyrAlaAsnPheCysSerGlyProCysPro 49 ::	

1045 GGCAAGATCCCT.....GGCATGGTGGTGGATCGCTG 1076 854 TCATCGCACCTAAGCGCTACAAGGCCAACTACTGCTCCGGCCAGTGCGAG 903 904 TACATGTTCATGCAAAAATATCCGCATACC......CATTTGGTGCA 944 93 GlyArgThrProLysValGluGlnLeuSerAsnMetValValLysSerCy 109 50 TyrLeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAs 66 66 nThrLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspL 83 83 euGluProLeuThrIleLeuTyrTyr....val 92 seq\_documentation\_block:
Sequence 1, Application US/08765875
SEQUENCE:
SEQUENCE:
SEQUENCE:
SEQUENCE:
SEQUENCES:
STORES:
STORES:
STORES:
STATE:
COUNTRY:
COUNTRY:
COUNTRY:
SIPER
COUNTRY:
COUNTRY seq\_name: /cgn2\_6/ptodata/2/ina/5B\_COMB.seq:US-08-765-875-1 SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/765,875
FILING DATE:
CLASSIFICATION: PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/706,958
FILING DATE:
APPLICATION NUMBER: US/08/272,763
FILING DATE: 08-UUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: TUMARKIN PH.D., LISA A.
REGISTRATION NUMBER: P-38,347
REFERENCE/DOCKET NUMBER: PD641
TELEDPHONE: 619/455-5100
TELEPHONE: 619/455-5100
TELEPAX: 619/455-5100 MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS TOPOLOGY: linear MOLECULE TYPE: DNA (genomic) IMMEDIATE SOURCE: CLONE: HUMAN GDF-11 LENGTH: 1393 base pairs TYPE: nucleic acid STRANDEDNESS: single COMPUTER READABLE FORM: MEDIUM TYPE: Floppy CDS 54..1274 1077 TGGCTGCTCT 1086 109 sLysCysSer 112 CLONE: HUM.;
FEATURE:
NAME/KEY:
LOCATION:
US-08-765-875-1

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1092 TACATGTTCATGCAAAATATCCGCATACC......CATTTGGTGCA 1132
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                                                                                                                                                                                                                                                                                                                         16 sValArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpV 33
                                                                                                                                                                                                                                                                                                                                                                                                                     33 alHisGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysPro 49
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    Sequence 1, Application US/08795671
    Patent No. 6008434
    GENERAL INFORMATION:
    APPLICANT: Se-Jin Lee and Alexandra McPherron
    TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-11
    NUMBER OF SEQUENCES: 9
    CORRESPONDENCE ADDRESS:
                                                Gaps: 5
Percent Identity: 36.667
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPRIATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                  Align seg 1/1 to: US-08-765-875-1 from: 1 to: 1393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: California
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: HAILE, PH.D., LISA A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07265/106001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/795,671 FILING DATE: February 6, 1997
                   203.00
3.076
55.000
                                                                                                            alignment_block:
TGFB3P x US-08-765-875-1
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                     Quality:
Ratio:
                                                       Percent Similarity:
alignment_scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             93 GlyArgThrProLysValGluGlnLeuSerAsnMetValValLysSerCy 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9 ArgAsnLeu.....GluGluAsnCysCy 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   33 alHisGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysPro 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      50 TyrLeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAs 66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16 sValArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpV 33
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    Sequence 3, Application US/08891789B
    Fatent No. 6103466
    GENERAL INFORMATION:
    TITLE OF INVENTION: Double-Muscling in Mammals
    TUMBER OF SEQUENCES: 52
    CORRESPONDENCE ADDRESS:
    ADDRESSEE: Blake, Cassels & Graydon
    STREET: Box 25, Commerce Court West
    CITY: Toronto
                                                                                                                                                                                                                                                                                                                                                                                                                Gaps: 5
Percent Identity: 36.667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Align seg 1/1 to: US-08-795-671-1 from: 1 to: 1393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    83 euGluProLeuThrIleLeuTyrTyr......
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
TELEFAX: 619/678-5099
                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                     INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1393 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                          203.00
3.076
55.000
                                                                                                                                                                                                      IMMEDIATE SOURCE:
CLONE: HUMAN GDF-11
                                                                                                                                                                                                                                                                         CDS
54..1274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           . alignment_block:
TGFB3P x US-08-795-671-1
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Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Similarity:
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US-08-795-671-1
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52

NUMBER OF SEQUENCES:

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seq_documentation_block:
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1011 .........CTTGTGCACAGCAAACCCCAGAGGTTCAGCGGCCC 1048
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    964 CIGGAGAAIGIGAAITIGTATITITICCAAAAGIAICCICAIACCCAI... 1010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         93 lyArgThrProLysVal...GluGlnLeuSerAsnMetValValLysSer 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28 uGlyTrpLysTrpValHisGluProLysGlyTyrTyrAlaAsnPheCysS 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  60 ThrValLeuGlyLeuTyrAsnThrLeuAsnProGluAlaSerAlaSerPr 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12 GluGluAsnCysCysValArgProLeuTyrIleAspPheArgGlnAspLe 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            erGlyProCysPro.....TyrLeuArgSerAlaAspThrThrHisSer 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq_name: /cgn2_6/ptodata/2/ina/6A_COMB.seq:US-08-891-789B-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    76 oCysCysValProGlnAspLeuGluProLeuThrIleLeuTyrTyrValG
                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3 1/2 inch, 1.4 Mb storage COMPUTER: COMPAQ, IBM PC compatible OPERATING SYSTEM: MS-DOS 5.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Percent Identity: 39.423
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Double-Muscling in Mammals
                                                                                                                                                   SOFTWARE: WORD PERFECT
CURRENT APPLICATION DATA:
PAPLICATION NUMBER: US/08/891,789B
FILING DATE: July 14, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Hunt, John C.
REGISTRATION NUMBER: 36,424
REFERENCE/DOCKET NUMBER: 52836/00004
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 863-4344
TELEPHONE: (416) 863-263
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_documentation_block:
    sequence 1, Application US/08891789B
    Patent No. 6103466
        GENERL INFORMATION:
        APPLICANT: Grobet, Luc; Georges,
        TITLE OF INVENTION: Double-Muscli
                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 1240 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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64.423
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|1149 TGTGGGTGTTCA 1160
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                M5L 1A9
'RY: Canada
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Ontario
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Ratio:
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US-08-891-789B-3
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                     ZIP: M5L
COUNTRY:
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1022 .........CTTGTGCACCAGAGAACCCCAGAGGTTCAGGCGGCCC 1059
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  93 lyArgThrProLysVal...GluGlnLeuSerAsnMetValValLysSer 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               45 erGlyProCysPro.....TyrLeuArgSerAlaAspThrHisSer 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60 ThrValLeuGlyLeuTyrAsnThrLeuAsnProGluAlaSerAlaSerPr 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          76 oCysCysValProGlnAspLeuGluProLeuThrIleLeuTyrTyrValG 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28 uGlyTrpLysTrpValHisGluProLysGlyTyrTyrAlaAsnPheCysS 45
                                                                                                                                                              COMPUTER REACHER FORM:
MEDIUM TYPE: Diskette, 3 1/2 inch, 1.4 Mb storage COMPUTER: COMPA, IBM PC compatible COMPUTER: COMPA, IBM PC compatible OPERATING SYSTEM: MS-DOS 5.1
SOFTWARE: WORD PERFECT CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/891,789B
FILING DATE: July 14, 1997
ATORNEY/AGENT INFORMATION:
NAME: Hunt, John C.
REGISTRATION NUMBER: 36,424
REFERENCE/DOCKET NUMBER: 52836/0004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12 GluGluAsnCysCysValArgProLeuTyrIleAspPheArgGlnAspLe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps: 4
Percent Identity: 39.423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Align seg 1/1 to: US-08-891-789B-1 from: 1 to: 1196
                               Graydon
CORRESPONDENCE ADDRESS:
ADDRESSEE: Blake, Cassels & Gra
STREET: Box 25, Commerce Court
                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 863-4344
TELEFAX: (416) 863-2653
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1196 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 201.50
3.053
63.462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TGFB3P x US-08-891-789B-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                109 CysLysCysSer 112
                                                                      CITY: Toronto
STATE: Ontario
ZIP: M5L 1A9
COUNTRY: Canada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
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APPLICANT: Anthony J. Mason
APPLICANT: Peter H. Seeburg
TITLE OF INVENTION: Nucleic Acid Encoding the Alpha or Beta Chains of Inhibin a
NUMBER OF SEQUENCES: 44
    67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
                                                                                                                                                                                                                                                                                                                                                          seq_name: /cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-197-792-42
                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US/08/197,792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NOMBER: US/08/19/1/19
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/958414
FILING DATE: 08-OCT-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/744207
FILING DATE: 12-AUG-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/215466
FILING DATE: 05-JUL-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 06/906729
FILING DATE: 31-DEC-1986
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 06/906729
FILING DATE: 31-DEC-1986
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 06/906729
FILING DATE: 06/906729
FILING DATE: 06/906729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                 seq_documentation_block:
; Sequence 42, Application US/08197792
; Patent No. 5525488
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 07-FEB-1986
PRIOR APPLICATION DATA: 06/783910
FILING DATE: 03-0CT-1985
ATTORNEY/AGENT INFORMATION:
NAME: Hasak, Janet E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: patin (Generatech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28,616
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1633 bases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Hasak, Janet E. REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 1633 bases
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                94080
                                                          APPLICANT: MURKAMI, KAZUO
APPLICANT: UENO, NACTO
APPLICANT: UENO, VAGTO
APPLICANT: ATO, YUKIO
TITLE OF INVENTION: XENOPUS LAEVIS BONE MORPHOGENETIC PROTEINS AND USE THE
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dike, Bronstein, Roberts & Cushman
STREET: 130 Water Street
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        237 ATCAGATAAATTATTGCATGGGCCTTTGCCCAATGCATATCCTGGAGCC 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23 pPheArgGlnAspLeuGlyTrpLys...TrpValHisGluProLysGlyT 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10 AsnLeuGluGluAsn..........CysCysValArgProLeuTyrIleAs 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     39 yrTyrAlaAsnPheCysSerGlyProCysPro...TyrLeuArgSerAla 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps: 7
Percent Identity: 36.842
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                40302-FWC-DIV
                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM: DOS
SOFTWARE: FESTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/455,550
FILING DATE: 31-MAY-1995
CLASSIFICATION 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/056,564
FILING DATE: 30-APR-1993
APPLICATION NUMBER: 07/577,892
FILING DATE: 105-SEP-1990
ATTORNEY/AGENT INFORMATION:
NAME: Eisenstein, Romald I
REGISTRATION NUMBER: 30628
Sequence 2, Application US/08455550
Patent No. 5670338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 40
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEPAX: 617-523-6440
                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEX: 200291
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 687 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        200.50
2.571
68.421
                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
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TGFB3P x US-08-455-550-2
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                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                      USA
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; ORIGINAL SOURCE:
US-08-455-550-2
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ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                  COUNTRY: U
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1294 AGTGCCCGAGCCATATAGCAGGCACGTCCGGGTCCTCACTGTCCTTCCAC 1343
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1197 IGCIGIAAGAAACAGIICIIIGICAGIIIICAAG...GACAICGGCIGGAA 1243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            90 yrTyr...ValGlyArgThrProLysValGluGlnLeuSerAsnMetVal 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     59 SerThrValLeuGlyLeuTyrAsnThrLeu.....AsnProGluAlaSe 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                73 rAlaSerProCysCysValProGlnAspLeuGluProLeuThrIleLeuT 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31 s...TrpValHisGluProLysGlyTyrTyrAlaAsnPheCysSerGlyP 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              47 roCysPro.....TyrLeuArgSerAlaAspThrThrHis 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15 CysCysValArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length: 107
Gaps: 5
Percent Identity: 37.383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Align seg 1/1 to: US-08-459-850-42 from: 1 to: 1633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 297P2D5 TELECOMMUNICATION INFORMATION:
                                                                                                         APPLICATION NOMBER: 12-AUG-1991
PRIOR APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: 07/215466
FILING DATE: 05-JUL-1988
PRIOR APPLICATION DATA: 06/906729
APPLICATION NUMBER: 06/906729
FILING DATE: 31-DEC-1986
PRIOR APPLICATION DATA: APPLICATION NUMBER: 06/827710
FILING DATE: 07-FEB-1986
PRIOR APPLICATION DATA: APPLICATION NUMBER: 06/783910
FILING DATE: 03-OCT-1985
ATTORNEY/AGENT INFORMATION:
                                             FILING DATE: 08-OCT-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/744207
                        APPLICATION NUMBER: 07/958414
FILING DATE: 08-0CT-1992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: 415/225-1896
TELEFAX: 415/952-9881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELERX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Hasak, Janet E. REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           200.00
2.703
69.159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS: single
    PRIOR APPLICATION DATA:
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TGFB3P x US-08-459-850-42
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Anthony J. Mason
APPLICANT: Peter H. Seeburg
TITLE OF INVENTION: Nucleic Acid Encoding the Alpha or
TITLE OF INVENTION: Beta Chains of Inhibin and Method for Synthesizing Polypeptide
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : ||||:::|||
1244 TGACTGGATCATTGCTCCCTCTGGCTATCATGCCAACTACTGCGAGGGTG 1293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1344 TCAACAGTCATCAACCACTACCGCATGCGGGGCCATAGCCCCTTTGCCAA 1393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          90 yrTyr...ValGlyArgThrProLysValGluGlnLeuSerAsnMetVal 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SerThrValLeuGlyLeuTyrAsnThrLeu.....AsnProGluAlaSe 73
                                                                                                                                                                                                                                                                                                                                                                                                                 31 s...TrpValHisGluProLysGlyTyrTyrAlaAsnPheCysSerGlyP 47
                                                                                                                                                                                                                                                                                                                      15 CysCysValArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLy 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq_name: /cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-459-850-42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    73 rAlaSerProCysCysValProGlnAspLeuGluProLeuThrileLeuT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             47 roCysPro.....TyrLeuArgSerAlaAspThrThrHis
                                                                                                                                                            Percent Identity: 37.383
                                                                                                                                                                                                                                                                             from: 1 to: 1633
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MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: patin (Generach)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,850
FILING DATE: 02-UN-1995
CLASSIFICATION: 435
PRIOR APPLICATION 1435
APPLICATION DATE: 08-197792
FILING DATE: 17-FEB-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Genembech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seq_documentation_block:
    sequence 42, Application US/08459850
    patent No. 5665568
        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                           Align seg 1/1 to: US-08-197-792-42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1494 GTGGAGGAGTGTGGGTGCTCA 1514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      106 ValLysSerCysLysCysSer 112
                                                                                                            200.00
2.703
69.159
                                                                                                                                                                                                       alignment_block:
TGFB3P x US-08-197-792-42
linear
                                                                                                              Quality:
Ratio:
                                                                                                                                                          Percent Similarity:
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; TOPOLOGY:
US-08-197-792-42
                                                                                         alignment_scores:
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tgfb3p.rni

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seq_documentation_block:

Sequence 32, Application US/08197792

Sequence 32, Application US/08197792

Patent No. 5525488

GENERAL INFORMATION:

APPLICANT: Anthony J. Mason

TITLE OF INVENTION:

NUMBER OF SEQUENCES: 44

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.

STREET: 460 Point San Bruno Blvd

CITY: South San Francisco

STATE: California

CONTRY: USA
                                                                                                            1197 IGCIGIAAGAAACAGIICITIIGICAGIIICAAG...GACAICGGCIGGAA 1243
                                                                                                                                                                                                   1444 ACTATGATGATGGTCAAAACATCATCAAAAAGGACATTCAGAACATGATC 1493
                                                                                                                                                                                                                                                                                                                                                                                                              1344 TCAACAGTCATCAACCACTACCGCATGCGGGGCCATAGCCCCTTTGCCAA 1393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           90 yrTyr...ValGlyArgThrProLysValGluGlnLeuSerAsnMetVal 105
                                                                                                                                                                     31 s...TrpValHisGluProLysGlyTyrTyrAlaAsnPheCysSerGlyP 47
                                                                                                                                                                                                                                                                   47 roCysPro.....TyrLeuArgSerAlaAspThrThrHis 58
                                                                                                                                                                                                                                                                                                                                                                 59 SerThrValLeuGlyLeuTyrAsnThrLeu.....AsnProGluAlaSe 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                             73 rAlaSerProCysCysValProGlnAspLeuGluProLeuThrIleLeuT 90
                                                                          15 CysCysValArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLy 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_name: /cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-197-792-32
                             to: US-08-459-214-42 from: 1 to: 1633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US/08/197,792
16-FEB-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
PRIOR APPLICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/958414
FILING DATE: 08-0CT-1992
PRIOR APPLICATION NUMBER: 07/744207
FILING DATE: 12-AUG-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/215466
APPLICATION NUMBER: 07/215466
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FILING DATE: 31-DEC-1986
PRIOR APPLICATION DATA: 06/827710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1494 GIGGAGGAGTGTGGGTGCTCA 1514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           106 ValLysSerCysLysCysSer 112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 94080
                             Align seg 1/1
                                                                                                                                        APPLICANT: Anthony J. Mason
APPLICANT: Peter H. Seeburg
TITLE OF INVENTION: Nucleic Acid Encoding the Alpha or
TITLE OF INVENTION: Beta Chains of Inhibin and Method for Synthesizing Polypeptide
TITLE OF INVENTION: Using such Nucleic Acid
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
seq_name: /cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-459-214-42
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COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPRRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                      STREET: Generatech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         омыЕR: US/08/459,214
02-JUN-1995
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PRIOR APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 17 FEB. 1994

PRIOR APPLICATION DATA:
APPLICATION DATE: 07/958414

FILING DATE: 08 **OCT**-1992

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/744207

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/215466

PRIOR APPLICATION DATA: 07/215466

PRIOR APPLICATION DATA: 05**-011988

PRIOR APPLICATION DATA: 05**-011988

PRIOR APPLICATION DATA: 06**-011988

PRIOR APPLICATION DATA: 06**-011988

PRIOR APPLICATION DATA: 06**-011988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: 06/827710
FILING DATE: 07-FEB-1986
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 06/783910
FILING DATE: 03-OCT-1985
ATTORNEY/AGENT INFORMATION:
                                               NAME: Hasak, Janet E.
REGISTRATION NUMBER: 28,616
REFERENCE/DOCKET NUMBER: 297
TELECOMMUNICATION:
TELEPHONE: 415/225-1896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEX: 910/3/1-7168
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2.703
69.159
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TGFB3P x US-08-459-214-42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 1633 bases
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 03 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Quality:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-459-214-42
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988 IGCIGIAAGAAGCAGIICITIGICAGIIICAAG...GACAICGGCIGGAA 103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15 CysCysValArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLy 31
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                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
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                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,850
FILING DATE: 02-UUN-1995
                                                                                                                                                                                                                                          FILING DATE: 02-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/197792
FILING DATE: 17-FEB-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/958414
FILING DATE: 08-OCT-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/744207
FILING DATE: 12-AUG-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/215466
FILING DATE: 05-JUL-1988
PRIOR APPLICATION DATA: 06/906729
FILING DATE: 31-DEC-1966
PRIOR APPLICATION DATA: 06/906729
FILING DATE: 07-FEB-1986
PRIOR APPLICATION DATA: 06/827710
FILING DATE: 03-OCT-1985
APPLICATION NUMBER: 06/82710
FILING APPLICATION DATA: NUMBER: 06/82710
FILING DATE: 03-OCT-1985
APPLICATION NUMBER: 28,616
RESISTRATION NUMBER: 28,616
RESISTRATION NUMBER: 28,616
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                                                                                                                             COMPUTER: IBM PC compatible
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS
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69.159
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TGFB3P x US-08-459-850-32
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              California
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                                      USA
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STRANDEDNESS
                                                            94080
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US-08-459-850-32
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    Sequence 32, Application US/08459850
    APPLICANT: Anthony J. Mason
    APPLICANT: Anthony J. Mason
    APPLICANT: Peter H. Sebelucit
    TITLE OF INVENTION: Using such Nucleic Acid
    NUMBER OF SEQUENCES: 44
    CORRESPONDENCES: 44
    ADDRESSE: Genentech, Inc.
    STREET: 460 Point San Bruno Blvd
    CITY: South San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1135 TCGACGGTCATCAACCACTACCGCATGCGCGCCCACAGCCCCTTCGCCAA 1184
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|1085 AGTGCCCCAGCCACATAGCGGCACGTCGGGCTCCTCGCTCTCGTTCCAC 1134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1235 ACTACGACGACGGCAGAACATCATCAAGAAGGACATCCAGAACATGATC 1284
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dulity: 200.00 Length: 107
Ratio: 2.703 Gaps: 5
Percent Similarity: 69.159 Percent Identity: 37.383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              from: 1 to: 3588
                                                                                         28,616
HER: 297P2D4
APPLICATION NUMBER: 06/783910
FILING DATE: 03-0CT-1985
ATTORNEY AGENT INFORMATION:
NAME: Hasak, Janet E.
                                                                                                            REFERENCE DOCKET NUMBER: 2970
RELECOMMUNICATION INFORMATION:
TELEPHONE: 415/255-1896
TELEFAX: 415/952-981
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CARACTER STICS:
LENGTH: 3588 bases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Align seg 1/1 to: US-08-197-792-32
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                                                                        NAME: Hasak, Janet E. REGISTRATION NUMBER: 2
                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TGFB3P x US-08-197-792-32
                                                                                                                                                                                                                                                                                                                                                                linear
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US-08-197-792-32
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seq_documentation_block:
    Sequence 1, Application US/0845550
    Patent No. 5670338
    GENERAL INFORMATION:
    APPLICANT: WORAKAMI, KAZUO
    APPLICANT: WENO, YUKIO
    APPLICANT: KATO, YUKIO
    TITLE OF INVENTION: XENOPUS LAEVIS BONE MORPHOGENETIC PROTEINS AND USE THE CORRESPONDENCE ADDRESS:
    CORRESPONDENCE ADDRESS:
    ADDRESSEE: Dike, Bronstein, Roberts & Cushman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1135 TCGACGGTCATCAACCACTACCGCATGCGCGGCCACAGCCCCTTCGCCAA 1184
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31 s...TrpValHisGluProLysGlyTyrTyrAlaAsnPheCysSerGlyP 47
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Identity: 37.383
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130 Water Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IEM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ VERSION 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/455,550
FILING DATE: 31-MAX-1995
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Align seg 1/1 to: US-08-459-214-32
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; SEQUENCE CHARACTERISTICS:
; LENGTH: 3588 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLLGY: linear
US-08-459-214-32
                                                                                                                                                                                                                                                                                                                                                                                                                                        200.00
2.703
69.159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TGFB3P x US-08-459-214-32
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CITY: Boston
STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                           alignment_scores:
Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ratio:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 32, Application US/08459214
Sequence 32, Application US/08459214
Patent No. 5716810
GENERAL INFORMATION:
APPLICANT: Anthony J. Mason
APPLICANT: Peter H. Seeburg
TITLE OF INVENTION: Nucleic Acid Encoding the Alpha or
TITLE OF INVENTION: Beta Chains of Inhibin and Method for Synthesizing Polypeptide
TITLE OF INVENTION: Using such Nucleic Acid
1185 CCTCAAGTCGTGCTGCGTCCCCAAGCTGAGGCCCATGTCCATGCTGT 1234
                                                                                                                                                                                                                                                                                                                                                                                                     90 yrTyr...ValGlyArgThrProLysValGluGlnLeuSerAsnMetVal 105
                                                                                                                                             73 rAlaSerProCysCysValProGlnAspLeuGluProLeuThrIleLeuT 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_name: /cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-459-214-32
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2IP: 94080.
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
ACTUM TYPE: 15.25 inch, 360 Kb floppy disk
COMPATIBLE
C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC COMPUTER: OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: patin (Genentech) CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/459,214 FILLING DATE: 02-UN-1995 CLASSIFICATION: 435 PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/197792 FT.ING DATE: 17-FEB-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      297P2D6
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PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: 0/958414

FILING DATE: 08-OCT-1992

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 0/7/44207

FILING DATE: 12-A0G-1991

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 0/215466

FILING DATE: 05-JUL-1988

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 0/906729

APPLICATION NUMBER: 0/906/906729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1285 GTGGAGGAGTGCGGGTGCTCC 1305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 29
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         106 ValLysSerCysLysCysSer 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEX: 910/371-7168 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_documentation_block
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TYPE: nucleic acid STRANDEDNESS: single Quality: 195.00 Ratio: 2.868 nilarity: 66.019 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy CORRESPONDENCE ADDRESS: alignment\_block: TGFB3P x US-08-278-729A-24 MOLECULE TYPE: CDNA linear CITY: HOPKINTON ; NAME/KEY: CDS ; LOCATION: 1..1 US-08-278-729A-24 USA Ratio: Percent Similarity: COUNTRY: US ZIP: 01748 alignment\_scores: TOPOLOGY: APPLICANT: STATE: 917 CAGCATCAAATCCTGCTGTGTGCCCTCTAAGCTTAGAGCTATGTCCATGT 966 euTyrTyr...ValGlyArgThrProLysValGluGlnLeuSerAsnMet 104 15 CysCysValArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLy 31 HisSerThrValLeuGlyLeuTyrAsnThr.....LeuAsnProGluAl 72 aSerAlaSerProCysCysValProGlnAspLeuGluProLeuThrIleL 89 31 s...TrpValHisGluProLysGlyTyrTyrAlaAsnPheCysSerGlyP 47 seq\_name: /cgn2\_6/ptodata/2/ina/5A\_COMB.seq:US-08-278-729A-24 47 roCysProTyrLeuArgSerAlaAspThrThr...... Percent Identity: 38,889 to: US-08-455-550-1 from: 1 to: 1667 Gaps: 40302-FWC-DIV PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/056,564
FILING DATE: 30-APR-1993
APPLICATION NUMBER: 07/577,892
FILING DATE: 05-SEP-1990
ATTONEY/AGENT INFORMATION: 1017 ATTGTGGAGGAATGTGGCTGCTCA 1040 NAME: Eisenstein, Ronald I REGISTRATION NUMBER: 30628 REFERENCE/DOCKET NUMBER: 403( TELECOMMUNICATION INFORMATION: TELEPHONE: 617-523-3400 105 ValValLysSerCysLysCysSer 112 TELEFAX: 617-523-6440
TELEX: 200291
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENOTH: 1667 base pairs
TYPE: nucleic acid
STRANDEDNESS: single GENERAL INFORMATION:
APPLICANT: SMART, JOHN
APPLICANT: OPPERMANN, HERMAN 2.689 68.519 Quality: 199.00 TGFB3P x US-08-455-550-1 linear TOPOLOGY: line MOLECULE TYPE: HYPOTHETICAL: N ; ANTI-SENSE: NO ; FRAGMENT TYPE: ; ORIGINAL SOURCE: US-08-455-550-1 Percent Similarity: Ratio: alignment\_scores: alignment\_block Align seg 1/1

28

72

83

1204 ATCGTCCAGACCCTGGTCCACCTGCTGGAGCCCCAAGAAGGTGCCCAAGCC 1253 APPLICANT: PANG, ROY H.L.
TITLE OF INVENTION: MORPHOGENIC PROTEIN SCREENING METHOD NUMBER OF SEQUENCES: 33 ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES STREET: 45 SOUTH STREET 30 p...LysTrpValHisGluProLysGlyTyrTyrAlaAsnPheCysSerG 46 60 ThrValLeuGlyLeuTyrAsnThrLeuAsnProGluAlaSerAlaSerPr 76 76 oCysCysValProGlnAspLeuGluProLeuThrIleLeuTyrTyrValG 93 46 lyProCysProTyrLeuArgSerAlaAsp.....ThrThrHisSer Align seg 1/1 to: US-08-278-729A-24 from: 1 to: 1368 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/278,729A
FILING DATE: 20-JUL-1994
CLASSIFICATION: 435 Gaps: 4 Percent Identity: 39.806 ATTORNEY/AGENT INFORMATION:
NAME: PITCHER ESG., EDMUND R.
REGISTRATION NUMBER: 27,829
REFERENCE/DOCKET NUMBER: CRP-058CPFW
TELECOMMUNICATION INFORMATION:
TELEPHONE: (508) 435-6911
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS: OZKAYNAK, ENGIN KUBERASAMPATH, THANGAVEL RUEGER, DAVID C. LENGTH: 1368 base pairs

```
APPLICANT: KUBGER, DAVID C.
APPLICANT: KUBGER, DAVID C.
APPLICANT: RUEGER, DAVID C.
APPLICANT: OPPERMANN, HERMAN
APPLICANT: COHEN, CHARLES M.
APPLICANT: PANG, ROY H.L.
TITLE OF INVENTION: MORPHOGENIC-INDUCED PERIODONTAL TISSUE
TITLE OF INVENTION: REGENERATION.
ROWBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
                              1057 AGCTGCCAGATGCAGACCCTGTACATAGACTTCAAG...GATCTGGGCTG 1103
93 ly...ArgThrProLysValGluGlnLeuSerAsnMetValValLysSer 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14 AsnCysCysValArgProLeuTyrIleAspPheArgGlnAspLeuGlyTr 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES STREET: 45 SOUTH STREET CITY: HOPKINTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30 p...LysTrpValHisGluProLysGlyTyrTyrAlaAsnPheCysSerG 46
                                                                                                                                                                                                 seq_name: /cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-155-343A-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SISTEM: PC-LUDS,MS-LUDS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/155,343A
FILING DATE: 15-NOV-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: FENTON ESQ., GILLIAN M.
REGISTRATION NUMBER: 36,508
REFERENCE/DOCKET NUMBER: CRP-067FW
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRAI: (617) 248-7560
TELEFRAI: (617) 248-7100
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 1368 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  to: 1368
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 01748
COMPUTER READABLE FORM:
MEDIUM TYPE: Flopy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                 Sequence 24, Application US/08155343A Patent No. 5656593 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Quality: 195.00
Ratio: 2.868
nilarity: 66.019
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TGFB3P x US-08-155-343A-24
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; LOCATION: 1..1365
US-08-155-343A-24
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                                                                                                                                                                                                                                               seq_documentation_block:
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                                                                                                                                            1354 TGCGGGTGC 1362
                                                                                                109 CysLysCys 111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: F
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seq\_documentation\_block:
; Sequence 24, Application US/08406672
; Patent No. 5674404
; General INFORMATION:
APPLICANT: COHEN, CHARLES M.
APPLICANT: COPERANN, HERMANN
APPLICANT: OPPERANN, HERMANN
APPLICANT: OFPERANN, HERMANN
APPLICANT: OFFERN, DAVID C.
APPLICANT: PANG, ROY H.L.
TITLE OF INVENTION: TREATMENT TO PREVENT LOSS OF AND/OR
TITLE OF INVENTION: INCREASE BONE MASS IN METABOLIC BONE DISEASES
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESSE:
SPECIAL OFFERN ADMINITED. 93 ly...ArgThrProLysValGluGlnLeuSerAsnMetValValLysSer 108 60 ThrValLeuGlyLeuTyrAsnThrLeuAsnProGluAlaSerAlaSerPr 76 76 oCysCysValProGlnAspLeuGluProLeuThrIleLeuTyrTyrValG 93 ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES STREET: 45 SOUTH STREET CITY: HOPKINTON 46 lyProCysProTyrLeuArgSerAlaAsp.....ThrThrHisSer SOFTWARES PATENTIN Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/406,672
FILING DATE: 20-AMR-1995
CLASSIETCATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 752,857
FILING DATE: 30-AUG-1991
PRIOR APPLICATION NUMBER: US 667,274 CRP-060CN MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS FILING DATE: 11-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: FENTON ESG., GILLIAN M.
REGISTRATION NUMBER: 36,508 REFERENCE/DOCKET NUMBER: CF TELEPHONE: (617) 248-7560 TELEPAX: (617) 248-7100 INFORMATION FOR SEO ID NO: 24: SEQUENCE CHARACTERISTICS: LENCTH: 1368 base pairs TYPE: nucleic acid STRANDEDNESS: single ZIP: 01748
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy 1354 TGCGGGTGC 1362 109 CysLysCys 111 STATE: MA

1057 AGCTGCCAGATGCAGACCCTGTACATAGACTTCAAG...GATCTGGGCTG 1103 1154 GCGAGTGCAATTTCCCGCTCATGCGCATGAACGCCACGAACCATGCG 1203 ||||||||:::||| | 1254 CTGCTGCGCTCCGAGCCTGGGAGCACTACCCGTTCTGTACCACCTGA 1303 93 ly...ArgThrProLysValGluGlnLeuSerAsnMetValValLysSer 108 14 AsnCysCysValArgProLeuTyrIleAspPheArgGlnAspLeuGlyTr 30 30 p...LysTrpValHisGluProLysGlyTyrTyrAlaAsnPheCysSerG 46 46 lyProCysProTyrLeuArgSerAlaAsp.....ThrThrHisSer 59 60 ThrValLeuGlyLeuTyrAsnThrLeuAsnProGluAlaSerAlaSerPr 76 76 oCysCysValProGlnAspLeuGluProLeuThrIleLeuTyrTyrValG 93 APPLICANT: SMART, JOHN
APPLICANT: OPPERMANN, HERMAN
APPLICANT: OZKAYTNAK, ENGIN
APPLICANT: CZKAYTNAK, ENGIN
APPLICANT: RUBERASAMPATH, THANGAVEL
APPLICANT: RUGERR, DAVID C.
APPLICANT: COHEN, CHARLES M.
APPLICANT: COHEN, CHARLES M. E: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES 45 SOUTH STREET seq\_name: /cgn2\_6/ptodata/2/ina/5A\_COMB.seq:US-08-643-563A-24 Gaps: 4
Percent Identity: 39.806 Align seg 1/1 to: US-08-406-672-24 from: 1 to: 1368 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA: Sequence 24, Application US/08643563A Patent No. 5707810 GENERAL INFORMATION: 195.00 2.868 66.019 alignment\_block: TGFB3P x US-08-406-672-24 1..1365 MOLECULE TYPE: CDNA STREET: 45 SOUTH CITY: HOPKINTON STATE: MA seq\_documentation\_block 1354 receeerec 1362 ; NAME/KEY: CDS ; LOCATION: 1..1 US-08-406-672-24 109 CysLysCys 111 Quality: Ratio: Percent Similarity: 01748 ADDRESSEE: alignment\_scores: COUNTRY:

GENERAL INFORMATION:
APPLICANT: KUBERASAMPATH, THANGAVEL
APPLICANT: RUEGER, DAVID C.
APPLICANT: OPPERMANN HERMAN
APPLICANT: COHEN, CHARLES M.
APPLICANT: PANG, ROY H.L.
TITLE OF INVENTION: MORPHOGENIC-INDUCED PERIODONTAL TISSUE 1057 AGCTGCCAGATGCAGACCCTGTACATAGACTTCAAG...GATCTGGGCTG 1103 1204 ATCGTCCAGACCCTGGTCCACCTGCTGGAGCCCAAGAAGGTGCCCAAGCC 1253 1104 GCATGACTGGATCATCGCACCAGAGGCTATGGCGCCTTCTACTGCAGCG 1153 93 ly...ArgThrProLysValGluGlnLeuSerAsnMetValValLysSer 108 30 p...LysTrpValHisGluProLysGlyTyrTyrAlaAsnPheCysSerG 46 46 lyProCysProTyrLeuArgSerAlaAsp.....ThrThrHisSer 59 60 ThrValLeuGlyLeuTyrAsnThrLeuAsnProGluAlaSerAlaSerPr 76 14 AsnCysCysValArgProLeuTyrIleAspPheArgGlnAspLeuGlyTr 30 76 oCysCysValProGlnAspLeuGluProLeuThrIleLeuTyrTyrValG 93 seq\_name: /cgn2\_6/ptodata/2/ina/5A\_COMB.seq:US-08-643-763A-24 Align seg 1/1 to: US-08-643-563A-24 from: 1 to: 1368 Ouality: 195.00 Length: 103 Ratio: 2.868 Gaps: 4 Percent Similarity: 66.019 Percent Identity: 39.806 ATTORNEY AGENT INFORMATION:
NAME: TWOMEY ESQ., MICHAEL J.
REGISTRATION NUMBER: 38.349
REFERENCE/DOCKET NUMBER: CRP-058CN2
TELECOMMUNICATION INFORMATION:
TELEPRAX: (508) 435-6951
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHRACTERISTICS:
LENGTH: 1368 base pairs
TYPE: nucleic acid
TYPE: nucleic acid US/08/643,563A ; Sequence 24, Application US/08643763A ; Patent No. 5733878 APPLICATION NUMBER: US/08 FILING DATE: 06-MAY-1996 alignment\_block: TGFB3P x US-08-643-563A-24 TOPOLOGY: linear MOLECULE TYPE: CDNA 1..1365 1354 TGCGGGTGC 1362 CLASSIFICATION: seg\_documentation\_block ; NAME/KEY: CDS ; LOCATION: 1..1 US-08-643-563A-24 109 CysLysCys 111 alignment\_scores: FEATURE

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14 AsnCysCysValArgProLeuTyrIleAspPheArgGlnAspLeuGlyTr 30 :::|| ::::|| ::::: ||||||||||||||| 1057 AGCTGCCAGATGCAGACCTGTACATAGACTTCAAG...GATCTGGGCTG 1103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1204 ATCGTCCAGACCCTGGTCCACCTGCTGGAGCCCCAAGAAGGTGCCCAAGCC 1253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       93 ly...ArgThrProLysValGluGlnLeuSerAsnMetValValLysSer 108
...JUKESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES STREET: 45 SOUTH STREET CITY: HOPKINTON STREET CONTINE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30 p...LysTrpValHisGluProLysGlyTyrTyrAlaAsnPheCysSerG 46
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               76 oCysCysValProGlnAspLeuGluProLeuThrIleLeuTyrTyrValG 93
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                                                                                                                                                              COUNTRY: USA
2IP: 01748
COMPUTER REDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBN PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/643,763A
FILING DATE: 06-MAY-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: FENTON ESQ., GILLIAN M.
REGISTRATION NUMBER: 36,508
REFERENCE/DOCKET NUMBER: CRP-067CN
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: (617) 248-7560
TELEFAX: (617) 248-7560
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
FWATH: 1368 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Align seg 1/1 to: US-08-643-763A-24 from: 1 to: 1368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps: 4
Percent Identity: 39.806
TITLE OF INVENTION: REGENERATION NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 1368 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Quality: 195.00
Ratio: 2.868
Percent Similarity: 66.019
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TGFB3P x US-08-643-763A-24
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MOLECULE TYPE: CDNA
FEATURE:
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; LOCATION: 1..1
US-08-643-763A-24
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APPLICANT: COHEN. CHARLES M.
APPLICANT: COHEN. CHARLES M.
APPLICANT: CHERASAMPATH, THANGAVEL
APPLICANT: RUGEER, DAVID C.
APPLICANT: RUGEER, DAVID C.
APPLICANT: OPPERMANN, HERMANN
APPLICANT: PANG, ROY H.L.
APPLICANT: SAMAT, JOHN E.
TITLE OF INVENTION: MORPHOGEN TREATMENT OF GASTROINTESTINAL
TITLE OF INVENTION: ULCERS.
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: APARENT ADDINISTRATOR, CREATIVE BIOMOLECULES
STREET: 45 SOUTH STREET
CITY: HOPKINTON
STATE: MA
COUNTRY: USA
COUNTRY: USA
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Percent Identity: 39.806
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PATENTIN RELEASE #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/462,623
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: FENTON ESG., GILLIAN M.
REGISTRATION NUMBER: 36,508
REFERENCE/DOCKET NUMBER: CRP-074CN
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/445,882
FILING DATE: 22-MAY-1995
ATTORNEY/AGENT INFORMATION:
                                                                                      seq_documentation_block:
; Sequence 24, Application US/08462623
; Patent No. 5739107
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 01748
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (508) 435-9001
TELEPAX: (508) 435-6951
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 1368 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Quality: 195.00
Ratio: 2.868
nilarity: 66.019
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: single
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TGFB3P x US-08-462-623-24
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1..1365
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1354 TGCGGGTGC 1362
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ) NAME/KEY:
; LOCATION:
US-08-462-623-24
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1104 GCATGATCATCGCACCAGAGGCTATGGCGCCTTCTACTGCAGCG 1153 1204 ATCGTCCAGACCCTGGTCCACCTGGAGCCCCAAGAAGGTGCCCAAGGC 1253 1304 ACGACGAGAATGTGAACCTGAAAAAGTATAGAAACATGATGTGAAATCC 1353 93 ly...ArgThrProLysValGluGlnLeuSerAsnMetValValLysSer 108 60 ThrValLeuGlyLeuTyrAsnThrLeuAsnProGluAlaSerAlaSerPr 76 30 p...LysTrpValHisGluProLysGlyTyrTyrAlaAsnPheCysSerG 46 APPLICANT: SMRT, JOHN
APPLICANT: OPPERMANN, HERMAN
APPLICANT: OZKAYNAK, ENGIN
APPLICANT: KUBERSAMPATH, THANGAVEL
APPLICANT: RUBERSAMPATH, THANGAVEL
APPLICANT: PANG, ROY H.L.
APPLICANT: COHEN, CHARLES M.
APPLICANT: COHEN, COHEN, MORPHOGENIC PROTEIN SCREENING METHOD NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS: SSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES 1: 45 SOUTH STREET HOPKINTON seq\_name: /cgn2\_6/ptodata/2/ina/5A\_COMB.seq:US-08-451-953A-24 SOFTWARE PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/451,953A
FILING DATE: 26-MAY-1995
CLASSIFICATION: 435
ATTONNEY/AGENT INFORMATION:
NAME: PITCHER ESQ., EDWIND R.
REGISTRATION NUMBER: 27,829
REFERENCE/POCKET NUMBER: 27,829
REFERENCE/POCKET NUMBER: 27,829
RELEPHONE: (508) 435-9001
TELEPHONE: (508) 435-9001
TELEPHONE: (508) 435-651
INFORMATION FOR SEQ ID NO: 24: SEQUENCE CHARACTERISTICS:
LENGTH: 1368 base pairs 46 lyProCysProTyrLeuArgSerAlaAsp. seq\_documentation\_block:
; Sequence 24, Application US/08451953A
; Patent No. 5741641 MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS TYPE: nucleic acid STRANDEDNESS: single COMPUTER READABLE FORM: MEDIUM TYPE: Floppy 1..1365 TOPOLOGY: linear MOLECULE TYPE: CDNA 1354 receserec 1362 GENERAL INFORMATION: 109 CysLysCys 111 ; NAME/KEY: CDS ; LOCATION: 1..1 US-08-451-953A-24 USA COUNTRY: UZIP: 01748 ADDRESSEE: STREET: STATE:

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1057 AGCTGCCAGATGCAGACCTGTACATAGACTTCAAG...GATCTGGGCTG 1103
                                                                                                                                                                                                                                                                                                                                     1154 GCGAGTGCAATTTCCCGCTCAATGCGCACATGAACGCCACGAACCATGCG 1203
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| 1254 CTGCTGCGCTCCGAGCTGGGAGCACTACCGTTCTGTACCACCTGA 1303
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                                                                                                                                                                                                                      14 AsnCysCysValArgProLeuTyrIleAspPheArgGlnAspLeuGlyTr 30
                                                                                                                                                                                                                                                                                                            30 p...LysTrpValHisGluProLysGlyTyrTyrAlaAsnPheCysSerG 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60 ThrValLeuGlyLeuTyrAsnThrLeuAsnProGluAlaSerAlaSerPr 76
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 24, Application US/08445468A
Patent No. 5849686
GENERAL INFORMATION:
APPLICANT: KUBERASAMPATH, THANGAVEL
APPLICANT: OPPERMANN, HERMAN
APPLICANT: PANG, ROY H.L.
APPLICANT: COPIEN, CHARLES M.
TITLE OF INVENTION: MORPHOGEN-INDUCED LIVER REGENERATION
NUMBER OF SEQUENCES: 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES STREET: 45 SOUTH STREET CITY: HOPKINTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq_name: /cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-445-468A-24
                                                                                                                                                                                                                                                                                                                                                                                                   46 lyProCysProTyrLeuArgSerAlaAsp.....ThrThrHisSer
                                                                                                                                                                                 to: 1368
                                                                Percent Identity: 39.806
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/445,468A
FILING DATE: 22-MAY-1995
                         Length:
                                                  Gaps:
                                                                                                                                                                               from: 1
                                                                                                                                                                             Align seg 1/1 to: US-08-451-953A-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY AGENT INFORMATION:
NAME: FENTON ESQ., GILLIAN M.
REGISTRATION NUMBER: 36,508
REFERENCE/DOCKET NUMBER: CRP-
                  195.00
2.868
66.019
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                          alignment_block:
TGFB3P x US-08-451-953A-24
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                       Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           USA
                                                                Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: US
ZIP: 01748
alignment_scores:
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CRP-072FW2

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1104 GCATGACTGGATCATCGCACCAGAGGGCTATGGCGCCTTCTACTGCAGCG 1153
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APPLICANT: CHARTETE, MARC F.
APPLICANT: KUBERASAMPATH, THANGAVEL
APPLICANT: NUBERASAMPATH, THANGAVEL
APPLICANT: OPPERAANN, HERMANN
APPLICANT: OPPERAANN, HERMANN
APPLICANT: OANG, ROY H.L.
APPLICANT: SMART, JOHN E.
TITLE OF INVENTION: MORPHOGEN TREATMENT FOR LIMITING
TITLE OF INVENTION: PROLIFFERATION OF EPITHELIAL CELLS.
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30 p...LysTrpValHisGluProLysGlyTyrTyrAlaAsnPheCysSerG 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    60 ThrValLeuGlyLeuTyrAsnThrLeuAsnProGluAlaSerAlaSerPr 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14 AsnCysCysValArgProLeuTyrIleAspPheArgGlnAspLeuGlyTr 30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_name: /cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-461-397A-24
                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps: 4
Percent Identity: 39.806
                                                                                                                                                                                                                                                                                                                                                                                            Length:
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APPLICANT: COREN, CHARLES M.
APPLICANT: CHARETTE, MARC F.
APPLICANT: KUBERASAMPATH, THANGAVEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7560
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 1368 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                            Quality: 195.00
Ratio: 2.868
Percent Similarity: 66.019
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TGFB3P x US-08-445-468A-24
                                                                                                                                                                                     TOPOLOGY: linear MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                             1..1365
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                                                                                                                                                                                                                                    FEATURE:
NAME/KEY: CDS
                                                                                                                                                                                                                                                                             ; LOCATION:
US-08-445-468A-24
                                                                                                                                                                                                                                                                                                                                                                         alignment_scores:
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1154 GCGAGTGCAATTTCCCGCTCAATGCGCACATGAACGCCACGAACCATGCG 1203
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Identity: 39.806
                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Align seg 1/1 to: US-08-461-397A-24 from: 1
                                                                                                                                                                                                                CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,397A
FILING DATE: 05-UN-1995
CLESSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: PITCHER ESO, EDMUND R.
REGISTRATION NUMBER: 27,829
REFERENCE/DOCKET NUMBER: CRP-074FW2
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: 617/248-7100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 1368 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
45 SOUTH STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             195.00
2.868
66.019
                                                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       alignment_block:
TGFB3P x US-08-461-397A-24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
                     HOPKINTON
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Ratio:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Similarity:
                                                                                     01748
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; LOCATION:
US-08-461-397A-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            alignment_scores:
                                          STATE: M
COUNTRY:
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seq\_name: /cgn2\_6/ptodata/2/ina/5B\_COMB.seq:US-08-912-088-24

1354 TGCGGGTGC 1362

alignment\_block: APPLICANT: OPPERANN, HERMAN
APPLICANT: OPPERASAMPATH, THANGAVEL
APPLICANT: RUBERASAMPATH, THANGAVEL
APPLICANT: RUGGER, DAVID C.
APPLICANT: PANG, ROY H.L.
APPLICANT: COHEN, CHARLES M.
TITLE OF INVENTION: MORPHOGENIC PROTEIN SCREENING METHOD NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS: ADDRESS: ADDRESSE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES STREET: ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES STREET: ADDRESSEE: ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES STREET: ADDRESSEE: 30 p...LysTrpValHisGluProLysGlyTyrTyrAlaAsnPheCysSerG 46 14 AsnCysCysValArgProLeuTyrIleAspPheArgGlnAspLeuGlyTr 30 46 lyProCysProTyrLeuArgSerAlaAsp.....ThrThrHisSer 59 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/912,088 Percent Identity: 39.806 Align seg 1/1 to: US-08-912-088-24 from: 1 to: 1368 NAME: PITCHER ESG., EDMUND R. REGISTRATION NUMBER: 27,829
REFERENCE/DOCKET NUMBER: CRP-058CPFW
TELECOMMUNICATION INPORMATION: CLASSIFICATION: PRIOR APPLICATION DATA: APPLICATION NUMBER: US 08/278,729 Sequence 24, Application US/08912088 Patent No. 5994131 TELEPHONE: (508) 435-9001 TELEFAX: (508) 435-6951 INFORMATION FOR SEQ ID NO: 24: ATTORNEY/AGENT INFORMATION: NAME: PITCHER ESG. FINM SEQUENCE CHARACTERISTICS: LENGTH: 1368 base pairs TYPE: nucleic acid STRANDEDNESS: single 195.00 2.868 66.019 SMART, JOHN ZIP: 01748 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy alignment\_block: TGFB3P x US-08-912-088-24 1..1365 MOLECULE TYPE: CDNA linear seq\_documentation\_block HOPKINTON alignment\_scores: Quality: USA Ratio: Percent Similarity: CITY: HOPKIN STATE: MA COUNTRY: USI ZIP: 01748 FILING DATE: FILING DATE ; NAME/KEY: ; LOCATION: US-08-912-088-24

Sequence 24, Application US/08278730A
Patent No. 6022853
GENERAL INFORMATION:
APPLICANT: KUBERASAMPATH, THANGAVEL
APPLICANT: COHEN, CHARLES M.
APPLICANT: COPERN, DAVID C.
APPLICANT: POPERMANN, HERMAN
APPLICANT: PANG, ROY H.L.
TITLE OF INVENTION: MORPHOGENIC-ENRICHED DIETARY COMPOSITION
NUMBER OF SEQUENCES: 33 1154 GCGAGTGCAATTTCCCGCTCAATGCGCACATGAACGCCACGAACCATGCG 1203 93 ly...ArgThrProLysValGluGlnLeuSerAsnMetValValLysSer 108 60 ThrValLeuGlyLeuTyrAsnThrLeuAsnProGluAlaSerAlaSerPr 76 76 oCysCysValProGlnAspLeuGluProLeuThrIleLeuTyrTyrValG 93 ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES STREET: 45 SOUTH STREET CITY: HOPKINTON seq\_name: /cgn2\_6/ptodata/2/ina/6A\_COMB.seq:US-08-278-730A-24 Gaps: 4 Percent Identity: 39.806 SOFTWARE: PATENTIN RELEASE #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/278,730A FILING DATE: 2-JULY-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: FENTON ESq., GILLIAN M.
REGISTRATION NUMBER: 36,508 REFERENCE/DOCKET NUMBER: CRP-071FW TELECOMMUNICATION INFORMATION: TELEPHONE: (617) 248-7560 MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS TELEPHONE: (617) 248-7560
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS: LENGTH: 1368 base pairs 195.00 2.868 66.019 TYPE: nucleic acid STRANDEDNESS: single COMPUTER READABLE FORM: MEDIUM TYPE: Floppy CORRESPONDENCE ADDRESS: 1..1365 linear seg\_documentation\_block 1354 TGCGGGTGC 1362 109 CysLysCys 111 NAME/KEY: CDS USA Quality: Percent Similarity: TOPOLOGY: li COUNTRY: US ; IOCATION: US-08-278-730A-24 alignment\_scores:

tgfb3p.rni

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FILING DATE: 30-AUG-1991
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                                                                                                                                                                                                 1204 ATCGTCCAGACCCTGGTCCACCTGGTGGCCCCAAGAAGGTGCCCAAGCC 1253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  93 ly...ArgThrProLysValGluGlnLeuSerAsnMetValValLysSer 108
                                                                                                                                                                      30 p...LysTrpValHisGluProLysGlyTyrTyrAlaAsnPheCysSerG 46
                                                                                                                                                                                                                                                                                                                                             60 ThrValLeuGlyLeuTyrAsnThrLeuAsnProGluAlaSerAlaSerPr 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: RUBERASAMPATH, THANGAVEL
APPLICANT: PANG, ROY HL
APPLICANT: OPPERRANNN, HERMANN
APPLICANT: OFBERANNN, HERMANN
APPLICANT: COHEN, CHARLES M
APPLICANT: COHEN, CHARLES M
APPLICANT: OZAYNAK, ENGIN
APPLICANT: SWART, JOHN E
TITLE OF INVENTION: INFLAMMATORY RESPONSE
NUMBER OF SEQUENCES: 33
CORRESPONDENE ADDRESS:
ADDRESSEE: CREATIVE BIOMOLECULES, INC.
                                                                                                                                                                                                                                                                                                                                                                                                                              76 oCysCysValProGlnAspLeuGluProLeuThrIleLeuTyrTyrValG
                                                                                  14 AsnCysCysValArgProLeuTyrIleAspPheArgGlnAspLeuGlyTr
                                                                                                                                                                                                                                                         46 lyProCysProTyrLeuArgSerAlaAsp.....ThrThrHisSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seg_name: /cgn2_6/ptodata/2/ina/6A_COMB.seq:US-08-445-467-24
                                          to: 1368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/445,467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 35 SOUTH STREET
CITY: HOPKINTON
STATE: MA
COUNTRY: USA
ZIP: 01748
COMPUTED: 05
                                        to: US-08-278-730A-24 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/753,059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/165,511
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/07/938,336 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                UMBER: US 07/667,274
11-MAR-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 24, Application US/08445467
Patent No. 6077823
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
TGFB3P x US-08-278-730A-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
FILING DATE: 11-MAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1354 TGCGGGTGC 1362
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE
                                        Align seg 1/1
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1154 GCGAGTGCAATTTCCCGCTCAATGCGCACATGAACGCCACGAACCATGCG 1203 1204 ATCGTCCAGACCCTGGTCCACCTGCTGGAGCCCAAGAAGGTGCCCAAGCC 1253 30 p...LysTrpValHisGluProLysGlyTyrTyrAlaAsnPheCysSerG 46 60 ThrValLeuGlyLeuTyrAsnThrLeuAsnProGluAlaSerAlaSerPr 76 46 lyProCysProTyrLeuArgSerAlaAsp......ThrThrHisSer 59 seq\_name: /cgn2\_6/ptodata/2/ina/6A\_COMB.seq:US-08-480-515A-24 14 AsnCysCysValArgProLeuTyrIleAspPheArgGlnAspLeuGlyTr Gaps: 4 Percent Identity: 39.806 from: 1 to: 1368 APPLICATION NUMBER: US 07/752,764
FILING DATE: 30-AuG-1991
ATTORNEY/AGENT INFORMATION:
NAME: PITCHER ESQ, EDMUND R
REGISTRATION NUMBER: 27,829
REFERENCE/DOCKET NUMBER: CRP-059CP.APP
TELECOMMUNICATION INFORMATION:
TELEPAX: 617/248-7000
INFORMATION FOR SEQ ID NO: 24:
LENGTH: 1368 base pairs Length: APPLICANT: KUBERASAMPATH, THANGAVEL APPLICANT: PANG, ROY H.L. APPLICANT: OPPERMANN, HERMANN Align seg 1/1 to: US-08-445-467-24 RUEGER, DAVID C. COHEN, CHARLES M. 2.868 66.019 TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear alignment\_scores: Quality: 195.00 PRIOR APPLICATION DATA: TGFB3P x US-08-445-467-24 TOPOLOGY: linear MOLECULE TYPE: CDNA 1..1368 1354 TGCGGGTGC 1362 109 CysLysCys 111 CDS Percent Similarity: Ratio: NAME/KEY: APPLICANT: APPLICANT: APPLICANT: ; US-08-445-467-24 alignment\_block FEATURE:

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APPLICANT: SMART, JOHN E.
TITLE OF INVENTION: MORPHOGEN TREATMENT OF ORGAN TRANSPLANTS
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1057 AGCTGCCAGATGCAGACCTGTACATAGACTTCAAG...GATCTGGGCTG 1103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             93 ly...ArgThrProLysValGluGlnLeuSerAsnMetValValLysSer 108
                                                                      ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES STREET: 45 SOUTH STREET CITY: HOPKINTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30 p...LysTrpValHisGluProLysGlyTyrTyrAlaAsnPheCysSerG 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60 ThrValLeuGlyLeuTyrAsnThrLeuAsnProGluAlaSerAlaSerPr 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14 AsnCysCysValArgProLeuTyrIleAspPheArgGlnAspLeuGlyTr 30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Align seg 1/1 to: US-08-480-515A-24 from: 1 to: 1368
                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,515A FILING DATE: 07-JUN-1995
ATTORNEY: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Percent Identity: 39.806
                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: FENTON ESQ., GILLIAN M.
REGISTRATION NUMBER: 36,508
REFERENCE/DOCKET NUMBER: CRP-068FWC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7560
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 1368 base pairs
                                                                                                                                                            COUNTY: USA
ZIP: 01748
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Quality: 195.00
Ratio: 2.868
nilarity: 66.019
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: single
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TGFB3P x US-08-480-515A-24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ratio:
Percent Similarity:
                                                                                                                        CITY: HOPK
STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; NAME/KEY:
; LOCATION:
US-08-480-515A-24
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seq_name: /cgn2_6/ptodata/2/ina/6B_COMB.seq:US-08-271-556A-1
                                                                                                                                                                                                                                                                                                    APPLICANT: RUBERASAMPATH, THANGAVEL
APPLICANT: PANG, ROY HL
APPLICANT: OPPERRANN, HERMANN
APPLICANT: COHEN, DAVID
APPLICANT: COHEN, CHARLES M
TITLE OF INVENTION: 60A PROTEIN-INDUCED MORPHOGENESIS
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/271,556A
FILING DATE: 07-JUL-1994
CLASSIFICATION NUMBER: US 07/945,292
FILING DATE: 15-SEP-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/667,274
FILING DATE: 11-MAR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/667,274
FILING DATE: 30-AUG-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/753,059
FILING DATE: 30-AUG-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: CREATIVE BIOMOLECULES, INC
STREET: 45 SOUTH STREET
CITY: HOPKINTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR DATE:
PRIOR DATE:
APPLICATION NUMBER: US 07/752,764
FILING DATE: 30-AGG-1991
PROOR PROCESSION NUMBER: US 07/752,857
FILING DATE: 30-AGG-1991
PRIOR APPLICATION NUMBER: US 07/923,780
FILING DATE: 31-AUL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/922,813
FILING DATE: 31-AUL-1992
PRIOR APPLICATION NUMBER: US 07/922,813
FILING DATE: 31-AUL-1992
ATTORNEY/AGGNT INFORMATION:
NAME: FENTON, GILLIAN N
NAME: FENTON NUMBER: 36,508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER: 36,508
REFERENCE/DOCKET NUMBER: CRP-066FW
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                  seq_documentation_block:
. Sequence 1, Application US/08271556A
.; Patent No. 6211146
.; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 1368 base pairs
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                                                            1354 TGCGGGTGC 1362
109 CysLysCys 111
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ZIP: 01748
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COCATION:
US-08-271-556A-1
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tgfb3p.rni

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1057 AGCTGCCAGACGCTGTACATAGACTTCAAG...GATCTGGGCTG 1103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
TITLE OF INVENTION: MORPHOGEN-ENRICHED DIETARY COMPOSITION
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                            1154 GCGAGTGCAATTTCCCGCTCAATGCGCACATGAACGCCACGAACCATGCG 1203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq_name: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:PCT-US93-07190-24
                                                                                                                                                                                                                                                                                                 30 p...LysTrpValHisGluProLysGlyTyrTyrAlaAsnPheCysSerG 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9/
                                                                                                                                                                                                               46 lyProCysProTyrLeuArgSerAlaAsp.....ThrThrHisSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60 ThrValLeuGlyLeuTyrAsnThrLeuAsnProGluAlaSerAlaSerPr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    93 ly... ArgThrProLysValGluGlnLeuSerAsnMetValValLysSer
                                              Gaps: 4
Percent Identity: 39.806
                                                                                                                                                                       Align seg 1/1 to: US-08-271-556A-1 from: 1 to: 1368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                        Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: CREATIVE BIOMOLECULES, INC. STREET: 35 SOUTH STREET CITY: HOPKINTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: KELLENT NOWBER: PCT/US93/07190
NAME: KELLENT NOWBER: 34,637
REGISTRATION NUMBER: 34,637
REFERENCE/DOCKET NUMBER: CRP-071
TELEPHONE: 617/248-7000
TELEFAX: 617/248-7100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 01748
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                    195.00
2.868
66.019
                                                                                                                            TGFB3P x US-08-271-556A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1354 TGCGGGTGC 1362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           109 CysLysCys 111
                      Quality:
Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: MA
alignment_scores:
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                                                                                                        alignment_block
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TITLE OF INVENTION: MORPHOGEN-INDUCED NERVE REGENERATION AND TITLE OF INVENTION: REPAIR
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS: 1204 ATCGTCCAGACCCTGGTCCACCTGCTGGAGCCCCAAGAAGGTGCCCAAGCC 1253 seq\_name: /cgn2\_6/ptodata/2/ina/PCTUS\_COMB.seq:PCT-US93-07231-24 93 ly...ArgThrProLysValGluGlnLeuSerAsnMetValValLysSer 108 30 p...LysTrpValHisGluProLysGlyTyrTyrAlaAsnPheCysSerG 46 60 ThrValLeuGlyLeuTyrAsnThrLeuAsnProGluAlaSerAlaSerPr 76 46 lyProCysProTyrLeuArgSerAlaAsp.....ThrThrHisSer 59 76 oCysCysValProGlnAspLeuGluProLeuThrIleLeuTyrTyrValG 93 14 AsnCysCysValArgProLeuTyrIleAspPheArgGlnAspLeuGlyTr to: 1368 Percent Identity: 39.806 ZIP: 01748
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA: Gaps: Length: ADDRESSEE: CREATIVE BIOMOLECULES, INC. STREET: 35 SOUTH STREET
CITY: HOPKINTON
STATE: MASSACHUSETTS
COUNTRY: USA PCT/US93/07231 Align seg 1/1 to: PCT-US93-07190-24 CLASSIFICATION:
CLASSIFICATION:
ATTORNEX/AGENT INFORMATION:
NAME: KELLEY, ROBIN D. 195.00 2.868 66.019 TGFB3P x PCT-US93-07190-24 APPLICATION NUMBER: TOPOLOGY: linear MOLECULE TYPE: CDNA 1..1368 1354 TGCGGGTGC 1362 109 CysLysCys 111 CDS Percent Similarity: Quality: Ratio: · NAME/KEY: COCATION: PCT-US93-07190-24 alignment\_scores alignment\_block: FEATURE:

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; LOCATION:
PCT-US93-08742-24
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CORRESPONDENCE ADDRESS:
ADDRESSEE: CREATIVE BIOMOLECULES, INC.
STREET: 45 SOUTH STREET
CITY: HOPKINTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1154 GCGAGTGCAATTTCCCGCTCAATGCGCACATGAACGCCACGAACCATGCG 1203
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; Sequence 24, Application PC/TUS9308742
; GENERAL INFORMATION:
REGISTRATION NUMBER: 34,637
REFERENCE/DOCKET NUMBER: CRP-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/248-7000
TELEPA: 617/248-7100
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 1368 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 01748
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                    195.00
2.868
66.019
                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                             alignment_block:
TGFB3P x PCT-US93-07231-24
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COUNTRY: USZ
ZIP: 01748
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PCT-US93-07231-24
                                                                                                                                                                                                                                                                   NAME/KEY:
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1104 GCATGACTGGATCATCGCACCAGGGGCTATGGCGCCTTCTACTGCAGGG 1153
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/08742
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NAME: KELLEY ESQ, ROBIN D.
REGISTRATION NUMBER: 34,637
REFRENCE/DOCKET WUMBER: CRP-067
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/248-7170
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; Sequence 24, Application PC/TUS9308808
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 24: SEQUENCE CHARACTERISTICS: LENGTH: 1368 base pairs TYPE: nucleic acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Quality: 195.00
Ratio: 2.868
Percent Similarity: 66.019
                                                                                                                                                             PRIOR APPLICATION DATA: APPLICATION NUMBER:
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TGFB3P x PCT-US93-08742-24
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                                                                                                                 FILING DATE:
CLASSIFICATION:
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1057 AGCTGCCAGATGCAGACCTGTACATAGACTTCAAG...GATCTGGGCTG 1103
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14 AsnCysCysValArgProLeuTyrIleAspPheArgGlnAspLeuGlyTr 30
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Percent Identity: 39.806
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/08808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Align seg 1/1 to: PCT-US93-08808-24 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                         CRP-072
                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE DOCKET NUMBER: CRP-
TELECOMOUNICATION INFORMATION:
TELEPHONE: 617/248-7477
TELEFAX: 617/248-7100
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 1368 base pairs
TYPE: NUCLEIC acid
STRANDEDNESS: SINGLE
                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: KELLEY ESQ, ROBIN D.
REGISTRATION NUMBER: 34,637
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66.019
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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Quality: 195.00
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TGFB3P x PCT-US93-08808-24
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PCT-US93-08808-24
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MORPHOGEN TREATMENT OF GASTROINTESTINAL
seq_name: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:PCT-US93-08885-24
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                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 01748
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFWWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                           ADDRESSEE: CREATIVE BIOMOLECULES, INC. STREET: 45 SOUTH STREET CITY: HOPKINTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: PCT/US93/08885
                                                                                                                                                          seq_documentation_block:
    Sequence 24, Application PC/TUS9308885
    GENERAL INFORMATION:
    APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CRP-074
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ATTORNEY/AGENT INFORMATION:
NAME: KELLEY ESQ, ROBIN D.
REGISTRATION NUMBER: 34,637
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TELECOMMUNICATION INFORMATION
TELEPHONE: 617/248-7477
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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2.868
66.019
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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                     TITLE OF INVENTION: MOI TITLE OF INVENTION: ULC NUMBER OF SEQUENCES: 3: CORRESPONDENCE ADDRESS:
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TGFB3P x PCT-US93-08885-24
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                                                      109 CysLysCys 111
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PCT-US93-08885-24
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1204 ATCGTCCAGACCCTGGTCCTGCTGGAGCCCCAAGAAGGTGCCCAAGAGCC 1253 || ||| ||| ::: 1154 GCGACTGCAATTTCCCGCTCAATGCGCACATGAACGCCACGAACCATGCG 1203 ||||||||:::||| |1254 CTGCTGCGCTCCGACCAGGGGGGGACACTACCCGTTCTGTACCACCTGA 1303 46 lyProCysProTyrLeuArgSerAlaAsp.....ThrThrHisSer 59 60 ThrValLeuGlyLeuTyrAsnThrLeuAsnProGluAlaSerAlaSerPr 76 76 oCysCysValProGlnAspLeuGluProLeuThrIleLeuTyrTyrValG 93 seq\_name: /cgn2\_6/ptodata/2/ina/5A\_COMB.seq:US-07-718-274A-1 SOFTWARES: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/718,274A
FILING DATE: 19910620
CLASSIFICATION: 435
PIOOR APPLICATION NUMBER: US 07/415,555
FILING APPLICATION DATA:
APPLICATION NUMBER: US 07/415,555
FILING APPLICATION DATA:
APPLICATION NUMBER: US 07/256,034
FILING DATE: 11-0CT-1988
ATTORNEX/AGENT INFORMATION: STREET: Two First National Plaza, 20 South Clark STREET: Street ADDRESSEE: Marshall, O'Toole, Gerstein, Murray ADDRESSEE: Bicknell seq\_documentation\_block:
 Sequence 1, Application US/07718274A
 Patent No. 528476
 GENERAL INFORMATION:
 APPLICANT: Grinna, Lynn
 APPLICANT: Parsons, Thomas F.
 APPLICANT: Theofan, Georgia
 TITLE OF INVENTION: Osteogenic Factor
 NUMBER OF SEQUENCES: 63
 CORRESPONDENCE ADDRESS: 27129/9430 ZIP: 60603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPPERATING SYSTEM: PC-DOS/MS-DOS NAME: Sharp, Jeffrey S.
REGISTRATION NUMBER: 31,879
REFERENCE/DOCKET NUMBER: 27.
TELECOMMUNICATION INFORMATION: TELEPHONE: (312) 346-5750
TELEFAX: (312) 984-9740
TELEAX: 25-3856
INPORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 417 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single MOLECULE TYPE: CDNA CITY: Chicago STATE: Illinois COUNTRY: USA 1..417 1354 TGCGGGTGC 1362 inear 109 CysLysCys 111 NAME/KEY: CDS LOCATION: 1...

320 CGCAGCTCAATGCCATCTCCGTCTTTCGATGACAGCTCCAACGTC 369 220 CCTCTGAACTCCTACATGAACGCCACCAACCACCACCACGTGCAGACGT 269 10 AsnLeuGluGluAsn.....CysCysValAr 18 18 gProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLys...TrpValH 34 34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50 51 LeuArgSerAla.....AspThrThrHisSerThrValLeuGlyLe 64 APPLICANT: MCCOY, John
APPLICANT: MULTAY, Beth
APPLICANT: Wolfman, Nail
TITLE OF INVENTION: MUTANTS OF BONE MORPHOGENIC PROTEINS
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc - Legal Affairs 81 lnAspLeuGluProLeuThrIleLeuTyrTyrValGlyArgThrProLys 97 seq\_name: /cgn2\_6/ptodata/2/ina/5A\_COMB.seq:US-08-163-877-9 ADDRESSEE: Genetics Institute, Inc - Legal Affairs STREET: 87 CambridgePark Drive CITY: Cambridge STATE: Massachusetts
COUNTRY: USA Percent Identity: 34.783 to: US-07-718-274A-1 from: 1 to: 417 OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/163,877 Length: Gaps: 5219 Sequence 9, Application US/08163877 Patent No. 5399677 GENERAL INFORMATION: ATTORNEY/AGENT INFORMATION:
NAME: Lazar, Steven R.
REGISTRATION NUMBER: 32,618
REFERENCE/DOCKET NUMBER: GI
TELECOMMUNICATION INFORMATION: COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible 189.00 2.662 61.739 TGFB3P x US-07-718-274A-1 OPERATING SYSTEM: SOFTWARE: PatentI seq\_documentation\_block: CLASSIFICATION: Percent Similarity: alignment\_scores: Quality: Ratio: FILING DATE: 02140 US-07-718-274A-1 Align seg 1/1 alignment\_block

COUNTRY

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170 TCGCGCCTGAAGGCTACGCCGCCTACTGTGAGGGGGAGTGTGCCTTC 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              220 CCTCTGAACTCCTACATGAACGCCACCAACCACGCCATCGTGCAGACGCT 269
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10 AsnLeuGluGluAsn.....CysCysValAr 18
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STREET: Two First National Plaza, 20 South Clark
STREET: Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps: 5
Percent Identity: 34.783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Align seg 1/1 to: US-08-163-877-9 from: 1 to: 417
; TELEPHONE: 617 876-1170 x 8260
; TELEFAX: 617 876-5851
; INPORMATION FOR SEQ ID NO: 9:
SEQUENCH: 417 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Grinna, Lynn
APPLICANT: Parsons, Thomas F.
APPLICANT: Theofan, Georgia
TITLE OF INVENTION: Osteogenic Factor
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq_documentation_block:
; Sequence 1, Application US/08149106
; Patent No. 5411941
                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2.662
61.739
                                                                                                                                                                                                                                                                                                                                                                                                                                                            189.00
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TGFB3P x US-08-163-877-9
                                                                                                                                                                                                                                                                                                                    NAME/KEY: CDS
LOCATION: 1..417
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: Illinois
                                                                                                                                                                                                                                                                       ORGANISM: bmp-7
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Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                      alignment_scores:
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170 TCGCGCCTGAAGGCTACCCCCTACTACTGTGAGGGGGAGTGTGCCTTC 219
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                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/149,106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             to: 417
                                                                                                                                 APPLICATION DATE:
CLASSIFICATION: 514
FILING DATE:
APPLICATION DATA:
APPLICATION NUMBER: US 07/415,555
FILING DATE: 04 -0CT-1989
PRIOR APPLICATION NUMBER: US 07/256,034
FILING DATE: 11-0CT-1988
ATTORNEY/AGENT INFORMATION:
NAME: Sharp, Joffrey S.
REGISTRATION NUMBER: 27129/9430
FELERALOZOCKET NUMBER: 27129/9430
TELEPHONE: (312) 346-5750
TELEPHONE: (312) 984-9740
TELEPHONE: (312) 984-9740
TELEPHONE: (312) 984-9740
TELEPHONE: CA-3856
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 417 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps:
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                                                                        OPERATING SYSTEM: PC-DOS/MS-DOS
                                     E: Floppy disk
IBM PC compatible
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61.739
               COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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TGFB3P x US-08-149-106-1
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MOLECULE TYPE: CDNA
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   Quality:
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60603
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; LOCATION:
US-08-149-106-1
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98 Val...GluGlnLeuSerAsnMetValValLysSerCysLysCys 111

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E: Marshall, O'Toole, Gerstein, Murray & Borun
6300 Sears Tower, 233 South Wacker Drive
                                                                      seq_name: /cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-298-021-1
370 ATCCTGAAGAAAAACAGAAGATGGTGGGCCCGGGCCTGTGGCTGC 414
                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Grinna, Lynn
APPLICANT: Parsons, Thomas F.
APPLICANT: Theofan, Georgia
TITLE OF INVENTION: Heterodimeric Osteogenic Factor
NUMBER OF SEQUENCES: 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/298,021
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/149,106
FILING DATE: 11-0CT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/718,274
FILING DATE: 20-UN-1991
PRIOR APPLICATION NUMBER: US 07/415,555
FILING DATE: 04-0CT-1989
PRIOR APPLICATION NUMBER: US 07/256,034
FILING DATE: 11-0CT-1988
APPLICATION NUMBER: US 07/256,034
FREISTRATION NUMBER: 31,879
REGISTRATION NUMBER: 31,879
REGISTRATION NUMBER: 31,879
REGISTRATION NUMBER: 31,879
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TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-64023
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                   seq_documentation_block:
    Sequence 1, Application US/08298021
    Patent No. 5508263
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312/474-0448
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 417 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   189.00
2.662
61.739
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TGFB3P x US-08-298-021-1
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; LOCATION: 1..4
US-08-298-021-1
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Ratio:
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STATE:
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73 AACGTGGCAGAAAAAGCAGCAGCAACAAGAGCAGGCCTGTAAGAAGCA 122
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APPLICANT: Nell M. WOLFMAN and John MCCOY
TITLE OF INVENTION: MUTANTS OF BONE MORPHOGENIC PROTEINS
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_name: /cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-360-914B-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98 Val...GluGlnLeuSerAsnMetValValLysSerCysLysCys 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Genetics Institute, Inc - Legal Affairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/360,914B
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/163,877
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ATTORNEY/AGENT INFORMATION:
NAME: LAZAr, Steven R.
REGISTRATION NUMBER: 32,618
REFERENCE/DOCKET NUMBER: GI 521'
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617,498-8260
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; Sequence 9, Application US/08360914B
; Patent No. 5756308
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INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
10 AsnLeuGluGluAsn.....
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STATE: Massachusetts
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220 CCTCTGAACTCCTACATGAACGCCACCAACCACCCATCGTGCAGACGCT 269 320 CGCAGCTCAATGCCATCTCCGTCTTCTACTTCGATGACAGCTCCAACGTC 369 ......CysCysValAr 18 18 gProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLys...TrpValH 34 64 uTyrAsnThrLeuAsnProGluAlaSerAlaSerProCysCysValProG 81 81 lnAspLeuGluProLeuThrIleLeuTyrTyrValGlyArgThrProLys 97 seq\_documentation\_block:
 Sequence 9, Application US/08741589A
 Patent No. 5804416
 GENERAL INFORMATION:
 TITLE OF INVENTION: MUTANTS OF BONE MORPHOGENIC PROTEINS NUMBER OF SEQUENCES: 13
 CORRESPONDENCE ADDRESS: seq\_name: /cgn2\_6/ptodata/2/ina/5A\_COMB.seq:US-08-741-589A-9 51 LeuArgSerAla.....AspThrThrHisSerThrValLeuGlyLe ADDRESSEE: Genetics Institute, Inc - Legal Affairs STREET: 87 CambridgePark Drive Percent Identity: 34.783 Align seg 1/1 to: US-08-360-914B-9 from: 1 to: 417 SOFTWARE: PatentIn Release #1.0, Version #1.25 Length: Gaps: CLASSIFTCATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/163,877
FILING DATE: December 7, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Lazar, Steven R. CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/741,589 ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Flopy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS 2.662 61.739 CITY: Cambridge STATE: Massachusetts COUNTRY: USA Quality: 189.00 alignment\_block: TGFB3P x US-08-360-914B-9 10 AsnLeuGluGluAsn.. 1..417 Percent Similarity: Ratio: FILING DATE: ; NAME/KEY: ; LOCATION: US-08-360-914B-9 alignment\_scores:

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220 CCTCTGAACTCCTACATGAACGCCACCAACCACCACCACCACCACGCCATCGTGCAGACGCT 269
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; Sequence 9, Application PC/TUS9413181
GENERAL INFORMATION:
APPLICANT: GENETICS INSTITUTE, INC.
TITLE OF INVENTION: MOTANTS OF BONE MORPHOGENIC PROTEINS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  51 LeuArgSerAla......AspThrThrHisSerThrValLeuGlyLe
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STREET: 87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                         Percent Identity: 34.783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Align seg 1/1 to: US-08-741-589A-9 from: 1 to: 417
                                                                                                                                                                                                                                                                                                                                                                      Length:
                                                                                                                                                                                                                                                                                                                                                                                              Gaps:
                GI 5219B-DIV
       REFERENCE/DOCKET NUMBER: 517 EPERENCE/DOCKET NUMBER: 61 TELECOMMUNICATION INFORMATION: 617 498-6260
TELEPHONE: 617 498-6260
TELEFAX: 617 876-5851
INFORMATION FOR SEQ ID NO: 9: SEQUENCE CHARACTERISTICS:
LENGTH: 417 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
TOPOLOGY: linear
REGISTRATION NUMBER: 32,618
                                                                                                                                                                                                                                                                                                                                                                      189.00
2.662
61.739
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                                                                                                                                                                                                                                                                                                                                                                                                                                              alignment_block:
TGFB3P x US-08-741-589A-9
                                                                                                                                                                                                                          ORGANISM: bmp-7
                                                                                                                                                                                                             ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                          Quality:
                                                                                                                                                                                                                                                                                                                                                                                                           Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                          Ratio:
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                                                                                                                                                                                                                                                                 NAME/KEY:
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US-08-741-589A-9
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270 GGTCCACTTCATCAACCGGAAACGGTGCCCAAGCCCTGCTGTGCGCCCA 319
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps: 5
Percent Identity: 34.783
                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentIn Release #1.0, Version #1.25
CURREW APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/13181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               to: 417
                                                                                                                                                      PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/163,877
FILING DATE: December 7, 1993
ATTORNEV/AGENT INFORMATION:
NAME: Lazar, Steven R.
REGISTRATION NUMBER: 32,618
REFERENCE/DOCKET NUMBER: GI 5219-PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617 498-8260
TELEPAX: 617 876-5851
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 417 base pairs
TYPE: nucleic acid
STRANDENESS: double
TOPOLOGY: Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               from: 1
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMDUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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2.662
61.739
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: DNA ORIGINAL SOURCE:
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                                                                                                                                             FILING DATE:
CLASSIFICATION:
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Ratio:
Percent Similarity:
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LOCATION:
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ьe /note="pel B is the leader sequence from the pectate lyase gene of Erwinia carotovora." /label- "Bone D"
//note-"Bone D is the subunit of human osteogenic protein (U.S. Patent No. 5851802 5,284,756 e.g., Fig. 6, Example 9, ID NOs: 1 and 2." residues 549-557 RWATION: /label- XhoI RWATION: /note="residues 549-557 comprise stop codon and XhoI site. /note="residues 1-65 comprise EcoRI site to begining of B." APPLICANT: Better, Marc D.
TITLE OF INVENTION: Methods for Recombinant Microbial Production of
TITLE OF INVENTION: Fusion Proteins and BPI-Derived Peptides
NUMBER OF SEQUENCES: 265 NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/621,803
FILING DATE: 22-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Borun, Michael F.
REGISTRATION NUMBER: 25,447
REFERENCE/DOCKET NUMBER: 21129/33199
TELECOMMUNICATION INFORMATION: COUNTRY: United States of America ZIP: 60606-6402 COMPUTER READABLE FORM: MEDIUM TYPE: Ploppy disk /label= pel B /label= EcoRI MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS Sequence 248, Application US/08621803 Patent No. 5851802 GENERAL INFORMATION: TELEPHONE: 312/474-6300 TELEFAX: 312/474-0448 residues 1-65 TELEFAX: 312/474-0448 TELEX: 25-3856 INFORMATION FOR SEQ ID NO: FEATURE:
NAME/KEY: misc\_feature
'~~\*\*TON: AA 1-22 LENGTH: 557 base pairs TYPE: nucleic acid STRANDEDNESS: single NAME/KEY: misc\_feature NAME/KEY: misc\_feature NAME/KEY: misc\_feature SEQUENCE CHARACTERISTICS protein AA 23-161 LOCATION: AA 23-161 OTHER INFORMATION: OTHER INFORMATION: OTHER INFORMATION: OTHER INFORMATION: LOCATION: residues OTHER INFORMATION: OTHER INFORMATION: OTHER INFORMATION: OTHER INFORMATION: LOCATION: 66..548 LOCATION: AA 1-22 OTHER INFORMATION: LOCATION: residues OTHER INFORMATION: OTHER INFORMATION: linear seq\_documentation\_block: CITY: Chicago STATE: Illinois TOPOLOGY: line MOLECULE TYPE: p ORIGINAL SOURCE: NAME/KEY: CDS US-08-621-803-248 ORGANISM FEATURE: FEATURE

115

Length:

Quality: 189.00

alignment\_scores:

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FEATURE:
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OTHER INFORMATION: /label=pel B /note="pel B is the leader sequence
OTHER INFORMATION: from the pectate lyase gene of Erwinia
OTHER INFORMATION: carottovora."
FEATURE:
NAME/KEY: misc_feature
LOCATION: (23)..(161)
OTHER INFORMATION: /label="Bone D" /note="Bone D is the subunit of
OTHER INFORMATION: human osteogenic protein (see, U.S; Patent No. 6242219)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq_documentation_block:
Sequence 1, Application US/09271970
Patent No. 624219
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
TITLE OF INVENTION: Improved Methods for Recombinant Peptide Production
TITLE OF INVENTION: Improved Methods for Recombinant Peptide Production
CURRENT FILING DATE: 1109-110410910;
CURRENT APPLICATION NUMBER: US/09/271,970
CURRENT FILING DATE: 1999-03-18
SOFTWARE: Patentin Ver. 2.0
SOFTWARE: Patentin Ver. 2.0
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OTHER INFORMATION: /label= ECORI /note="residues 1-65 comprise ECORI OTHER INFORMATION: site to beginning of pel B."
FEATURE:
LOCATION: misc_feature
LOCATION: (1)..(22)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        204 AACGIGGCAGAGACAGCAGCAGCGACCAGAGGCAGGCCIGIAAGAAGCA 253
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98 Val...GluGlnLeuSerAsnMetValValLysSerCysLysCys 111
  Gaps: 5
Percent Identity: 34.783
                                                                                                                                                    Align seg 1/1 to: US-08-621-803-248 from: 1 to: 557
2.662
61.739
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LOCATION: (66)..(548)
FEATURE:
NAME/KEY: misc_feature
                                                                       alignment_block:
TGFB3P x US-08-621-803-248
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Ratio:
Percent Similarity:
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ORGANISM: Human
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No. 6242219: 1
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CURRENT APPLICATION NUMBER: US/09/271,970
CURRENT FILING DATE: 1999-03-18
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 7
                                                                          NAME/KEY: misc_feature

: LOCATION: (549)..(557)

: OTHER INFORMATION: /label=XHOI /note="residues 549-557 comprise stop

: OTHER INFORMATION: codon and XhoI site."
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LOCATION: (1)..(65)
OTHER INFORMATION: /label=EcoRI /note="residues 1-65 comprise EcoRI
OTHER INFORMATION: 5,284,756 e.g., Fig. 6, Example 9, Seq ID OTHER INFORMATION: and 2."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       204 AACGTGGCAGAGCAGCAGCAGCGACCAGAGGCAGGCCTGTAAGAAGCA 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : |||||||:::::||||||| |||||||||||::: |||:::
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98 Val...GluGlnLeuSerAsnMetValValLysSerCysLysCys 111
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                                                                                                                                                                                                                                                                                                                Gaps: 5
Percent Identity: 34.783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Align seg 1/1 to: US-09-271-970-1 from: 1 to: 557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 7, Application US/09271970; Patent No. 6242219; GENERAL INFORMATION; APPLICANT: Better, Marc D.; APPLICANT: Gavit, Patrick D.
                                                                                                                                                                                                                                                                                   189.00
2.662
61.739
                                                                                                                                                                                                                                                                                                                                                                                         alignment_block:
TGFB3P x US-09-271-970-1
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Ratio:
Percent Similarity:
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ORGANISM: Human
FEATURE:
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FEATURE:
NAME/KEY: misc_feature
LOCATION: (23)..(161)
OTHER INFORMATION: /label="Bone D" /note="Bone D is the subunit of
OTHER INFORMATION: human osteogenic protein (see, U.S. Parent No. 6742219
OTHER INFORMATION: 5,284,756 e.g., Fig. 6, Example 9, Seq ID No. 6242219: 1
OTHER INFORMATION: and 2."
                                                                                                                                                                                                                                                                                             FEATURE:
NAME/KEY: misc_feature
LOCATION: (162)..(166)
OTHER INFORMATION: /label=cleavage linker /note="Ala-Leu-Asp-Pro-Pro
OTHER INFORMATION: linking sequence with Asp-Pro cleavage site."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc_feature
LOCATION: (600)..(610)
OTHER INFORMATION: /label-xhoI /note="residues 600-610 comprise stop
OTHER INFORMATION: codon and XhoI site."
                                       NAME/KEY: misc_feature
LOCATION: (1)..(22)
OTHER INFORMATION: /label-pel B /note="pel B is the leader sequence
OTHER INFORMATION: from the pectate lyase gene of Erwinia
OTHER INFORMATION: caratovora."
                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: (167)..(178)
OTHER INFORMATION: /label=peptide sequence /note="BPI-derived
OTHER INFORMATION: peptide."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  351 CCTCTGAACTCCTACATGAACGCCACCAACCACGCCATCGTGCAGACGCT 400
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OTHER INFORMATION: site to beginning of pel B."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length:
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Ratio: 2.662
Percent Similarity: 61.739
                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
NAME/KEY: misc_feature
LOCATION: (167)..(178)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            alignment_block:
TGFB3P x US-09-271-970-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       alignment_scores:
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4444	3 4 4 6 4 6 5 6 6 6 6 6 6 6 6 6 6 6 6 6 6	36 4 4 3 7 6	4 8 4	255	41.	43	5 5 5 5 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	20001	9 8 8 8 1 9 72 72 73 15	4 4 4 4 4 5 5 5 5 5	37.	322	4 4 0 0	<b>4</b> 4	101	104	4 4	35.	300	37.	35(	30.23	35,47	
31.5 31.5 31.5	30.08 30.08 30.09 30.09	30.0 29.8 29.8	29.5 29.4	29.4	29.1	78.0 78.0 78.0 78.0	78.8.8 78.8.8 78.8.8	28.7 28.7 28.7 28.7	222222 28888 2444 2544	28.2 27.8 27.8	27.4 27.1	27.1 27.1 27.0	26.9	26.9 26.9	26.9 26.8	26.7	26.1	25.9	25.6	25.1 25.0	24.7	23.3 22.1 21.4	21.1	
200 200 200 200 200	197 : 5 193 191 : 5 190	190 189 189 188.5	186.5 186.5 186.5	186.5	184.5	183	182.5 182.5 182.5	182 182 182 182 181.5	180 180 180	179 179 176	174 172	171.5 171.5 171	170.5	170.5 170.5	170.5 170	169	165.5	164.5	162.5	159 158.5	156.5 149.5	148 140 135.5	135.5 133.5 133.5	
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version 4.5 - 2000 Compugen Ltd.	<pre>:56 ; Search time 16.82 Seconds (without alignments) 511.755 Million cell updates/sec</pre>	RTPKVEQLSNMVVKSCKCSX 113		residues	arameters: 219241		ries		4: plr4:* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	SUMMARIES	Description	transforming growt transforming growt transforming growt			transforming growt transforming growt				transforming growt transforming growt			transforming growt transforming growt transforming growt	activin beta E cha vgr protein - rat bone morphogenetic	Vg-1-related prote inhibin beta-A cha
GenCore vers Copyright (c) 1993 - 2	protein search, using sw model October 30, 2001, 08:49:56	TGFB3P 634 1 ALDTNYCFRNLEENCCVRPL.	BLOSUM62 Gapop 10.0 , Gapext 0.5	219241 seqs, 76174552 re	hits satisfying chosen parameters	length: 0 length: 200000000	: Minimum Match 0% Maximum Match 100% Listing first 100 summaries	PIR_68:* 1: pir1:* 2: pir2:* 3: pir3:*	<pre>4: plr4:* is the number of results ater than or equal to the rived by analysis of the.</pre>	s Query	Match Length DB ID	000	412 2 409 2	412 2 112 2	414 1 414 2	442 2	413 1 390 1	390 315	390 1 390 2	390 2 390 2	390 2 391 2	130 2 373 2 382 2	350 2 207 2 513 1	510 425
	OM protein - pr Run on:	Title: Perfect score: Sequence:	Scoring table:	Searched:	Total number of	Minimum DB seq Maximum DB seq	Post-processing	Database :	Pred. No. score gre and is de		No. Score	1 633 2 633 3 630												

inhibin beta-A cha inhibin beta-A cha inhibin beta-A cha inhibin beta-A cha activin beta D cha TGF-beta-related p activin beta-A cha cetivin beta-A cha cetivin beta-B cha beta-B cha inhibin beta-B cha inhibin beta-B cha activin beta B 1 bone morphogenetic bone morphogenetic contini beta B cha activin beta B cha activin beta B cha activin beta B cha activin beta C cha steegenic protein - S inhibin beta-B cha activin beta C cha cartivin beta C cha bone morphogenetic cortivin firiffi bone morphogenetic bone morphogenetic fruit fil bone morphogenetic

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A; Reference number: A41262; MUID:91342629
A; Accession: A41262
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A: Residues: 1-410 < wILL>
A: Wolccule type: mRNA
A: Residues: 1-410 < wILL>
A: Conserreferences: 638 M32745; NID:9201949; PIDN:AAA40422.1; PID:9201950
B: Denhez, F.; Lafyatis, R.; Kondalah, P.; Roberts, A.B.; Sporn, M.B.
Growth Factors 3, 139-146, 1990
A: Title: cloning by polymerase chain reaction of a new mouse TGF-beta, mTGF-beta3.
A: Reference number: A61039; MVID:91000714
A: Accession: A61039
A: Molecule type: mRNA
A: Residues: 1-410 < CDEN
A: Watrin, F.; Scotto, L.; Assoian, R.K.; Wolgemuth, D.J.
Cell Growth Differ: 2, 77-83, 1991
A: Title: Cell lineage specificity of expression of the murine transforming growth factor
A: Reference number: A61225; MVID:91299576
A: Status: translation not shown
A: Molecule type: mRNA
A: Residues: 285-410 < wMar>
C: Superfamily: inhibin
C: Keywords: 91ycoprotein; growth factor; growth regulation
B: 1-21/Domain: propeptide #status predicted < ROC
C: Superfamily: signal sequence #status predicted < ROC
C: Superfamin: signal sequence #status predicted < ROC
F: 22-299/Domain: propeptide #status predicted < ROC
F: 22-299/Domain: propeptide #status predicted < ROC
F: 22-209/Domain: propeptide #status predicted < ROC
F: 22-209/Domain: propeptide #status predicted < ROC
F: 22-209/Domain: prodicted | Assoin |
                                                                                                                                                                                                                                                    C; Species: Mus musculus (house mouse)
C; Date: 03-Apr-1992 #sequence_revision 03-Apr-1992 #text_change 16-Jul-1999
C; Accession: A41397; A61225
C; Accession: A41397; A61225
R; Miller, D.A.; Lee, A.; Matsui, Y.; Chen, E.Y.; Moses, H.L.; Derynck, R.
Mol. Endocrinol. 3, 1926-1934, 1989
A; Title: Complementary DNA cloning of the murine transforming growth factor-beta3 (TGFbe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: mRNA
A; Residues: 1-412 <TEN>
A; Cross-references: GB-103241; NID:g339551; PIDN:AAA61161.1; PID:g339552
A; Cross-references: GB-103241; NID:g339551; PIDN:AAA61161.1; PID:g339552
R; Arrick, Ba. Liee, A.L.; Grendell, R.L.; Derynck, R.
Mol. Cell. Biol. 11, 4306-4313, 1991
A; Title: Inhibition of translation of transforming growth factor-beta3 mRNA by its 5' un
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A; Reference number: A36169
A; Reference number: A36169
A; Reference number: A36169
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 410;
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100.0%; Pred. No. 7.2e-57;
11ve 0; Mismatches 0;
                                                                                                                                                                                                                     transforming growth factor beta-3 precursor - mouse
ALIGNMENTS
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A; Accession: A41397
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Best Local Sim
Matches 112;
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C; Species: Rattus norvegicus (Norway rat)
C; Date. 03-Mar-1995
C; Date. 03-Mar-1995
C; Accession: A55706; B40699; S36042
R; Wang, J.; Kuliszewski, M.; Yee, W.; Sedlackova, L.; Xu, J.; Tseu, I.; Post, M.
J B101. Chem. 270, 2722-2728, 1995
A; Title: Cloning and expression of glucocorticoid-induced genes in fetal rat lung fib A; Reference number: A55706; MUID:95155340
                                                                                           A.; Wen, D.; Tamm, J.; Graycar, J.L.; Rhee,
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                                                                                                                                                                                                                                                                                                                                                                              Across-references: GDB:120437; OMIM:190230
A;Map position: 14924-14924
A;Introns: 118/1; 172/3; 216/1; 252/1; 309/2; 360/3
C;Superfamily: inhibin
C;Keywords: growth factor; homodimer
F;1-27/Domain: signal sequence #status predicted <SIG>F;8-300/Domain: propeptide #status predicted <PRO>F;301-412/Product: transforming growth factor beta-3 #status predicted <MAT>
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A;Residues: 3-412 <DER>
A;Cross-references: EMBL:X14885; NID:937075; PIDN:CAA33024.1; PID:91200236
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A;Residues: 157-211 <MCK>
A;Cross-references: EMBL:X71903; NID:g311326; PIDN:CAA50722.1; PID:g311327
C;Superfamily: inhibin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 ALDTNYCFRNLEENCCVRPLYIDFRQDLGWKWVHEPKGYYANFCSGPCPYLRSADTTHST 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 ALDTNYCFRNLEENCCVRPLYIDFRQDLGWKWVHEPKGYYANFCSGPCPYLRSADTTHST 60
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R:Derynck, R.; Lindquist, P.B.; Lee, A.; Wen, D.; Tamm, J.; Grayoz
EMBO J. 7, 3737-3743, 1988
A;Title: A new type of transforming growth factor-beta, TGF-beta3.
A;Reference number: S01824; MUID:89091120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Note: it is uncertain whether Met-1 is the initiator R;MCKinnon, R.D.; Piras, G.; Ida Jr., J.A.; Dubois-Dalcq, M. J. Cell Biol. 121, 1397-1407, 1993
A;Title: A role for TGF-beta in oligodendrocyte differentiation.
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llarity 99.1%; Pred. No. 1.4e-56;
Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 633; DB 2;
Pred. No. 7.2e-57;
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Matches 112; Conservative
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A; Residues: 1-410 <WAN>
A; Cross-references: GB:U03491
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Matches 111; Conserv
A; Molecule type: DNA
A; Residues: 1-48 <ARR>
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C;Species: Gallus gallus (chicken)
C;Species: Gallus gallus (chicken)
C;Date: 17-ul-1992 #sequence_revision 17-Jul-1992 #text_change 16-Jul-1999
C;Accession: A39489; A61018; S25849
R;Burc, D.W.; Paton, I.R.
DNA Cell Biol. 10, 723-734, 1991
A;Title: Molecular cloning and primary structure of the chicken transforming growth f A;Reference number: A39489; MUID:92075163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rydkowlew, S.B.; Dillard, P.J.; Sporn, M.B.; Roberts, A.B.
Growth Factors 2, 123-133, 1990
A;Title: Complementary deoxyribonucleic acid cloning of an mRNA encoding transforming A; Reference number: A61018; MUID:90253805
A;Accession: A61018
A;Scarsus: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-94,'G',96-244,'L',246-412 <JAK>
                                                                                                                                               C;Accession: S01825
R;Derynck, R.; Lindquist, P.B.; Lee, A.; Wen, D.; Tamm, J.; Graycar, J.L.; Rhee, L.;
EMBO J. 7, 3737-3743, 1988
A;Title: A new type of transforming growth factor-beta, TGF-beta3.
A;Reference number: S01824; MUID:89091120
A;Accession: S01825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PIDN:CAA41101.1; PID:g833616; GB:X59082;
                                                                                                                                                                                                                                                                                                                                                                                             C;Keywords: growth factor
F;1-25/Domain: signal sequence #status predicted <SIG>
F;26-29//Domain: propeptide #status predicted <PRO>
F;298-409/Product: transforming growth factor beta-3 #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       <MAT>
                                                                             transforming growth factor beta-3 precursor - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 16-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 ALDINYCFRNLEENCCVRPLYIDFRQDLGWKWVHEPKGYYANFCSGPCPYLRSADTTHST 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C; Superfamily: inhibin
C; Keywords: growth factor; growth regulation; mitogen; transformation
F;1-26/Domain: signal sequence #status predicted <SIG>
F;27-300/Domain: propeptide #status predicted <PRO>
F;301-412/Product: transforming growth factor beta-2 #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 ALDINYCFRNLEENCCVRPLYIDFRQDLGWKWVHEPKGYYANFCSGPCPYLRSADTIH$T
                                                                                                                                                                                                                                                                                                                                                A;Cross-references: EMBL:X14150; NID:g2127; PIDN:CAA32363.1; PID:g2128
C;Superfamily: inhibin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 409;
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79.5%; Pred. No. 2.6e-47;
iive 15; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    transforming growth factor beta-2 precursor - chicken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 621; DB 2;
Pred. No. 1.2e-55;
1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Introns: 115/1; 169/3; 214/1; 251/1; 309/2; 360/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Cross-references: GB:X58071; NID:g63810;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 110; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-412 <BUR>
                                                                                                                                                                                                                                                                                                A; Molecule type: mRNA A; Residues: 1-409 <DER>
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Matches 8
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A; Residues: 1-412 <JAK>
A; Residues: 1-412 <JAK>
A; Residues: 1-812 <JAK>
A; Cross-references: GB.M31154; NID:g212758; PIDN:AAA49089.1; PID:g212759
B; Burt, D.W.; Paton, I.R.; Dey, B.R.
J. Mol. Endocrinol. 7, 175-183, 1991
A; Title: Comparative analysis of human and chicken transforming growth factor-beta-2 and A; Reference number: S25850; MUID:92134496
                                                                                                                                                                                                                                                                                                                         growth fact
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                                                                                                                                                                                         C; Species: Gallus gallus (chicken)
C; Species: Gallus gallus (chicken)
C; Date: 13-uui-1990 #sequence_revision 13-Jul-1990 #text_change 16-Jul-1999
C; Accession: A34939; S25850; S36125; S36124; I51181
R; Jakowlew, S.B.; Dillard, P.J.; Kondalah, P.; Sporn, M.B.; Roberts, A.B.
Mol. Endocrinol. 2, 747-755, 1988
A; Title: Complementary deoxyribonucleic acid cloning of a novel transforming A; Reference number: A34939; MuID:89096666
A; Accession: A34939
A; Status: preliminary; not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Molecule,type: DNA,
A;Residues: 1-117 <BUR>
A;Cross-references: EMBL:X58127; NID:g63815; PIDN:CAA41128.1; PID:g63816
A;Accession: S36125
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VLGLYNTLNPEASASPCCVPQDLEPLTILYYVGRTPKVEQLSNMVVKSCKCS 112
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                                                                                                                                                                        growth factor beta-3 precursor - chicken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 ALDINYCFRNLEENCCVRPLYIDFRQDLGWKWVHEPKGY
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A; Status: preliminary
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Best Local S
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Associated with that in the long form of the human sequences, a clone identical yielding a sequence with that in the long form of the human sequence (Sequencemily: inhibin c; Keywords: alternative splicing; glycoprotein; growth factor; growth regulation; hom F;1-19/Domain: signal sequence #status predicted <SIG> F;0-302/Domain: propertide #status predicted <PRO> F;303-414/Peroduct: transforming growth factor beta-2 #status predicted <MMT> F;72,140,241/Binding site: carbohydrate (Asn) (covalent) #status predicted
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A:Title: Structural and sequence analysis of TGF-beta-2 cDNA clones predicts two diff A;Ritle: Structural and sequence analysis of TGF-beta-2 cDNA clones predicts two diff A;Reference number: A90960; MUID:89090808
A;Accession: A31249
A;Status: not compared with conceptual translation
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N;Alternate names: gliablastoma-derived T-cell suppressor factor
C;Species: Homo sapiens (man)
C;Date: 01-Dec-1989 #sequence_revision 19-Oct-1995 #text_change 16-Jul-1999
C;Accession: S06216, A31249
R;de Martin, R.; Haendler, B.; Hofer-Warbinek, R.; Gaugitsch, H.; Wrann, M.; Schluese
EMBO J. 6, 3673-3677, 1987
                                                                                                                                                                                                                                                                                                                            A;Title: Structural and sequence analysis of TGF-beta-2 cDNA clones predicts two diff A;Reference number: A90960; MUID:89090808
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                                                                                  A; Molecule type: mRNA
A; Residues: 1-414 <HANN
A; Cross-references: GB:J03585; NID:g176495; PIDN:AAA35358.1; PID:g176496
A; Cross-references: GB:goalonce, including the amino end of the active peptide,
A; Note: part of this sequence, including the amino end of the active peptide,
B; Webb, N.R.; Madisen, L.; Rose, T.M.; Purchio, A.F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 ALDINYCFRNLEENCCVRPLYIDFRQDLGWKWVHEPKGYYANFCSGPCPYLRSADTTHST 60
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R;Webb, N.R.; Madisen, L.; Rose, T.M.; Purchio, A.F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 VLGLYNTLNPEASASPCCVPQDLEPLTILYYVGRTPKVEQLSNMVVKSCKCS 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           84.4%; Score 535; DB 1; Length 414; 79.5%; Pred. No. 6.7e-47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             363 VLSLYNTINPEASASPCCVSQDLEPLTLYYIGKTPKIEQLSNMIVKSCKCS
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Pred. No. 6.7e-47;
Pred. no. 6.7e-47;
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        A; Reference number: A34005; MUID:88124824
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ilarity 79.5%;
Conservative 1
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C; Superfamily: inhibin
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                     transforming growth factor beta-2*- bovine

Nalterate, manes: cartilage-inducing factor B, MGF-a; milk growth factor a

C; Species: Bos primigenius taurus (cattle)

C; Actession: A6139; Ma2380; S15389

R; Jin, Y.; Cox, D.A.; Knecht, R.; Raschdorf, F.; Cerletti, N.

J; Protein Chem. 10, 565-575, 1991

A; Reference number: A6139; MuD1:92189724

A; Reference number: A6139; MuD1:92189724

A; Reference number: A6139; MuD1:92189724

A; Residues: 1-112 cJIN

A; Residues: 1-112 cJIN

A; Residues: 1-12 cJIN

A; Reference number: A25485; MUD1:97137406

A; Reference number: A25485; MUD1:97137406

A; Reference number: A25485

A; Reference number: A67439; MUD1:9713730

A; Reference number: A67439; MUD1:97129307

A; Rickentine tupe: A774, A774,
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N;Alternate names: BSC-1 cell growth inhibitor; cartilage-inducing factor B; polyergin
C;Species: Csrcoppithecus aethiops (green monkey, grivet)
C;Date: 23-Mar-1990 #sequence_revision 19-Oct-1995 #text_change 18-Jun-1999
C;Accession: A34005
R;Hanks, S.K.; Armour, R.; Baldwin, J.H.; Maldonado, F.; Spiess, J.; Holley, R.W.
Proc. Natl. Acad. Sci. U.S.A. 85, 79-82, 1988
A;Title: Amino acid sequence of the BSC-1 cell growth inhibitor (polyergin) deduced from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eur. J. Blochem. 197, 353-358, 1991
A;Title: Isolation and characterisation of milk growth factor, a transforming-growth-fact
A;Reference number: S15389; MUID:91224126
A;Accession: S15389
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301 ALDAAYCFRNVQDNCCLRPLYIDFKRDLGWKWIHEPKGYHANFCAGACPYLWSSDTQHSR 360
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A;Accester coule type: protein
A;Molecule type: protein
A;Residues: 1-16,'XX',19 <COX>
A;Experimental source: milk
C;Superfamily: inhibin
C;Superfamily: inhibin
C;Keywords: growth factor; growth regulation; heterodimer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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                                                                                                                   84.4%; Score 535; DB 2; Lv 79.5%; Pred. No. 1.7e-47; ive 14; Mismatches 9;
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89; Conservative
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Best Local S
Matches 89
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R;Roberts, A.B.; Rosa, F.; Roche, N.S.; Coligan, J.E.; Garfield, M.; Rebbert, M.L.; K Growth Factors 2, 135-147, 1990
A;Title: Isolation and characterization of TGF-beta2 and TGF-beta5 from medium condit A;Reference number: A61036; MUID:90253806
                                                                                                                                                                                                                                                   transforming growth factor beta-2 precursor - mouse
C;Species: Mus musculus (house mouse)
C;Decies: Mus musculus (house mouse)
C;Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 18-Jun-1999
C;Accession: A40148
R;Miller, D.A.; Lee, A.; Pelton, R.W.; Chen, E.Y.; Moses, H.L.; Derynck, R. Mol. Endocrinol. 3, 1108-1114, 1389
A;Title: Murine transforming growth factor-beta2 cDNA sequence and expression in adul A;Reference number: A40148; MUID:90014832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Across references: EMBL:X57413; NID:g54772; PIDN:CAA40672.1; PID:g54773
C; Comment: None of the three predicted glycosylation sites is in the mature protein.
C; Superfamily: inhibin
C; Keywords: glycoprotein; growth factor; growth regulation; homodimer; mitogen
C; L1-19/Domain: signal sequence #status predicted <RIG>
F; 1-19/Domain: propertide #status predicted <RIG>
F; 303-414/Product: transforming growth factor beta-2 #status predicted <AMAT>
F; 72,140,241/Binding site: carbohydrate (Asn) (covalent) #status predicted
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C; Superfamily: inhibin
C; Superots: glycoprotein; growth factor; growth regulation; homodimer; mitogen
E;1-19/Domain: signal sequence #status predicted <SIG>
F;20-301/Domain: propeptide #status predicted <PRO>
F;302-413/Product: transforming growth factor beta-2 #status predicted <MAT>
F;72,140,241/Binding site: carbohydrate (Asn) (covalent) #status predicted
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C;Date: 12-Feb-1993 #sequence_revision 19-Oct-1995 #text_change 18-Jun-1999
C;Date: 12-Feb-1993 #sequence_revision 19-Oct-1995 #text_change 18-Jun-1999
C;Accession: S09510; And 10-Dey, N.; Dawid, I.B.
Nucleic Acids Res. 18, 2185, 1990
A;Tille: The sequence of TGF-beta2 from Xenopus laevis.
A;Reference number: S09510; MUID:90245678
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A;Residues: 1-413 <REB>
A;Cross-references: EMBL:X51817; NID:g414789; PIDN:CAA36116.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         83.6%; Score 530; DB 1; Length 41 78.6%; Pred. No. 2.2e-46; ive 14; Mismatches 10; Indels
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76.8%; Pred. No. 5.8e-45;
ive 14; Mismatches 12;
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A,Molecule type: protein
A:Residues: 302-307,'X',309-315,'XX',318-319 <ROB>
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Best Local Similarity 76.89
Matches 86; Conservative
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A; Residues: 1-414 <MIL>
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A:Accession: A54627; WUID:92110032
A:Accession: A54627; WUID:92110032
A:Residues: 1-11.'L', 33-115 <NOW>
A:Residues: 1-12.'L', 33-115 <NOW>
A:Residues: 1-13.'L', 33-115 <NOW>
A:Residues: 1-13.'L', 33-115 <NOW>
A:Residues: 1-13.'L', 33-115 <NOW>
A:Reference number: A26740; WUID:87271633
A:Reference number: A26740; WUID:87271633
A:Reference number: A26740; WUID:87271633
A:Reference number: A26740; WUID:87271633
A:Residues: 31-381-(IKE)
A:Residues: 31-381-(IKE)
A:Residues: 31-381-(IKE)
A:Residues: 331-442 <NAR>
A:Residues: 311-442 <NAR>
A:Residues: 311-443 <NAR>
A:Residues: 311-443 <NAR>
A:Residues: 311-443 <NAR>
A:Residues: 311-444 <COMPLIANA
A:Residues: 311-444 SOURCE A:Residues and Sequence analysis of TGF-beta-2 CDNA clones predicts two differe A:Reference number: A90960; WUID:8909080
A:Accession: B31249
A:Accession: B3124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A,Accession: A29478
A;Molecule type: mRNA
A;Residues: 1-442 <MADA
A;Cross-references: GB:M19154; GB:M22045; GB:M22046; NID:g339549; PIDN:AAA50404.1; PID:g
A;Cross-references: adenocarcinoma
A;Experimental source: adenocarcinoma
R;Noma, T.; Glick, A.B.; Geiser, A.G.; O'Reilly, M.A.; Miller, J.; Roberts, A.B.; Sporn,
Growth Factors 4, 247-255, 1991
                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Homo sapiens (man)
C;Date: 01-Dec-1989 #sequence_revision 19-Oct-1995 #text_change 16-Jul-1999
C;Accession: A2478; A54627; A26740; A29798; B31249
R;Madisen, L.; Webb, N.R.; Rose, T.M.; Marquardt, H.; Ikeda, T.; Twardzik, D.; Seyedin,
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R; Madisen, L.; Webb, N.R.; Rose, T.M.; Marquardt, H.; Ikeda, T.; Twardzik, D.;
DNA 7, 1-6, 1988
A; Title: Transforming growth factor-beta-2: cDNA cloning and sequence analysis. A; Reference number: A29478; MUID:88166349
1 ALDINYCFRNLEENCCVRPLYIDFRQDLGWKWVHEPKGYYANFCSGPCPYLRSADTTHST 60
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                                                                                                                                         transforming growth factor beta-2 precursor, long form - human
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A; Accession: S02267
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A; Residues: 1-390 CDEX
A; Colestinates: 1-390 CDEX
A; Colestinates: 1-390 CDEX
A; Colestinates: GB:M1317; NID:g201952; PIDN:AAA40423.1; PID:g201953
A; Colestinates: GB:M1317; NID:g201952; PIDN:AAA40423.1; PID:g201953
A; Note: the authors suggest that residues 8-23 could represent the hydrophobic core of a C; Comment: The mature protein is the carboxyl-terminal segment of a precursor polypeptid C; Superfamily: inhibin
C; Superfamily: inhibin
C; Superfamily: inhibin
C; Reywords: glycoprotein; growth factor; growth regulation; homodimer; mitogen; transfor F; 1-23/Domain: signal sequence #status predicted <SIG>
F; 1-23/Domain: propeptide #status predicted <PRO>
F; 24-246/Region: cell attachment (R-G-D) motif
F; 24-246/Region: cell attachment (R-G-D) motif
F; 279-390/Product: transforming growth factor beta-1 #status predicted
F; 82,136,176/Binding site: carbohydrate (Asn) (covalent) #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                              transforming growth factor beta-1 precursor - mouse
N;Alternate names: TGF type 2; TGF-beta
C;Species: Mus musculus (house mouse)
C;Decies: 04-Dec-1986 #sequence_revision 04-Dec-1986 #text_change 24-Nov-1999
C;Accession: A01396
R;Derynck, R; Jarrett, J.A.; Chen, E.Y.; Goeddel, D.V.
J Biol. Chem. 261, 4377-4379, 1986
A;Title: The murine transforming growth factor-beta precursor.
A;Reference number: A01396; MUID:86168129
11111111 : 1:11111 | 111111:111111:11111:1111 | 1| :| 1| :| 279 ALDINYCESSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSK 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 ALDINYCFRNLEENCCVRPLYIDFRQDLGWKWVHEPKGYYANFCSGPCPYLRSADTTHST 60
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Pred. No. 1.1e-43;
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77.78;
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transforming growth factor beta-1 precursor - bovine (fragment)
N;Alternate names: beta-TGF; cartilage-inducing factor-A; EGF-dependent TGF or dEGF;
C;Species: Bos primigenius taurus (cattle)
C;Date: 28-Feb-1992 #sequence_revision 28-Feb-1992 #text_change 16-Jul-1999
C;Accession: A40057; A42320; A05284; A24322; B61439
R;Van Obberghen-Schilling, E.; Kondalah, P.; Ludwig, R.L.; Sporn, M.B.; Baker, C.C.
Mol. Endocrinol. 1, 693-698, 1987
A;Title: Complementary deoxyribonucleic acid cloning of bovine transforming growth fa
A;Reference number: A40057; MUID:91042552
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A; Residues: 204-209, X*, 211-217, XX', 220-232 <JIN>
A; Residues: 204-209, X*, 211-217, XX', 220-232 <JIN>
Cicomment: This polypeptide is composed of two polypeptide chains cross-linked by dis C; Comment: Type II TGF does not bind to the EGF receptor and lacks intrinsic mitogenion. Cells grown in monolayer do not respond in a similar manner to these growth fact
A; Title: One of two subunits of masking protein in latent TGF-beta is a part of pro-T A; Reference number: $02267; MUID:89121078
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A; Residues: 204-218 RNDB>
A; Residues: 204-218 RNDB>
J. Biol. Chem. 261, 5693-5695, 1986
A; Title: Cartilage-inducing factor-A. Apparent identity to transforming growth factor
A; Reference number: A24322; MUID:86195954
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A; Residues: 1-315 <VANN
A; Residues: 1-315 <VANN
A; Residues: 1-315 <VANN
A; Residues: 1-315 <VANN
A; Cross-references: GB:M3571; NID:g163747; PIDN:AAA30778.1; PID:g163748
B; Ogawa, Y.; Schmidt, D.K.; Dasch, J.R.; Chang, R.J.; Glaser, C.B.
J. Biol. Chem. 267, 2325-2328, 1992
A; Title: Purification and characterization of transforming growth factor-beta2.3 and A; Reference number: A42320; MUID:92129307
A; Accession: A42320
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A.Residues: 30-32, X',34-38,'Q',40-42,'X',44 < OK2>
C.Superfamily: inhibin
C.Superfamily: inhibin
C.Superfamily: signal sequence #status predicted <SIG>
F:10-29/Domain: signal sequence #status predicted <SIG>
F:10-29/Domain: propebtide #status experimental <PRO>
F:244-246/Region: cell attachment (R-G-D) motif
F:279-390/Product: transforming growth factor beta-1 #status predicted <MAT>
F:82,136,176/Binding site: carbohydrate (Asn) (covalent) #status predicted
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A;Residues: 204-209, X', 211-217 <0GA>
R;Residues: 204-209, X', 211-217 <0GA>
R;Roberts, A.B.; Anzano, M.A.; Meyers, C.A.; Wideman, J.; Blacher, Biochemistry 22, 5692-5698, 1983
Biochemistry 22, 5692-5698, 1983
A;Title: Purification and properties of a type beta transforming gr. A;Reference number: A05284; MUID:84104793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 VLGLYNTLNPEASASPCCVPQDLEPLTILYYVGRTPKVEQLSNMVVKSCKCS 112
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A; Residues: 204-233 <SEX>.

R; Jin, Y.; Cox, D.A.; Rnecht, R.; Raschdorf, F.; Cerletti, N.

J. Protein Chem. 10, 565-575, 1991

J. Protein Chem. 10, 565-575, 1991

A; Title: Separation, purification, and sequence identification of

A; Reference number: A61439; MUID:92189724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             79.3%; Score 503; DB 2; Length 390; 77.7%; Pred. No. 1.1e-43; Live 10; Mismatches 15; Indels
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nes 87; Conserv
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Gaps

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transforming growth factor beta-1 precursor - green monkey
C;Species: Cercopithecus aethiops (green monkey, grivet)
C;Date: OS-Oct-1988 #sequence_revision 05-Oct-1988 #text_change 24-Nov-1999
C;Accession: A20960
R;Sharples, K.; Plowman, G.D.; Rose, T.M.; Twardzik, D.R.; Purchio, A.F.
DNA 6, 239-244, 1987
A;Teile: Cloning and sequence analysis of simian transforming growth factor-beta cDNA
A;Reference number: A20960; MUID:87246074
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                transforming growth factor beta-1 - dog
C;Species: Canis lupus familiaris (dog)
C;Date: 13-Jun-1995 #sequence_revision 14-Jul-1995 #text_change 24-Nov-1999
C;Accession: JC4023
R;Manning, A.M.; Auchampach, J.A.; Drong, R.F.; Slightom, J.L.
Gene 155, 307, 308, 1995
A;Tille: Cloning of a canine cDNA homologous to the human transforming growth factor-A;Reference number: JC4023; MUID:95237630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Accession: JC4023
A;Molecule type: mRNA
A;Residues: 1-390 <MAN>
A;Cross-references: GB:L34956; NID:g516071; PIDN:AAA51458.1; PID:g516072
C;Comment: This factor plays a multifunctional role as a regulator of mammalian cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Superfamily: inhibin
C;Keywords: growth factor; transforming protein
F;288-390/Product: transforming growth factor beta 1 #status predicted <MAT>
        C; Keywords: glycoprotein; growth factor; homodimer; mitogen; transformation F;1-18/Domain: signal sequence #status predicted <SIG>F;19-278/Domain: propeptide #status predicted <PRO>F;19-278/Domain: propeptide #status predicted <PRO>F;244-246/Region: cell attachment (R·G-D) motif F;249-390/Product: transforming growth factor beta-1 #status experimental <P:82,136,176/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             279 ALDTNYCFSSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSK 338
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A;Cross-references: GB:M16658; NID:g176552; PIDN:AAA35369.1; PID:g176553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 VLGLYNTLNPEASASPCCVPQDLEPLTILYYVGRTPKVEQLSNMVVKSCKCS 112
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C;Keywords: growth factor
F;1-16/Domain: signal sequence #status predicted <SIG>
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Matches 86;
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N.Alternate names: growth-inhibitory factor; TGF type 2; TGF-beta

C.Species: Homo sapiens (man)

C.Species: A.S. Fibe. 1986

R.Sperynck, R.; Rhee, L.; Chen, E.Y.; Van Tilburg, A.

Nucleic Acids Res. 15, 3188-3189, 1987

A.Title: Intron-exon structure of the human transforming growth factor-beta precursor generated enumber: A27513

A.Molecule type: DNA

A.Residues: 1-390 (DER-A)

A.Residues: 1-390 (DER-A)

A.Residues: 1-390 (DER-A)

A.Reference sapiens (B.X05839) (B.Y00112; NID:g37097; FIDN:CAA29283.1; PID:g1212989

R.Derynck, R.; Jarrett, J.A.; Chen, E.Y.; Eaton, D.H.; Bell, J.R.; Assoian, R.K.; Robert Nature 316, 701-702, 1985

A.Reference number: A01395; MUID:85296301

A.Recession: A01395

A.Residues: 1-9, P', 11-24, P', 26-159, R', 160-390 (DE2-A)

A.Residues: 1-9, P', 11-24, P', 26-159, R', 160-390 (DE2-A)

A.Residues: 1-9, P', 11-24, P', 26-159, R', 160-390 (DE2-A)

A.Residues: 1-9, P', 11-24, P', 26-159, R', 160-390 (DE2-A)

A.Residues: 1-9, P', 11-24, P', 26-159, R', 160-390 (DE2-A)

A.Residues: 1-9, P', 11-24, P', 26-159, R', 160-390 (DE2-A)

A.Residues: 1-9, P', 11-24, P', 26-159, R', 160-390 (DE2-A)

A.Residues: 1-9, P', 11-24, P', 26-159, R', 160-390 (DE2-A)

A.Residues: 1-9, P', 11-24, P', 26-159, R', 160-390 (DE2-A)

A.Residues: 1-9, P', 11-24, P', 26-159, R', 100-390 (DE2-A)

A.Residues: 1-9, P', 11-24, P', 26-159, R', 100-390 (DE2-A)

A.Residues: 1-9, P', 11-24, P', 26-159, R', 100-390 (DE2-A)

A.Residues: 1-9, R', 100-300 (DE2-A)

A.Residues: 1-9, R'
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A; Residues: 279-390 <RES>
A; Molecule type: mRNA
A; Residues: 279-390 <RES>
A; Cross-references: GB:M38449; NID:q339557; PIDN:AAA36735.1; PID:g339558
A; Stam, K.; Stewart, A.A.; Qu, G.Y.; Iwata, K.K.; Fenyoe, D.; Chait, B.T.; Marshak, D.R. Blochem. J. 305, 87-92, 1995
A; Title: Physical and biological characterization of a growth-inhibitory activity puriff
A; Reference number: S53444
A; Recession: S5344
A; Accession: S5344
A; Accession: S5344
A; Reliminary
A; Molecule type: protein
A; Residues: 279-297 <STA>
C; Comment: The mature protein is the carboxyl-terminal segment of a precursor polypeptic
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A; Residues: 279-295, XX', 298-301 < MAS>
A; Residues: 279-295, XX', 298-301 < MAS>
R; Urushizaki, Y.; Niitsu, Y.; Terui, T.; Koshida, Y.; Mahara, K.; Kohgo, Y.; Urushizaki, Tumor Res. 22, 41-55, 1987
A; Title: Cloning and expression of the gene for human transforming growth factor-beta in A; Reference number: 159664
                                                                                                                                                                                                                                                                                                                             ö
                                                                                             <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Superfamily: inhibin
C;Keywords: glycoprotein; growth factor; heterodimer
F;204-315/Product: transforming growth factor beta-1 #status experimental
F;7,61,101/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                   1 ALDINYCFRNLEENCCVRPLYIDFRQDLGWKWVHEPKGYYANFCSGPCPYLRSADTTHST 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 VLGLYNTLNPEASASPCCVPQDLEPLTILYYVGRTPKVEQLSNMVVKSCKCS 112
                                                                                                                                                                                                                                                Length 315;
                                                                                                                                                                                                                                                                                                                         15; Indels
                                                                                                                                                                                                                                        Query Match 78.9%; Score 500; DB 2; Best Local Similarity 76.8%; Pred. No. 1.8e-43; Matches 86; Conservative 11; Mismatches 15;
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A;Map position: 19q13.2-19q13.2
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Best Local Similarity 76.8%
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Best Local Similarity 76.89
Matches 86; Conservative
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                                                                                        : mrna
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                                                                                                                                                                                                                                                                                                                                                                      Aransforming growth factor beta-1 precursor - pig
N;Alternate names: TGF-beta
N;Alternate names: TGF-beta
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 05-Jun-1988 #sequence_revision 05-Jun-1988 #text_change 16-Jul-1999
C;Accession: A27512; A26356; I46657
R;Derynck, R.; Rhee, L.
Nucleic Acids Res. 15, 3187, 1987
A;Title: Sequence of the porcine transforming growth factor-beta precursor.
A;Reference number: A27512; MUID:87174844
A;Accession: A77512
A;Molecule type: mRNA
A;Residues: 1-390 <DER>
R;Cheifetz, S.; Weatherbee, J.A.; Tsang, M.L.S.; Anderson, J.K.; Mole, J.E.; Luccell 48, 409-415, 1987
A;Title: The transforming growth factor-beta system, a complex pattern of cross-A;Reference number: A90890; MUID:87102890
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transforming growth factor beta-1 - sheep
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 19-Dec-1997 #squence_revision 19-Dec-1997 #text_change 24-Nov-1999
C;Accession: 146463; S45115
R;Woodall, C.J.; McLaren, L.J.; Watt, N.J.
Gene 150, 371-373, 1994
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                                                                                                                                             1 ALDTNYCFRNLEENCCVRPLYIDFRQDLGWKWVHEPKGYYANFCSGPCPYLRSADTTHST 60
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A;Cross-references: GB:M23703; NID:g755044; PIDN:AAA64616.1; PID:g755045
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  transforming growth factor beta #status predicted
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                                                            ; Score 500; DB 2; Length 39; Pred. No. 2.3e-43; 11; Mismatches 15; Indels
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A; Residues: 279-322 CCHE>
B; Kondaiah, P.; Van Obberghen-Schilling, E.; Ludwig, T. Biol. Chem. 263, 18313-18317, 1988
A; Title: cDNA cloning of porcine transforming growth A; Reference number: 146657; MUID:89054010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Score 500; DB 2;
; Pred. No. 2.3e-43;
11; Mismatches 15
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A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                         78.9%;
ilarity 76.8%;
Conservative 11
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76.8%;
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A;Gene: TGFB; TGF-beta-1
C;Superfamily: inhibin
C;Keywords: growth factor
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Best Local Similarity
Matches 86; Conserv
                                                                               Similarity
F;17-390/Product:
                                                                                                       86;
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                                                              Query Match
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transforming growth factor beta-1 precursor - chicken
C;Species: Gallus gallus (chicken)
C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 24-Nov-1999
C;Accession: S01413
R;Jakowlew, S.B.; Dillard, P.J.; Sporn, M.B.; Roberts, A.B.
Nucleic Acids Res. 16, 8730, 1988
A;Title: Nucleotide sequence of chicken transforming growth factor-beta 1 (TGF-beta 1 A;Reference number: S01413; MUID:88335639
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C; Species: Mesocricetus auratus (golden hamster)
C; Species: 02-Unl-1996 #sequence_revision 04-Oct-1996 #text_change 24-Nov-1999
C; Date: 02-Unl-1996 #sequence_revision 04-Oct-1996 #text_change 24-Nov-1999
C; Am. Or 148196
R; Wong, D.T.; Donoff, R.B.; Yang, J.; Song, B.Z.; Matossian, K.; Nagura, N.; Elovic, Am. J. Pathol. 143, 130-142, 1993
A; Title: Sequential expression of transforming growth factors alpha and beta 1 by eos A; Reference number: 148196; MUID:93304479
A;Title: Sequence and chromosomal localisation of the gene encoding ovine latent A;Reference number: 146463; MUID:95121932
A;Accession: 146463
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A; Rossidues: 1-390 <WOO>
A; Cross-references: EMBL:X76916; NID:g496648; PIDN:CAA54242.1; PID:g496649
A; Note: submitted to the EMBL Data Library, December 1993
C; Superfamily: inhibin
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A;Cross-references: EMBL:X60296; NID:g396177; PIDN:CAA42838.1; PID:g396178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              279 ALDINYCESSTEKNCCVRQLYIDFRKDLGWKWIHEPRGYHANFCLGPCPYIWSLDTQYSK 338
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A;Residues: 1-301 <JAK>
A;Residues: 1-301 <JAK>
A;Cross-references: EMBL:X12373; NID:g63808; PIDN:CAA30933.1; PID:g63809
C;Superfamily: inhibin
C;Keywords: growth factor
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Pred. No. 2.3e-43;
                                                                                                                                                                                                                                                                                                                                                             ; Score 500; DB 2;
; Pred. No. 2.3e-43;
11; Mismatches 15
                                                                                                      A;Status: preliminary; translated from GB/EMBL/DDBJ
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A; Title: Isolation and characterization of TGF-beta2 and TGF-beta5 from medium condit A; Reference number: A61036; MUID:90253806
A; Accession: B61036; MUID:90253806
A; Accession: B61036
A; Molecule type: protein
A; Residues: 271-276, X', 278-284, XXX', 287-299 <ROB>
C; Superfamily: inhibin
C; Keywords: growth factor
F; 271-382/Product: transforming growth factor beta-5 #status experimental <MAT>
                                     M.L.; K
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Biochem. Biophys. Res. Commun. 231, 655-661, 1997
A;Title; Genes coding for mouse activin beta C and beta E are closely linked and exhi A;Reference number: JC5366; MUID:97224404
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   A;Cross-references: GB:J05180; NID:g214821; PIDN:AAA49968.1; PID:g214822
R;Roberts, A.B.; Rosa, F.; Roche, N.S.; Coligan, J.E.; Garfield, M.; Rebbert,
Growth Factors 2, 135-147, 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Species: Mus musculus (house mouse)
C;Date: 25-Apr-1997 #sequence_revision 09-May-1997 #text_change 29-Oct-1999
C;Accession: JC5241; JC5367
R;Fang, J.; Yin, W.; Smiley, E.; Wang, S.Q.; Bonadio, J.
Blochem. Blophys. Res. Commun. 228, 669-674, 1996
A;Title: Molecular cloning of the mouse activin beta E subunit gene.
A;Reference number: JC5241; MUID:97096313
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C;Date: 18-Feb-1994 #sequence_revision 26-May-1995 #text_change 16-Jul-1999
C;Accession: S37618
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A;Residues: 1-350 <FAN>
A;Cross-references: GB:U96386; NID:g2072521; PIDN:AAB53801.1; PID:g2072522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Cross-references: GB:U96386; NID:g2072521; PIDN:AAB53801.1; PID:g2072522 C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15 CCVRPLYIDFRQDLGWK-WVHEPKGYYANFCSGPC-PYLRS----ADTTHSTVLGLYNTL 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6 YCFRNLEENCCVRPLYIDFRQDLGWKWVHEPKGYYANFCSGPCPYLRSADTTHSTVLGLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10;
                                                                                                                                                                                                                                                                                                                                                                                                    Length 382;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            33; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               66 NTLNPEASASPCCVPQDLEPLTILYYVGRTPKVEQLSNMVVKSCKCS 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  336 NQNNPGASISPCCVPDVLEPLPIIYXVGRTAKVEQLSNMVVRSCNCS 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 69 NPEASASPCCVPQDLEPLTILY - - YVGRTPKVEQLSNMVVKSCKCS 112
                                                                                                                                                                                                                                                                                                                                                                                                    Score 439; DB 2;
Pred. No. 3.6e-37;
9; Mismatches 21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. 1e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 32.8%; Score 208; 42.5%; Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 activin beta E chain precursor - mouse
                                                                                                                                                                                                                                                                                                                                                                                                    69.2%;
72.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 42.5%
Matches 45; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              S37618
vgr protein - rat (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
Matches 77; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-350 <FA2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Introns: 99/3
C;Superfamily: inhibin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Accession: JC5241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Contents: liver
                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        qq
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Adjointing growth factor beta-4 precursor - chicken (fragment)
NiAlternate names: TGF-beta 4
C.Specias: Gallus gallus (chicken)
R.Burt, D.W.; Jakowlew, S.B.
Nol. Endocrinol. 6, 989-992, 1992
A.Title: Correction: a new interpretation of a chicken transforming growth factor-beta 4
A.Residues: 1-373 capux.
A.Residues: 1-373 capux.
A.Residues: 1-373 capux.
A.Note: sequence extracted from NCB1 backbone (NCB1N:10186, NCB1F:10187)
A.Note: this report corrects and reinterprets the sequence from reference A34941
A.Note: this report corrects and reinterprets the sequence from reference A34941
A.Note: this report corrects and reinterprets the sequence A34941
A.Note: this report corrects and reinterprets the sequence A34941
A.Note: this sequence has been corrected in A41918
A.Note: this sequence (fragment) #status predicted cMAT>
F.17Domain: signal sequence (fragment) #status predicted
F.17Domain: signal sequence (fragment) Residues: transforming growth factor
F.17Domain: signal sequence (fragment) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         transforming growth factor beta-5 precursor - African clawed frog
C;Species: Xenopus laevis (African clawed frog)
C;Date: 31-Dec-1993 #sequence_revision 03-Feb-1994 #text_change 16-Jul-1999
C;Accession. A34929; B61036
B;Kondaiah, P.; Sands, M.J.; Smith, J.M.; Fields, A.; Roberts, A.B.; Sporn, M.B.; Melton J. Biol. Chem. 265, 1089-1093, 1990
A;Title: Identification of a novel transforming growth factor-beta (TGF-beta5) mRNA in XA;Reference number: A34929; MUID:90110090
A;Molecule type: mRNA
                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ä
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                                                                    Gaps
                                                                                                                       1 ALDINYCFRNLEENCCVRPLYIDFRQDLGWKWVHEPKGYYANFCSGPCPYLRSADITHST 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            321 KVLALYNQHNPGASAAPCCVPQTLDPLPIIYYVGRNVRVEQLSNMVVRACKCS 373
                                                                                                                                                                                                                                                                             61 VLGLYNTLNPEASASPCCVPQDLEPLTILYYVGRTPKVEQLSNMVVKSCKCS 112
   Length 130;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 2; Length 373;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               72.7%; Score 461; DB 2; Length 37
71.7%; Pred. No. 2e-39;
ive 13; Mismatches 17; Indels
                                                              17; Indels
Score 488; DB 2;
Pred. No. 1.2e-42;
                                                           10; Mismatches
77.0%;
75.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best_Local Similarity 71.79
Matches 81; Conservative
                                                           85; Conservative
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: mRNA
A; Residues: 1-382 <KON>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                           Matches
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δ 셤 ò q

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A;Title: Recombinant vgr-1/BMP-6-expressing tumors induce fibrosis and endochondral b
A;Reference number: A54798; MUID:94375533
A;Accession: A54798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                    A;Status: preliminary
                                                                                                                                    A; Molecule type: mRNA
                                                                                                            A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Accession: B60856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Accession: 147072
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BAHU6
bone morphogenetic protein 6 precursor - human
C;Species: Homo sapiens (man)
C;Date: 18-Oct-1991 #sequence_revision 03-Aug-1995 #text_change 18-Jun-1999
C;Date: 18-Oct-1991 #sequence_revision 03-Aug-1995 #text_change 18-Jun-1999
C;Accession: B39263
R;Celeste, A.J.; Iannazzi, J.A.; Taylor, R.C.; Hewick, R.M.; Rosen, V.; Wang, B.A.; Wozn Proc. Natl. Acad. Sci. U.S.A. 87, 9843-9847, 1990
A;Title: Identification of transforming growth factor beta family members present in bon A;Reference number: A39263; MUID:91088608
             R; Sauermann, U.; Meyermann, R.; Schluesener, H.J.
A: Neurosci. Res. 33, 142-147, 1992
A:Title: Cloning of a novel TGF-beta related cytokine, the vgr, from rat brain: cloning A; Reference number: S37618
A; Accession: S37618
A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-207 <SAU>
A; Rossidues: 1-207 <SAU>
A; Cross references: EMBL:X58830; NID:957475; PIDN:CAA41634.1; PID:957476
A; Note: the sequence from Fig. 4 is inconsistent with that from Fig. 1 in having 88-Ser
C; Superfamily: inhibin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: GB:M60315; GB:M38694; NID:g339561; PIDN:AAA36737.1; PID:g339562
C;Genetics:
A;Gene: GDB:BMP6
A;Cross-references: GDB:127596; OMIM:112266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A Map position: 6pter-6qter
C; Superfamily: inhibin
C; Keywords: bone; glycoprotein
F; 1-23/Domain: signal sequence #status predicted <SIG>
F; 24-374/Domain: propeptide #status predicted <PRO>
F; 375-513/Product: bone morphogenetic protein 6 #status predicted <MAT>
F; 241, 269, 386, 404, 454/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                               4,
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Vg-1-related protein precursor - mouse
C;Species: Mus mmsculus (house mouse)
C;Date: 28-Oct-1994 #squence_revision 28-Oct-1994 #text_change 16-Jul-1999
C;Accession: A54798; A33925; S47442
R;Gitelman, S.E.; Kobrin, M.S.; Ye, J.Q.; Lopez, A.R.; Lee, A.; Derynck, R. J. Cell Biol. 126, 1595-1609, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SYNTANESELKTACKKHELYVSF-QDLGWQDWIIAPKGYAANYCDGECSFPLNAHMNATNHA 153
                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 TNYCFRNLEENCCVRPLYIDFRQDLGWK-WVHEPKGYYANFCSGPCPYLRSAD---TTHS 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 TNYCFRNLEENCCVRPLYIDFRQDLGWK-WVHEPKGYYANFCSGPCPYLRSAD---TTHS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
9
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                                                                                                                                                                                                                                                                                                                                                                       Length 207;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           460 IVQTLVHLMNPEYVPKPCCAPTKLNAISVLYFDDNSNVILKKYRNMVVRACGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 513;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            60 TVLGLYNTLNPEASASPCCVPQDLEPLTILYYVGRTPKV-EQLSNMVVKSCKC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60 TVLGLYNTLNPEASASPCCVPQDLEPLTILYYVGRTPKV-EQLSNMVVKSCKC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      43; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                       43; Indels
                                                                                                                                                                                                                                                                                                                                                                 32.5%; Score 206; DB 2; 37.2%; Pred. No. 9.5e-14; tive 22; Mismatches 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                32.5%; Score 206; DB 1; 37.2%; Pred. No. 2.5e-13; Live 22; Mismatches 43;
                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 37.29
Matches 42; Conservative
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Best Local Similarity
Matches 42; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Accession: B39263
A; Molecule type: mRNA
A; Residues: 1-513 <CEL>
                                                                                                                                                                                                                                                                                                                                                                       Query Match
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A; Molecule type: mRNA
A; Residues: 1-425 <FLE>
A; Cross-references: GB:L19218; NID:g310379; PIDN:AAC41621.1; PID:g310380
B; Leversha, L.J.; Robertson, D.M.; de Vos, F.L.; Morgan, F.J.; Hearn, M.T.W.; Wettenh
J. Endocrinol. 113, 213-221, 1987
A; Title: Isolation of inhibin from ovine follicular fluid.
A; Reference number: A60856; MUID:87224684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            inhibin beta-A chain precursor - sheep C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 15-Oct-1996 #sequence_revision 15-Oct-1996 #text_change 16-Jul-1999
C;Accession: 147072; B60856
R;Fleming, J.S.; Galloway, S.M.; Crawford, R.J.; Tisdall, D.J.; Greenwood, P.J.
Mol. Reprod. Dov. 40, 1-8, 1995
A;Title: Tissue-specific variation in the length of the 5' untranslated region of the A;Reference number: 147072; MUID:95217464
A;Cross-references: EMBL:X80992; NID:g530729; PIDN:CAA56917.1; PID:g530730
R;Cross-references: EMBL:X80992; NID:g530729; PIDN:CAA56917.1; PID:g530730
R;Lyons, K; Graycar, J.L.; Lee, A.; Hashmi, S.; Lindquist, P.B.; Chen, E.Y.; Hogan, Proc. Natl. Acad. Sci. U.S.A. 86, 4554-4558, 1989
A;Title: Vgr-1, a mammalian gene related to Xenopus Vg-1, is a member of the transfor A;Reference number: A33925; MUID:89282810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         398 SDYNGSELKTACKKHELYVSF-QDLGWQDWIIAPKGYAANYCDGECSFPLNAHMNATNHA 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  || : |: |: |: || || || 320 CCKKQFYVSFK-DIGWNDWIIAPSGYHANYCEGECPSHIAGTSGSSLSFHSTVINHYRMR 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 INYCFRNLEENCCVRPLYIDFRQDLGWK-WVHEPKGYYANFCSGPCPYLRSAD---TTHS 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ---YLRSADTTHSTVLGLYNTL 68
                                                                                                                                                                                                                                                                                                                               A;Molecule type: mRNÅ
A;Residues: 'M',74'K',76-85,'P',87-510 <LYO>
A;Cross-references: GB:J04566; NID:9202352; PIDN:AAA40548.1; PID:9202353
C;Superfamily: inhibin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Molecule type: protein
A;Residues: 310-312, X',314-319, XX',322 <LEV>
C;Comment: Inhibin suppresses follicle-stimulating hormone secretion.
C;Superfamily: inhibin
C;Keywords: disulfide bond; glycoprotein; gonad; heterodimer; hormone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60 TVLGLYNTLNPEASASPCCVPQDLEPLTILYYVGRTPKV-EQLSNMVVKSCKC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 425;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 510;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        69 -- NPEASASPCCVPQDLEPLTILYY - VGRTPKVEQLSNMVVKSCKCS 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GHSPFANLKSCCVPTKLRPMSMLYYDDGQNIIKKDIQNMIVEECGCS 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 32.3%; Score 205; DB 2; I
Best Local Similarity 37.2%; Pred. No. 3.1e-13;
Matches 42; Conservative 22; Mismatches 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  32.2%; Score 204; DB 2;
38.3%; Pred. No. 3.3e-13;
tive 20; Mismatches 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Status: preliminary; translated from GB/EMBL/DDBJ
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tgfb3p.rpr

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Soluble beta-A chain precursor - bovine
Nihlternate names: activin; mesoderm inducing factor
C.Species: Bos primigentus taurus (cattle)
C.Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C.Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C.Accession: S50899; Bas732; AA60660; B61548
R.Fihompson, D.A.; Cronin, C.N.; Martin, F.
Bur. 7 Blochem: 226, 771-764, 1994
A.Fitle: Genomic cloning and sequence analyses of the bovine alpha-, beta(A)- and bet
A.Fistus: preliminary
A.Fictus: preliminary
A.Fictus
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N;Alternate names: activin A; activin AB chain A; erythroid differentiation factor; m
C;Species: Homo sapiens (man)
C;Spate: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 08-Dec-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Reference number: A61548; MUD:86136989
A;Reference number: A61548; MUD:86136989
A;Reference number: A61548; MUD:86136989
A;Redience: 310-313 <FUX>
C;Genetics: 310-313 <FUX>
C;Genetics: 130/1
A;Introns: 130/1
C;Superfamily: inhibin
C;Keywords: disulfide bond; glycoprotein; gonad; heterodimer; homodimer; hormone F;1-28/Domain: signal sequence #status predicted <SIG>F;29-309/Domain: propeptide #status predicted <PRO>F;29-309/Domain: propeptide #status predicted <PRO>F;310-425/Product: beta-A inhibin/activin #status experimental <AM7>F;165/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15 CCVRPLYIDFRODLGWK-WVHEPKGYYANFCSGPCP----YLRSADTTHSTVLGLYNTL 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10;
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                                      424
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              69 -- NPEASASPCCVPQDLEPLTILYY - VGRTPKVEQLSNMVVKSCKCS 112
378 GHSPFANLKSCCVPTKLRPMSMLYYDDGQNIIKKDIQNMIVEECGCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       36;
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37.4%; Pred. No. 8.3e-13;
Live 21; Mismatches 36,
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Best Local Similarity
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A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1-4.4 <mas.
A; Cross-references: GB:X03266; NID:g2002; PIDN:CAA27020.1; PID:g2003
A; Cross-references: GF:X03266; NID:g2002; PIDN:CAA27020.1; PID:g2003
C; Comment: The source of this protein is ovarian follicular fluid.
C; Comment: The mature protein is the carboxyl-terminal segment of a precursor polypeptic if comment: Inhibin have been isolated (A and B) that differ in the amino-terminal c; Comment: Inhibin is secreted by ovaries or testes and inhibits the secretion of follit c; Superfamily: inhibin
C; Keywords: contraceptive, follitropin inhibitor; glycoprotein; gonad
C; Keywords: contraceptive, follitropin inhibitor; glycoprotein; gonad
C; Toomain: signal sequence *status predicted <NGC>
F; 1-20/Domain: propeptide *status predicted <NGC>
F; 309-424/Froduct: inhibin beta-A chain *status predicted
F; 165/Binding site: carbohydrate (Asn) (covalent) *status predicted
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A;Reference number: A60087; MUID:92155098
A;Accession: A60087
                                                                                                                                                                                S.Y.; Guillemin, R.;
                                                                                                                                                                                                                                                 A;Title: Complementary DNA sequences of ovarian follicular fluid inhibin show precursor A;Reference number: A93371; MUID:86092207
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                       inhibin beta-A chain precursor - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Bate: 13-Aug-1986 #sequence_revision 13-Aug-1986 #text_change 18-Jun-1999
C;Accession: A01393
E;Mason, A.J.; Hayfilck, J.S.; Ling, N.; Esch, F.; Ueno, N.; Ying, S.Y.; Gui
Nature 318, 659-663, 1985
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N;Alternate names: activin A; mesoderm-inducing factor WEHI-MIF
C;Species: Mus musculus (house mouse)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: A60087; 148265; S314440
B;Albano, R.M.; Godsave, S.F.; Huylebroeck, D.; Van Nimmen, K.; Isaacs, H.V.
Development 110, 435-443, 1990
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C;Superfamily: inhibin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Title: Activins are expressed in preimplantation mouse embryos and in
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A; Residues: 309-311, 'X', 313-318, 'XX', 321-325 <AL2>
R; Albano, R.M.; Groome, N.; Smith, J.C.
Development 117, 711-723, 1993
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Best Local Similarity 37.4%;
Matches 40; Conservative
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Best Local Similarity
Matches 40; Conserv
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A; Status: prelimina
                                                                                                                                                                                                                                                                                                                              A; Accession: A01393
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C;Species: Xenopus lacvis (African clawed frog)
C;Date: 27-Aug-1995 #sequence_revision 19-Oct-1995 #text_change 21-Jul-2000
C;Accession: JC4151
R;Oda, S:; Nishimatsu, S.; Murakami, K.; Ueno, N.
Biochem. Biophys. Res. Commun. 210, 581-588, 1995
A;Title: Molecular cloning and functional analysis of a new activin beta subunit: a d A;Reference number: JC4151; MUID:95275314
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A;Cross-references: GB:M84795; NID:g156729; PIDN:AAA28307.1; PID:g156730<br/>
A;Cross-references: GB:M84795; NID:g156729; PIDN:AAA28307.1; PID:g156730<br/>
A;Note: sequence extracted from NCBI backbone (NCBIN:106399, NCBIP:106400)<br/>
B;Wharton, K.A.; Thomsen, G.H.; Gelbart, W.M.<br/>
Proc. Natl. Acad. Sci. U.S.A. 88, 9214-9218, 1991<br/>
A;Title: Drosophila 60A gene, another transforming growth factor beta family member, A;Reference number: A41233; MUID:92021021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Title: Sequence, biochemical characterization, and developmental expression of a A;Reference number: A43918; MUID:92290120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           F;1-253/Domain: signal sequence #status predicted <SIG>
F;254-367/Product: activin beta D chain #status predicted <MAT>
F;64,155,161,208,230/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: GB:M77012; NID:g156727; PIDN:AAA28306.1; PID:g156728
C;Comment: This protein is a member of the transforming growth factor beta family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TGF-beta-related protein 60A precursor - fruit fly (Drosophila melanogaster) N;Alternate names: bone morphogenetic protein homolog precursor C;Species: Drosophila melanogaster C;Beteis: IO-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 17-Nov-2000 C;Accession: A43918; A41233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Residues: 1-367 < ODA>
A; Cross-references: DDBJ:D49543; NID:g961512; PIDN:BAA08494.1; PID:g961513
A; Experimental source: embryo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Doctor, J.S.; Jackson, P.D.; Rashka, K.E.; Visalli, M.; Hoffmann, F.M.
Dev. Biol. 151, 491-505, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10 NLEEN----CCVRPLYIDFRQDLGWK-WVHEPKGYYANFCSGPCPYLRS----ADTTHST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 VLGLYNTLNPEASASPCCVPQDLEPLTILYYVGRTPKV--EQLSNMVVKSCKCS 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13;
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                                                                                                    380 GHSPFANLKSCCVPTKLRPMSMLYYDDGQNIIKKDIQNMIVEECGCS 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                          -- NPEASASPCCVPQDLEPLTILYY - VGRTPKVEQLSNMVVKSCKCS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 19,00,
Pred. No. 1.3e-12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C; Keywords: glycoprotein; mesoderm
                                                                                                                                                                                                                                                                                                                                           activin beta D chain precursor
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Matches 41; Conserv
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A; Residues: 1-455 <WHA>
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A; Molecule type: mRNA
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                                                                                                                                                                                                                                           A:Status: preliminary
A:Molecule type: DNA
A:Molecule type: DNA
A:Molecule type: DNA
A:Residues: 1-426 craN>
A:Cross-references: EMBL:X57578; NID:928351; PIDN:CAA40805.1; PID:9825621
A:Note: the authors translated the codon GAG for residue 53 as Gly and GAG for residue
R:Stewart, A.G.; Miborrow, H.M.; Ring, J.M.; Crowther, C.E.; Forage, R.G.
A:Title: Human inhibin genes. Genomic characterisation and sequencing.
A:Reference number: A91366; MUID:87005283
C; Accession: S30488; B23556; B24248; A30884; S33351; PN0010
R; Tanimoto, K.; Handa, S.I.; Ueno, N.; Murakami, K.; Fukamizu, A.
DNA Seq. 2, 103-110, 1991
A; Title: Structure and sequence analysis of the human activin beta(A) subunit gene.
A; Reference number: S30488; MUID:92135888
A; Accession: S30488
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A; Molecule type: DNA
A; Racidues: 311-426 (STEE)
A; Cross-references: GB.X04447; NID:933928; PIDN:CAA28041.1; PID:933929
B; Mason, A.J.; Niall, H.D.; Seeburg, P.H.
Biochem, Biophys. Res. Commun. 135, 957-964, 1986
A; Title: Structure of two human ovarian inhibins.
A; Reference number: A90123; MUID:86186863
A; Recession: B24248
A; Molecule type: MRNA
A; Residues: 1-426 < AMAS
A; Cross-references: GB:M13436; NID:9186414; PIDN:AAA59168.1; PID:9307069
B; Murata, M.; Eto, Y.; Shibal, H.; Sakal, M.; Muramatsu, M.
Proc. Natl. Acad. Sci. U.S.A. 85, 2434-2438; 1988
A; Title: Erythroid differentiation factor is encoded by the same mRNA as that A; Accession: A30884; MUID:88190086
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A/Cross-references: GDB:119346; OMIM:147290
C/Cross-references: GDB:119346; OMIM:147290
C/Cross-references: GDB:119346; OMIM:14729
C/Cross-references: GDB:119346; OMIM:14729
C/Cross-references: GDB:119346; OMIM:14729
C/Cross-references: GDB:119346; OMIM:14729
C/Cross-references: GDB:119346; OMIM:147290
C/Cross-
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Best Local S
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9

Gaps

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C; Genetics:

Matches 15

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Inhibin beta-A chain precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: B40905; B40056
R;Esch, F.S.; Shimasaki, S.; Cooksey, K.; Mercado, M.; Mason, A.J.; Ying, S.Y.; Ueno, Mol. Endocrinol. 1, 388-396, 1987
A;Title: Complementary deoxyribonucleic acid (cDNA) cloning and DNA sequence analysis A;Reference number: A40905; MUID: 90331931
A;Accession: B40905
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Reference mumber: H.; Jones, P.B.C.; Hsueh, A.J.W.; Mayo, K.E.
Mol. Endocrinol. 1, 561-568, 1987
A;Title: Rat inhibin: molecular cloning of alpha- and beta-subunit complementary deox
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C;Species: Gallus gallus (chicken)
C;Species: Gallus gallus (chicken)
C;Date: 04-Sep-1997 #sequence_revision 04-Sep-1997 #text_change 16-Jul-1999
C;Accession: I51284
R;Houston, B.; Thorp, B.H.; Burt, D.W.
A; Molecular cloning and expression of bone morphogenetic protein-7 in the chic A;Reference number: I51284; MUID:95200473
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                                                                    260 ESNLCRRTDFYVDF-DDLNWQDWIMAPKGYDAYQCQGSCPNPMPAQLNATNHAIIQSLLH 318
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EENCCVR-PLYIDFRODLGWK-WVHEPKGYYANFCSGPCPYLRSAD---TTHSTVLGLYN 66
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A; Cross-references: GB:M37482; NID:g204936; PIDN:AAA41436.1; PID:g204937
C; Superfamily: inhibin
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A; Residues: 1-313 <HOU>
A; Cross-references: GB:S77477; NID:g957233; PIDN:AAB33846.1; PID:g957234
C; Superfamily: inhibin
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36.4%; Pred. No. 6.8e-12;
.ive 21; Mismatches 37; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 69 -- NPEASASPCCVPQDLEPLTILYY - VGRTPKVEQLSNMVVKSCKCS 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         378 GHSPFANLKSCCVPTKLRPMSMLYYDDGQNIIKKDIQNMIVEECGCS 424
                                                                                                                                    TLNPEASASPCCVPQDLEPLTILYY-VGRTPKVEQLSNMVVKSCKC 111
                                                                                                                                                                        SI | STRPDEVPPPCCVPTETSPLSILYMDVDKVIVIREYADMRVESCGC 364
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34.8%; Pred. No. 6.3e-12;
iive 22; Mismatches 39
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A;Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 30.19
Best Local Similarity 36.49
Matches 39; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Accession: B40056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 40;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cispecies: Cynops pyrrhogaster (Japanese Common newt)
Cibate: 15-Aug-1996 #sequence_revision 18-Oct-1996 #text_change 20-Jun-2000
Circession: JC4862
Biochem. Biophys. Res. Commun. 224, 451-456, 1996
A.Title: Expression of activin beta subunit genes in sertoli cells of newt testes.
A.Reference number: JC4862
A.Reference number: JC4862
A.Rocession: JC4862
A.Rocession: JC4862
A.Rocession: JC4862
A.Rocession: JC4862
A.Rocession: JC4863
A.Rocessio
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C. Species: Caenorhabditis elegans
C. Species: Caenorhabditis elegans
C. Species: L1-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 21-Jul-2000
C. Accession: T43286
R. Morita, K.; Chow, K.L.; Ueno, N.
Development 126, 1337-1347, 1999
A. Title: Regulation of body length and male tail ray pattern formation of Caenorhabditis
A. Reference number: Z22393; MUID:99146896
A. A. Title: Regulation of body length and male tail ray pattern formation of Caenorhabditis
A. Reference number: Z22393; MUID:99146896
A. A. Molecule type: mRNA
A. Molecule type: mRNA
A. Molecule type: mRNA
A. Molecule type: MRL. AF074395; NID:93328181; PIDN:AAC26791.1; PID:93328182
C. Genetics:
A. Genetics:
A. Map position: 5
C. Superfamily: inhibin
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                                                                                                                                                                     14 NCCVRPLYIDFRQDLGW-KWVHEPKGYYANFCSGPCPYLRSAD---TTHSTVLGLYNTLN 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                    9
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                                Length 455
                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         367 GYSPFTSVKSCCVPTKLRAMSMLYYDDGQNIIKKDIQNMVVEECGCS 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length
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                                                                                                                                                                                                                                                                                                          70 PEASASPCCVPQDLEPLTILYYVG-RTPKVEQLSNMVVKSCKC 111
                                                                                                                                                                                                                                                                                                                                                        37;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       activin beta-A chain precursor - Japanese common newt
                            Query Match 30.8%; Score 195; DB 2; Best Local Similarity 39.8%; Pred. No. 2.9e-12; Matches 41; Conservative 19; Mismatches 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 41; Conserv
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Best Local Similarity
Matches 42; Conserv
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A;Cross-references: GB:M60316; GB:M38695; NID:g339563; PIDN:AAA36738.1; PID:g339564 R;Oezkaynak, E.; Rueger, D.C.; Drier, E.A.; Corbett, C.; Ridge, R.J.; Sampath, T.K.; EMBO J. 9, 2085-2093, 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     F:1-29/Domain: signal sequence #status predicted <SIG>
7:30-29/Domain: propeptide #status predicted <PRO>
F:300-431/Product: bone morphogenetic protein 7 #status predicted <WAT>
F:187,302,321,372/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           activin beta B subunit - African clawed frog
C;Species: Xenopus laevis (African clawed frog)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 16-Jul-1999
C;Accession: 151199
R;Dohrmann, C.E.; Hemmati-Brivanlou, A.; Thomsen, G.H.; Fields, A.; Woolf, T.M. Dev. Biol. 157, 474-483, 1993
A;Title: Expression of activin mRNA during early development in Xenopus laevis. A;Reference number: 151199; MUID:93273083
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                || : ||||| :|| || || 266 CCRQQFYIDFRL-IGWNDWIIAPAGYYGNYCEGSCPAYLAGVPGSASSFHTAVVNQYRMR 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10 NLEEN-----CCVRPLYIDFRQDLGWK-WVHEPKGYYANFCSGPCPYLRSA---DTT 57
                                                                                                                                                                                                                                                                                                                                            A;Molecule type: mRNA
A;Residues: 1-431 <OEZ>
A;Cross-references: EMBL:X51801; NID:g35151; PIDN:CAA36100.1; PID:g35152
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                                                                                                                                                                                                                                  A;Title: OP-1 CDNA encodes an osteogenic protein in the TGF-beta family. A;Reference number: $10529; MUID:90291971 A;Accession: $10529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15 CCVRPLYIDFRQDLGWK-WVHEPKGYYANFCSGPCP-YLR----SADTTHSTVLGLYNT-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29.8%; Score 189; DB 1; Length 431; 34.8%; Pred. No. 1.1e-11; ive 22; Mismatches 39; Indels
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A;Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Cross-references: GDB:127597; OMIM:112267
A; Reference number: A39263; MUID:91088608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Keywords: bone; dimer; glycoprotein
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Matches 40; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Map position: 20pter-20qter C; Superfamily: inhibin
                                                                                                   A; Residues: 1-431 <CEL>
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                                                                      A; Molecule type: mRNA
                               A; Accession: C39263
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C;Species: Sus scrofa domestica (domestic pig)
C;Species: J-May-1988 #sequence_revision 21-May-1988 #text_change 30-Sep-1993
C;Accession: B26356
R;Cheifetz, S.; Weatherbee, J.A.; Tsang, M.L.S.; Anderson, J.K.; Mole, J.E.; Lucas, R.;
Cell 48, 409-415, 1987
A;Title: The transforming growth factor-beta system, a complex pattern of cross-reactive A;Reference number: A90890; MUID:87102890
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                                                               HSTVLGLYNTLNPEASASPCCVPQDLEPLTILYYVGRTPKV-EQLSNMVVKSCKC 111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 360;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     / Match 30.0%; Score 190; DB 2; Length 36 Local Similarity 37.3%; Pred. No. 7.3e-12; Length 36 ses 38; Conservative 19; Mismatches 39; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 189; DB 2; Length 43
Pred. No. 9.6e-13;
7; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 ALDTNYCFRNLEENCCVRPLYIDFRQDLGWKWVHEPKGYYANF 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  71 EASASPCCVPQDLEPLTILYYVGRTPKV-EQLSNMVVKSCKC 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 ALDAAYCFRNVQDNCCLRPLYIDFKRDLGXKXIHEPKGYNANF
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bone morphogenetic protein 7 precursor - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29.8%;
72.1%;
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Best Local Similarity 72.1
Matches 31; Conservative
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A; Residues: 1-43 <CHE>
C; Superfamily: inhibin
C; Keywords: growth factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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Matches
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A.; Woolf, T.M.; Melt

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Gaps

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C;Species: Bos primidents taurus (cattle)
C;Date: 01-Aug-1995 #sequence_revision 01-Sep-1995 #text_change 17-Mar-1999
C;Accession: S50899
R;Thompson, D.A.; Cronin, C.N.; Martin, F.
Eur. J. Biochem. 226, 751-764, 1994
A;Title: Genomic cloning and sequence analyses of the bovine alpha-, beta(A)- and bet y DNase I footprinting.
A;Reference number: S50897; MUID:95112839
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Accession: S10751
A;Molecule type: protein
A;Residues: 293-294,'GX',297-302,'XX',305-307 <SCH>
C;Comment: Activins A and B are homodimers of inhibin beta-A or inhibin beta-B, respebin beta-A and beta-B, respectively.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A Experimental source: testis
R; Schmelzer, C.H.; Button, L.E.; Tamony, C.M.; Schwall, R.H.; Mason, A.J.; Liegeois, Blochim. Biophys. Acta 1039, 135-141, 1990
A; Ittle: Purification and characterization of recombinant human activin B.
A; Reference number: S10751; MUID: 90304183
                                                                                                                                                                                                                                   A;Residues: 1-407 <MAS>
A;Reference number: A90123; MUID:86186863
        C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 01-Dec-2000 C;Accession: A40150; C24248; A40156; S10751 R;Mason, A.J.; Berkemeier, L.M.; Schwelzer, C.H.; Schwall, R.H. Mol. Endocrinol 3, 1352-1358, 1989 A;Title: Activin B; precursor sequences, genomic structure and in vitro activities. A;Reference number: A40150; MUID:90114200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            testicular inhibin beta-subunit mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                            A Molecule type: mRNA
A;Residues: 55-407 <MA2>
A;Residues: 55-407 <MA2>
A;Cross-references: 65-8M13437; NID:9186416; PIDN:AAA59169.1; PID:9186417
R;Feng, Z.M.; Bardin, C.W.; Chen, C.L.C.
Mol. Endocrinol. 3, 939-948, 1989
A;Title: Characterization and regulation of testicular inhibin beta-subur
A;Reference number: A40156; MUID:89295443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A)Cross-references: GDB:119347; OMIM:147390
A)Cross-references: GDB:119347; OMIM:147390
C)Superfamily: inhibin
C; Superfamily: inhibin gonad; heterodimer; homodimer; hormone
E;1-20/Domain: signal sequence #status predicted <PRO>
F;21-292/Domain: propeptide #status predicted <PRO>
F;23/Product: inhibin Deta-B chain #status predicted <AMI>
F;93/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 407;
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37.4%; Pred. No. 1.9e-11;
iive 21; Mismatches 35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Molecule type: mRNA
A;Residues: 22-46,'A',48-407 <
A;Cross-references: GB:M31632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                40; Conservative
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                                                                                                                                                                                         A; Accession: A40150
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C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Jul-1999
R;Accession: JH0690
R;Nishimatsu, S.; Suzuki, A.; Shoda, A.; Murskami, K.; Ueno, N.
Biochem. Biophys. Res. Commun. 186, 1487-1495, 1992
A;Title: Genes for bone morphogenetic proteins are differentially transcribed in A; Reference number: JH0690
A;Molecule type: mRNA
A;Residence: 1-426 cNIS5
A;Residence: 1-426 cNIS5
A;Residence: 1-426 cNIS5
A;Cross-references: GB:X65427; NID:g64591; PIDN:CAA45021.1; PID:g64592
A;Experimental source: oocyte
C;Superfamily: inhibin
C;Reywords: glycoprotein
F;283-426/Product: bone morphogenetic protein 7 #status predicted cMAT>
F;177,307,367/Binding site: carbohydrate (Asn) (covalent) #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 inhibin beta-B chain precursor - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 01-Dec-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         319 RFLKQACKKHELFVSFR-DLGWQDWIIAPEGYAAYYCDGECAFPLNSFMNATNHAIVQTL 377
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9 RNLEENCCVRPLYIDFRQDLGWK-WVHEPKGYYANFCSGPCPYLRSA---DTTHSTVLGL 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 426;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  378 VHFINPETVPKPCCAPTQLNGISVLYFDDSANVILKKYKNMVVQACGC 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 65 YNTLNPEASASPCCVPQDLEPLTILYYVGRTPKV-EQLSNMVVKSCKC 111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               41;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29.5%; Score 187; DB 2; 35.2%; Pred. No. 1.8e-11; ive 23; Mismatches 41;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 29.5%
Best Local Similarity 35.2%
Matches 38, Conservative
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Matches 40; Conserv
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Query Match 29.1
Best Local Similarity 36.4
Matches 39; Conservative
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Best Local Similarity
Matches 40; Conserv
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                                                                                                                                                                                                                         A; Gene: ZactbetaB
C; Superfamily: inhibin
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A;Residues: 133-411 <E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Status: preliminary A; Molecule type: DNA
                                                                          A; Molecule type: mRNA
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A; Residues: 1-7 <RES>
       A; Accession: I50103
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Inhibin beta-B chain - mouse (fragment)
Inhibin beta-B chain
Inhibin beta-B chain
Inhibin inhib
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Accession: I4835
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1-234 <RES>
A; Cross-references: EMBL:X83376; NID:9603571; PIDN:CAA58290.1; PID:9603572
B; Albano, R.M.; Grome, N. S. Smith, J.C.
B; Albano, R.M.; Grome, N. S. Smith, J.C.
A; Reference number: 148243; MUID:93321614
A; Accession: I4826
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Residues: 134, D', 136-255 <ALB>A; Residues: 134, D', 136-255 <ALB>A; Cross-references: EMBL:X69620; NID:950147; PIDN:CAA49326.1; PID:950148
C; Superfamily: inhibin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             150103
activin beta B - zebra fish
activin beta B - zebra fish
C;Species: Brachydanio rerio (zebra fish)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 16-Jul-1999
C;Accession: 150103
R;Wittbrodt, J;, Rosa, F.M.
Genes Dev. 8, 1448-1462, 1994
A;Title: Disruption of mesoderm and axis formation in fish by ectopic expression of acti
                                                                                                                                                                                                                                                                                                                                                                                                         7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15 CCVRPLYIDFRQDLGWK-WVHEPKGYYANFCSGPCP-YLR----SADTTHSTVLGLYNT- 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15 CCVRPLYIDFRQDLGWK-WVHEPKGYYANFCSGPCP-YLR----SADTTHSTVLGLYNT- 67
                                                                                                                                                                                                                                                                                                                                                                                                         11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11;
                                                                                                                                                                                                                                                                                                                              Length 408;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 255;
                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    363 GLNP-GTVNSCCIPTKLSTMSMLYFDDEYNIVKRDVPNMIVEECGCA 408
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -LNPEASASPCCVPQDLEPLTILYYVGRTPKVEQ-LSNMVVKSCKCS 112
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ilarity 37.4%; Pred. No. 1.8e-11;
Conservative 20; Mismatches 36;
                                                                                                                                                                                                                                                                                                                          ch 29.4%; Score 186.5; DB 2; 1 Similarity 37.4%; Pred. No. 1.9e-11; 40; Conservative 21; Mismatches 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Reference number: 148235; MUID:95344997
                          A; Molecule type: DNA
A; Residues: 1.408 < THO>
A; Cross-references: EMBL:U16240
C; Genetics:
A; Introns: 151/1
C; Superfamily: inhibin
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Best Local Similarity
Matches 40; Conserva
A;Status: preliminary
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Best Local 9
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Nylternate names: inhibin/activin beta B-chain
C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 03-Apr-1992 * *sequence_revision 01-Aug-1997 * text_change 16-Jul-1999
C;Accession: B41398; 153288; C40905
R;Feng, Z.M.; Li, Y.P.; Chen, C.L.C.
Role: Endocrinol: 3, 1914-1925, 1989
A;Title: Analysis of the 5'-flanking regions of rat inhibin alpha- and beta-B-subunit
A;Reference number: A41398; MUID:90190649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Title: Complementary deoxyribonucleic acid (cDNA) cloning and DNA sequence analysis A;Reference number: A40905; MUID:90331931 A;Accession: C40905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: GB:S72477; NID:g619268
R;Esch, F.S.; Shimasaki, S.; Cooksey, K.; Mercado, M.; Mason, A.J.; Ying, S.Y.; Ueno,
Mol. Endocrinol. 1, 388-396, 1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Title: Two messenger ribonucleic acids encoding the common beta B-chain of inhibin A;Reference number: I53288; MUID:94307180
A;Accession: I53288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: GB:M32756; GB:M32757; NID:g204943; PIDN:AAA1438.1; PID:g554460
R;Dykema, J.C.; Mayo, K.E.
Endocrinology 135, 702-711, 1994
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                                                               A;Residues: 1-393 <WIT>
A;Cross-references: EMBL:X76051; NID:g516356; PIDN:CAA53636.1; PID:g516357
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                          15 CCVRPLYIDFRQDLGWK-WVHEPKGYYANFCSGPCP-YLR----SADTTHSTVLGLYNT-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15 CCVRPLYIDFRQDLGWK-WVHEPKGYYANFCSGPCP-YLR----SADTTHSTVLGLYNT-
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                                                                                                                                                                                                                                                                                                  Length 393;
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                                                                                                                                                                                                                                                                                                                                                           Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         68 -LNPEASASPCCVPQDLEPLTILYYVGRTPKVEQ-LSNMVVKSCKCS 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               68 -LNPEASASPCCVPQDLEPLTILYYVGRTPKVEQ-LSNMVVKSCKCS 112
                                                                                                                                                                                                                                                                                        29.1%; Score 184.5; DB 2; 36.4%; Pred. No. 2.9e-11; tive 22; Mismatches 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 2;
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A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         inhibin beta-B chain precursor - rat
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4

Gaps

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Done morphogenetic protein-2 - mouse
C; Species: Mus musculus (house mouse)
C; Species: Mus musculus (house mouse)
C; Date: 10-Dec-1994 #sequence_revision 17-Nov-1995 #text_change 03-May-1996
C; Accession: 84535
R; Feng, J.Q.; Harris, M.A.; Ghosh-Choudhury, N.; Feng, M.; Mundy, G.R.; Harris, S.E. Biochim. Biophys. Acta 1218, 221-224, 1994
A; Title: Structure and sequence of mouse bone morphogenetic protein-2 gene (BMP-2): c
A; Reference number: 845355; MUID:94289485
A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Species: Rattus norvegicus (Norway rat)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 16-Jul-1999
C;Accession: S37073 #sequence_revision 06-Jan-1995 #text_change 16-Jul-1999
C;Accession: S37073 #sequence_revision 06-Jan-1995 #text_change 16-Jul-1999
Submitted to the EMBL Data Library, September 1993
A;Bescription: ODNA sequence of fetal rat calvarial osteoblast bone morphogenetic pro
A;Reference number: S37073
                   A.Molecule type: mRNA
A.Residues: 54-430 <0E2>
C.Comment: This protein induces bone formation.
C;Superfamily: inhibin
C;Keywords: glycoprotein
F;1-29/Domain: signal sequence #status predicted <SIG>
F;30-290/Domain: propeptide #status predicted <PRO>
F;291-430/Product: osteogenic protein.1 #status predicted <AMAT>
F;291-430/Product: osteogenic protein.1 #status predicted <AMAT>
F;186,301,320,371/Binding site: carbohydrate (Asn) (covalent) #status predicted
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A,Residues: 1-393 <FEN>
A;Cross-references: EMBL:Z25868; NID:g397950; PIDN:CAA81088.1; PID:g397951
C;Superfamily: inhibin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             329 CKKHELYVSFR-DLGWQDWIIAPEGYAAYYCEGECAFPLNSYMNATNHAIVQTLVHFINP 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     287 KRLKSSCKRHPLYVDF-SDVGWNDMIVAPPGYHAFYCHGECPFFLADHLNS--TNHAIVQ 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15 CCVRPLYIDFRQDLGWK-WVHEPKGYYANFCSGPCPYLRSA---DTTHSTVLGLYNTLNP 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9 RNLEENCCVRPLYIDFRQDLGWK-WVHEPKGYYANFCSGPCPY----LRSADTTHSTVL 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     344 TLVNSVNSKIPKA----CCVPTELSAISML-YLDENEKVVLKNYQDMVVEGCGC 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63 GLYNTLN---PEASASPCCVPQDLEPLTILYYVGRTPKV--EQLSNMVVKSCKC 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 393;
                                                                                                                                                                                                                                                                                                                                                                              Length 430;
                                                                                                                                                                                                                                                                                                                                                                                                                                             38; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : |||| | | :::||: : : : ||||::| | 388 DIVPKPCCAPTQLNAISVLYFDDSSNVILKKYRNMVVRACGC 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         71 EASASPCCVPQDLEPLTILYYVGRTPKV-EQLSNMVVKSCKC 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2;
                                                                                                                                                                                                                                                                                                                                                                              Query Match 28.9%; Score 183; DB 2; Best Local Similarity 35.3%; Pred. No. 4.5e-11; Matches 36; Conservative 22; Mismatches 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28.8%; Score 182.5; DB 2
37.7%; Pred. No. 4.6e-11;
iive 21; Mismatches 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      S37073
bone morphogenetic protein 2 - rat
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Matches 43; Conservative
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A; Residues: 1-394 <FEN>
C; Superfamily: inhibin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Accession: S37073
A; Status: preliminary
A;Accession: PQ0224
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                                              N.Alternate names: gact 2
C.Species: Carassius auratus (goldfish)
C.Species: Carassius auratus (goldfish)
C.Species: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 17-Mar-1999
C.Accession: PN0505
R.Ge, W.; Gallin, W.J.; Strobeck, C.; Peter, R.E.
Bicchem. Biophys. Res. Commun. 193, 711-717, 1993
A.Fitle: Cloning and sequencing of goldfish activin subunit genes: Strong structural con A.Reference number: PN0504; MUID:93290666
A.Accession: PN0505
A.Molecule type: DNA
A.Molecule type: DNA
A.Residues: 1-115 <GEW>
C.Superfamily: inhibin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    activin beta A chain - goldfish (fragment)

N.Alternate names: gact 18
C.Species: Carasaius auratus (goldfish)
C.Species: Carasaius auratus (goldfish)
C.Saccession: PNOS04
E.G. W.; Gallin, W.J.; Strobeck, C.; Peter, R.E.
Biochem. Biophys. Res. Commun. 193, 711-717, 1993
A.Title: Cloning and sequencing of goldfish activin subunit genes: Strong structural con A.Reference number: PNOS04
A.Accession: PNOS04
A.Accession: PNOS04
A.Accession: PNOS04
A.Residues: 1-115 cGEW>
C.Superfamily: inhibin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7;
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C; Species: Mus musculus (house mouse)
C; Species: Musculus (house mouse)
R; Oezkaynak, E.; Schnegelsberg, P.N.J.; Oppermann, H.
Biochem. Biophys. Res. Commun. 179, 116-123, 1991
A; Fitle: Murine osteogenic protein (OP-1): high levels of mRNA in kidney.
A; Reference number: JQ1184, MUID:91354237
A; Moccession: JQ1184
A; Wolecule type: DNA
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-120 <OEZ>A; Cross-references: EMBL:X56906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12 CCRQQFYIDFRL-IGWNDWIIAPAGYYGNYCEGSCPAYMAGVPGSASSFHTAVVNQYRMR 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15 CCVRPLYIDFRQDLGWK-WVHEPKGYYANFCSGPCP-YLR----SADTTHSTVLGLYNT- 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15 CCVRPLYIDFRQDLGWK-WVHEPKGYYANFCSGPCP----YLRSADTTHSTVLGLYNT- 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 115;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 37; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              68 -LNPEASASPCCVPQDLEPLTILYYVGRTPKV--EQLSNMVVKSCKC 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           68 -LNPEASASPCCVPQDLEPLTILYYVGRTPKVEQ-LSNMVVKSCKC 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28.9%; Score 183.5; DB 2; 36.8%; Pred. No. 9.9e-12; ive 21; Mismatches 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28.9%; Score 183; DB 2; 36.4%; Pred. No. 1.1e-11; iive 19; Mismatches 37;
                       tivin beta B-1 chain - goldfish (fragment)
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Matches 39; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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Gaps

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Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: mRNA
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Cipate: 16-Sep-192 #sequence_revision 03-Aug-1955 #text_change 18-Jun-1999
CiAccession: B3728; PC2178
RiWozney, J.M.; Rosen, V.; Celeste, A.J.; Mitsock, L.M.; Whitters, M.J.; Kriz, R.W.; Hew Science 242, 1528-1534, 1988
RiWozney, J.M.; Rosen, V.; Celeste, A.J.; Mitsock, L.M.; Whitters, M.J.; Kriz, R.W.; Hew Science 242, 1528-1534, 1988
A;Title: Novel regulators of bone formation: molecular clones and activities.
A;Reference number: A37278; MUID:89072730
A;Accession: B37278
A;Reference number: A37278; MUID:9179501; PIDN:AA51834.1; PID:9179502
A;Cross-references: GB:M22489; NID:9179501; PIDN:AA51834.1; PID:9179502
A;Cross-references: GB:M22489; NID:9179501; PIDN:AA51834.1; PID:9179502
A;Cross-references: GB:M22489; NID:9179501; PIDN:AA51834.1; PID:9179502
A;Title: Expression and characterization of human bone morphogenetic protein-2 in silkwc A;Reference number: PC2178; MUID:94266754
A;Reference number: PC2178; MUID:94266754
A;Residues: 290-295, XX, 297-304 <ISH:
A;Residues: 290-295, XX, 297-304 <ISH:
B;Rathore, S.; Hammerstone, K.M.; Dansereau, S.; Porter, T.J.
Brotein Sci. 4(Suppl.2), 4435, 1995
A;Reference number: A56704
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C; Genetics:
C; Geneti
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89
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                                                                                                                                                                                                                 290 KRLKSSCKRHPLYVDF-SDVGWNDWIVAPPGYHAFYCHGECPFPLADHLNS--TNHAIVQ 346
                                                                                                            Gaps
                                                                                                                                                                                     ---- LRSADTTHSTVL 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9 RNLEENCCVRPLYIDFRQDLGWK-WVHEPKGYYANFCSGPCPY----LRSADTTHSTVL 62
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                                                                                                                                                                                                                                                                                                                              GLYNTLN---PEASASPCCVPQDLEPLTILYYVGRTPKV--EQLSNMVVKSCKC 111
                                                                                                                                                                                                                                                                                                                                                                              TLVNSVNSKIPKA----CCVPTELSAISML-YLDENEKVVLKNYQDMVVEGCGC 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               63 GLYNTLN---PEASASPCCVPQDLEPLTILYYVGRTPKV--EQLSNMVVKSCKC 111
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                        Length 394;
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                                                                                                    Indels
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N.Alternate names: bone morphogenetic protein 2A; rhBMP2
                                                                                                    31;
                                                                                                                                                                         RNLEENCCVRPLYIDFRQDLGWK-WVHEPKGYYANFCSGPCPY-
                        DB 2;
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                28.8%; Score 182.5; DB 2 37.7%; Pred. No. 4.6e-11; ive 21; Mismatches 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 182.5; DB 1, Pred. No. 4.7e-11; 21; Mismatches 31
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A; Note: determination of amino ends
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                                                                                                Conservative
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Query Match
Best Local Similarity
Matches 43; Conserv
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Matches 43; Conserva
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RESULT

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Rinishimateu, S.; Suzuki, A.; Shoda, A.; Murakami, K.; Ueno, N.
Biochem. Biophys. Res. Commun. 186, 1487-1495, 1992
A/Title: Genes for bone morphogenetic proteins are differentially transcribed in earl A; Reference number: JH0687; MUID:92378616
A; Accession: JH0689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           transcribed in earl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Keywords: glycoprotein
F;285-398/Product: bone morphogenetic protein 2II #status predicted <MAT>
F;137,202,237,340/Binding site: carbohydrate (Asn) (covalent) #status predicted
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R; Plessow, S.; Koester, M.; Knoechel, W.
Biochim. Biophys. Acta 1089, 280-282, 1991
A;Tille: cDNA sequence of Xenopus laevis bone morphogenetic protein 2 (BMP-2).
A;Reference number: S16244; MUID:91274367
A;Accession: S16244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Xenopus lacvis (African clawed firog)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Jul-1999
C;Accession: JH0687; S16244
R;Nishimatsu, S.; Suzuki, A.; Shoda, A.; Murakami, K.; Ueno, N.
Biochem. Biophys. Res. Commun. 186, 1487-1495, 1992
A;Tilte: Genes for bone morphogenetic proteins are differentially transcribe A;Reference number: JH0687; MUID:92378616
C;Species: Xenopus laevis (African clawed frog C;Species: Xenopus laevis (African clawed frog) C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Jul-1999 C;Accession: JH0688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C:Keywords: dimer; glycoprotein
F;285-398/Product: bone morphogenetic protein 21 #status predicted <MAT>
F;137,202,340/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  292 KRLKSSCRRHPLYVDF-SDVGWNDWIVAPPGYHAFYCHGECPFFLADHLNS--TNHAIVQ 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    292 KRLKSSCRRHPLYVDF-SDVGWNDWIVAPPGYHAFYCHGECPFPLADHLNS--TNHAIVQ 348
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A;Residues: 1-6,'S',8-15,'V',17-232,'N',234-398 <PLE>
A;Cross-references: EMBL:X55031; NID:g64581; PIDN:CAA38850.1; PID:g64582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: mRNA
A;Residues: 1-398 <NIS>
A;Cross-references: GB:X63424; NID:964585; PIDN:CAA45018.1; PID:964586
                                                                                                                                                                                                                                                                                                                                                      A; Residues: 1-398 -NIS>
A; Cross-references: GB:X63425; NID:g64583; PIDN:CAA45019.1; PID:g64584
A; Experimental source: oocyte
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4.7e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28.8%; Score 182.5; DB 2; 37.7%; Pred. No. 4.7e-11; Live 21; Mismatches 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 182.5; DB 2;
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R; Hoetten, G.; Neidhardt, H.; Jacobowsky, B.; Pohl, J.
Blochem. Blophys. Res. Commun. 204, 646-652, 1994
A; Title: Cloning and expression of recombinant human growth/differentiation factor 5.
A; Reference number: JC2347; MUID:95071375
A; Accession: JC2347
A; Molecule type: DNA
A; Reidues: L501 < HOE>
A; Cross-references: GB:X80915; NID:9671524; PIDN:CAA56874.1; PID:9671525
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ë
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NyAlternate names: gact 11
NyAlternate names: gact 11
Sylvania auratus (goldfish)
C; Species: Carassius auratus (goldfish)
C; Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 17-Mar-1999
C; Accession: PNOSO6
R; Ge, W.; Gallin, W.J.; Strobeck, C.; Peter, R.E.
Biochem. Biophys. Res. Commun. 193, 711-717, 1993
A; Title: Cloning and sequencing of goldfish activin subunit genes: Strong structural
A; Reference number: PNOSO4; MUID: 93290666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C; Species: Strongylocentrotus purpuratus (purple urchin)
C; Date: 08-May-1995 #sequence_revision 21-Jul-1995 #text_change 20-Sep-1999
C; Accession: 552408
R; Ponce, M.R.; Micol, J.L.; Davidson, E.H.
submitted to the EMBL Data Library, February 1995
A; Poscription: SpDVR1, a member of the transforming growth factor-beta superfamily A; Reference number: 552408
A; Accession: 552408
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                                                                                                                                                                                                                                                                                                                                                                                  C:Reywords: glycoprotein
F:189/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:381-382/Cleavage site: Arg-Ala (unidentified proteinase) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 394 KNLKARCSRKALHVNPK-DMGWDDWIIAPLEYEAFHCEGLCEFPLRSHLEPTNHAVIOTL 452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9 RNLEENCCVRPLYIDFRQDLGW-KWVHEPKGYYANFCSGPCPY-LRS--ADTTHSTVLGL 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15 CCVRPLYIDFRQDLGWK-WVHEPKGYYANFCSGPCPYL----RSADTTHSTVLGLYNT- 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12 CCROOFYIDFRL-IGWNDWIIAPAGYYGNYCEGSCPAFLAGVPGSASSFHTAVVNQYRMR 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             68 -LNPEASASPCCVPQDLEPLTILYYVGRTPKVEQ-LSNMVVKSCKC 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SPDVR1 protein - sea urchin (Strongylocentrotus purpuratus)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 28.7%; Score 182; DB 2; L. Best Local Similarity 37.0%; Pred. No. 6.7e-11; Matches 40; Conservative 23; Mismatches 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28.6%; Score 181.5; DB 2
35.8%; Pred. No. 1.6e-11;
iive 20; Mismatches 37
                                                                                                                                                                                                                                                                    A;Gene: GDB:BMP9
A;Cross-references: GDB:433948
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A;Residues: 1-115 <GEW>
C;Superfamily: inhibin
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C;Superfamily: inhibin
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C;Species: Hono sapiens (man)
C;Species: Hono sapiens (man)
C;Date: 10-Feb-1995 #sequence_revision 10-Feb-1995 #text_change 17-Mar-2000
C;Date: 10-Feb-1995 #sequence_revision 10-Feb-1995 #text_change 17-Mar-2000
C;Coccasion: A5452
B;Chang, S.C.: Hoang, B.: Thomas, J.T.; Vukicevic, S.; Luyten, F.P.; Ryba, N.J.P.; Kozak J. Biol. Chem. 269, 28227-28234, 1994
A;Title: Cartilage-derived morphogenetic proteins. New members of the transforming growt A;Reference number: A55452; MUID:95050604
A;Refatus: preliminary
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-501 < CHA>
A;Cross-references: GB:U13660; NID:9600731; PID:9600732
                                                                                                                                              C;Species: Mus musculus (house mouse)
C;Date: 20-Oct-1994 #sequence_revision 10-Nov-1995 #text_change 17-Mar-2000
C;Date: 20-Oct-1994 #sequence_revision 10-Nov-1995 #text_change 17-Mar-2000
C;Accession: 843294
R;Storm, E.E.; Huynh, T.V.; Copeland, N.G.; Jenkins, N.A.; Kingsley, D.M.; Lee, S.J.
Nature 368, 639-643, 1994
A;Title: Limb alterations in brachypodism mice due to mutations in a new member of the A;Reference number: 843294; MUID:94195427
A;Stotus: preliminary
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C;Species: Homo sapiens (man)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 17-Mar-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 388 KNLKARCSRKALHVNFK-DMGWDDWIIAPLEYEAFHCEGLCEFPLRSHLEPTNHAVIQTL 446
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                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: mRNA
A; Residues: 1-495 <STO>
A; Cross-references: GB:U08337; NID:g488461; PIDN:AAA18778.1; PID:g488462
C; Superfamily: inhibin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cartilage-derived morphogenetic protein 1 precursor - human
                                                                                                                         bone morphogenetic protein-related protein (GDF5) - mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28.7%; Score 182; DB 2; 37.0%; Pred. No. 6.6e-11; ive 23; Mismatches 39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 182; DB 2;
Pred. No. 6.7e-11;
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37.0%;
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Best Local Similarity
Matches 40; Conserv
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Superfamily: inhibin
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Gaps

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C.Genetics:
A.Gene: Gdf6
C.Superfamily: inhibin
F.1-5/Domain: polybasic protease recognition site #status predicted <PPR>
F.1-5/Domain: polybasic protein homolog GDF6 (fragment) #status predicted
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                                          related activins,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                activin beta C precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 14-Peb-1997 #sequence_revision 13-Mar-1997 #text_change 26-Aug-1999
C;Accession: S70580
R;Lau, A.L.; Nishimori, K.; Matzuk, M.M.
Biochim. Biophys. Acta 1307, 145-148, 1996
A;Title: Structural analysis of the mouse activin beta-C gene.
A;Reference number: S70580; MUID:96283807
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bone morphogenetic protein homolog GDF6 precursor - mouse (fragment)
N/Alternate names: growth and differentiation factor 6
C.Species: Mus musculus (house mouse)
C.Date: 20-Oct-1994 #sequence_revision 07-Feb-1997 #text_change 26-May-2000
C.Accession: S43295
R.Storm, E.E.; Huynh, T.V.; Copeland, N.G.; Jenkins, N.A.; Kingsley, D.M.; I
Nature 368, 639-643, 1994
A.Title: Limb alterations in brachypodism mice due to mutations in a new mem A.Reference number: S43294; MUID:94195427
                                                                                                                                                                                                                                                                                                        A;Residues: 11125 <STO>
A;Cross-references: EMBL:U08338; NID:g488463; PIDN:AAA18779.1; PID:g488464
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                       18;
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                                                                                                                                                                                                                                                                                                                                                                                 68 LNPEASA-----SPCCVPQDLEPLTILYYVGRTPKVE-QLSNMVVKSCKCS 112
                                                                                                                                                                                                                                                                                                                                                                                                             68 LNPEASA-----SPCCVPQDLEPLTILYYVGRTPKVE-QLSNMVVKSCKCS 112
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                                          subset of
                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31;
          A;Cross-references: GB:U95962
C;Comment: Activin beta C and beta E form a distinct
                                                                                                                                                                                  28.4%; Score 180; DB 2; 37.8%; Pred. No. 7.4e-11; ive 20; Mismatches 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Molecule type: DNA
A;Residues: 1-352 <LAU>
A;Cross-references: EMBL:U40772
                                                                                                                                                                                Query Match 28.4
Best Local Similarity 37.8
Matches 42; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                         C;Genetics:
A;Introns: 105/3
C;Superfamily: inhibin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Superfamily: inhibin
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JC5366
activin beta C - mouse
C; Species: Mus musculus (house mouse)
C; Date: 28-May-1997 #sequence_revision 18-Jul-1997 #text_change 26-Aug-1999
C; Accession: JC5366
R; Fang, J; Wang, S.; Smiley, E.; Bonadio, J.
Blochem. Biophys. Res. Commun. 231, 655-661, 1997
A; Title: Genes coding for mouse activin beta C and beta E are closely linked and exhibit A; Accession: JC5366
A; Molecule type: DNA
A; Residues: 1-352 <FAN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ਹ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C.Species: Homo sapiens (man)
C.Date: 29-Mar-1995 #sequence_revision 26-May-1995 #text_change 29-Oct-1999
C.Date: 29-Mar-1995 #sequence_revision 26-May-1995 #text_change 29-Oct-1999
C.Accession: JC2466
R.Hoetten, G.; Neidhardt, H.; Schneider, C.; Pohl, J.
Blochem. Blophys. Res. Commun. 206, 608-613, 1995
A.Title: Clohing of a new member of the TGF-beta family: A putative new activin betaC A.Reference number: JC2466, MUID:95126961
A.Residues: JC2466
A.Molecule type: mRNA
A.Molecule type: mRNA
A.Residues: 1-352 (HOE>
A.Cross-references: GB:X82540; NID:9669154; PIDN:CAA57890.1; PID:9669155
A.Cross-references: liver
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F;19-236/Domain: propeptide #status predicted <PRO>
F;237-352/Product: activin beta C #status predicted <MAT>
F;110,143,161/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                          | : | : | :: | : | | | | 355 NSDWQCKRKNLEVNF - EDLDWQEWIIAPLGYVAFYCQGECAFPLNGHANATNHAIVQTLV 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                            10 NLEENCCVRPLYIDFRQDLGW-KWVHEPKGYYANFCSGPCPYLRSAD---TTHSTVLGLY
                                                                                                                                                                                                         .
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                                                                                                                                                         Length 461;
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37.4%; Pred. No. 7.4e-11;
Live 19; Mismatches 38; Indels
                                                                                                                                                                                                      42; Indels
                                                                                                                                                                                                                                                                                                                                              66 NTLNPEASASPCCVPQDLEPLTILYY-VGRTPKVEQLSNMVVKSCKC 111
                                                                                                                                                                                                                                                                                                                                                                            HMSPSHVPQPCCAPTKLSPITVLYYDDSRNVVLKKYKNMVVRACGC 460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         67 TLNPEASASPCCVPQDLEPLTILYYVGRTPKVE-QLSNMVVKSCKCS 112
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A; Residues: 1-461 <PON>
A; Crosz-references: EMBL: Z48313; NID:g673496; PID:g673497
C; Superfamily: inhibin
                                                                                                                                               28.5%; Score 181; DB 2; 34.6%; Pred. No. 7.8e-11; ive 22; Mismatches 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 64
2C2466
Inhibin beta-C chain precursor - human
N:Alternate names: activin beta C chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 Similarity 37.4%;
40; Conservative 1
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A,Cross-references: GDB:632884
A,Map position: 2cen-2q13
C,Superfamily: inhibin
C;Keywords: glycoprotein
                                                                                                                                                                                                 37; Conservative
                                                                                                                                                                        Local Similarity
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Matches 4
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A;Title: Limb alterations in brachypodism mice due to mutations in a new member of th A;Reference number: $43.294; MUID:941954.27 A;Accession: $43.296 A;Status: preliminary
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C;Date: 10-Feb-1995 #sequence_revision 10-Feb-1995 #text_change 26-May-2000
C;Datession: B5545
C;Accession: B5545
B;Chang, S.C.; Hoang, B.; Thomas, J.T.; Vukicevic, S.; Luyten, F.P.; Ryba, N.J.P.;
J. Biol. Chem. 269, 2827-28234, 1994
A;Title: Cartilage-derived morphogenetic proteins. New members of the transforming A;Reference number: A55452; MUID:95050604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Species: Mus musculus (house mouse)
C;Date: 20-Oct-1994 #sequence_revision 10-Nov-1995 #text_change 19-May-2000
C;Date: 20-Oct-1994 #sequence_revision 10-Nov-1995 #text_change 19-May-2000
C;Accession: 84326
R;Storm, E.E.; Huynh, T.V.; Copeland, N.G.; Jenkins, N.A.; Kingsley, D.M.; Lee, Nature 368, 639-643, 1994
                                                                                                                                                                                               44 REGRSECSRKSLHVDFK-ELGWDDWIIAPLDYEAYHCEGVCDFPLRSHLEPTNHAIIQTL 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    335 CSKKPLHVNFK-ELGWDDWIIAPLEYEAYHCEGVCDFPLRSHLEPTNHAIIQTLMNSMDP 393
                                                                              Gaps
                                                                                                                                                    67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9 RNLEENCCVRPLYIDFRQDLGW-KWVHEPKGYYANFCSGPCPY-LRS--ADTTHSTVLGL 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Molecule type: mRNÅ
A;Residues: 1-436 <CHA>
A;Cross-references: GB:U13661; NID:g632489; PIDN:AAA61416.1; PID:g632490
C;Superfamily: inhibin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: GB:U08339; NID:g488465; PIDN:AAA18780.1; PID:g488466
C;Superfamily: inhibin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cartilage-derived morphogenetic protein 2 precursor - bovine (fragment)
                                                                                                                                                    12 EENCCVRPLYIDFRQDLGWK-WVHEPKGYYANFCSGPCPYLRSAD---TTHSTVLGLYNT
                                                                              . 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            65 YNTLNPEASASPCCVPQDLEPLTILYYVGRTPKV-EQLSNMVVKSCKC 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27.8%; Score 176; DB 2; Length 15
37.0%; Pred. No. 7.7e-11;
ive 20; Mismatches 42; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27.6%; Score 175; DB 2; Length 43
37.3%; Pred. No. 3e-10;
ive 19; Mismatches 39; Indels
                                                                              40; Indels
                                                                                                                                                                                                                                                                                                                                                   68 LNPEASASPCCVPQDLEPLTILYYVGRTPKV-EQLSNMVVKSCKC 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          bone morphogenetic protein-related protein (GDF7) - mouse
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Score 179; DB 1;
Pred. No. 1.2e-10;
2; Mismatches 40
28.2%; Scc
35.2%; Pre
tive 22;
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Matches 38; Conservative
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Matches 40; Conservative
                                                                              Conservative
Query Match
Best Local Similarity
Matches 37; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 1-151 <STO>
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C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Date: 18-Oct-1991 #sequence_revision 03-Aug-1995 #text_change 18-Jun-1999
C; Date: 18-Oct-1991 #sequence_revision 03-Aug-1995 #text_change 18-Jun-1999
R; Celeste, A.J.; Iannazzi, J.A.; Taylor, R.C.; Hewick, R.M.; Rosen, V.; Wang, E.A.; Wozn Proc. Natl. Acad. Scl. U.S.A. 87, 9843-9847, 1990
A; Title: Identification of transforming growth factor beta family members present in bon A; Reference number: A39263; MUID:91088608
A; Rccession: A39263; MUID:91088608
A; Molecule type: mRNA
A; Residues: 1-454 < CEL>
A; Cross-references: GB:M60314; GB:M38693; NID:g339559; PIDN:AAA36736.1; PID:g339560
C; Genetics:
A; Genetics:
A; Genetics: GB:127595; OMIM:112265
A; Map position: 6pter-6qter
C; Superfamily: inhibin
C; Superfamily: inhibin
C; Superfamily: signal sequence #status predicted <SIG>F; 18-316/Domain: signal sequence #status predicted <PRO>F; 11.77/Domain: propeptide #status predicted <PRO>F; 11.7327, 345,395/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C. Species: Mus musculus (house mouse)
C. Species: Musculus (house mouse)
C. Accession: 14954
B. King, J.A.; Marker, P.C.; Seung, K.J.; Kingsley, D.M.
Dev. Biol. 166, 112-122, 1994
A. Accession: 14954
A. Molecule type: many
A. Molec
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                                                                                                                                                                                   CCVRPLYIDFRQDLGW-KWVHEPKGYYANFCSGPCPY-LRS--ADTTHSTVLGLYNTLNP 70
                                                                                                                                                                                                                          12 BENCCVRPLYIDFRQDLGWK-WVHEPKGYYANFCSGPCPYLRSAD---TTHSTVLGLYNT 67
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                                   Length 125;
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                                                                                                             Indels
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                                                                                                                                                                                                                                                                                                                                                                               Query Match 28.2%; Score 179; DB 2; L. Best Local Similarity 38.2%; Pred. No. 3.1e-11; Matches 39; Conservative 20; Mismatches 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                40;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                bone morphogenetic protein 5 precursor - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 28.2%
Best Local Similarity 35.2%
Matches 37; Conservative
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A;Title: Bone morphogenetic proteins and a signalling pathway that controls patternin A;Reference number: I50607; MUID:94163974 A;Accession: I50607
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C;Species: Bos primigenius taurus (cattle)
C;Date: 03-Mar-1994 #sequence_revision 03-Mar-1994 #text_change 17-Mar-1999
C;Accession: C42320
R;Ogawa, Y.; Schmidt, D.K.; Dasch, J.R.; Chang, R.J.; Glaser, C.B.
J. Biol. Chem. 267, 2325-2328, 1992
A;Title: Purification and characterization of transforming growth factor-beta2.3 and A;Reference number: A42320; MUID:92129307
                                                                                                                                                                                         A; Status: preliminary; nucleic acid sequence not shown; not compared with conceptual
                                                        R;Thomsen, G.; Woolf, T.; Whitman, M.; Sokol, S.; Vaughan, J.; Vale, W.; Melton, D.A. Cell 63, 485-493, 1990
A;Title: Activins are expressed early in Xenopus embryogenesis and can induce axial A;Reference number: A36192; MUID:91029481
A;Recession: A36192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Gallus gallus (chicken)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 16-Jul-1999
C;Accession: 150607
E;Francis, P.H.; Richardson, M.K.; Brickell, P.M.; Tickle, C.
Development 120, 209-218, 1994
          C;Date: 11-Jan-1991 #sequence_revision 11-Jan-1991 #text_change 15-Jun-1996
C;Accession: A36192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Cross-references: EMBL:X75914; NID:9472927; PIDN:CAA53513.1; PID:9472928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14 NCCVRPLYIDFRQDLGWK-WVHEPKGYYANFCSGPCPY----LRSADTTHSTVLGLYNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 353;
                                                                                                                                                                                                                                                                                                                                                       Length 102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             309 VNSKIPKA----CCVPTELSAISML-YLDENEKVVLKNYQDMVVEGGGG 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   68 LN---PEASASPCCVPQDLEPLTILYYVGRTPKV--EQLSNMVVKSCKC 111
                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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                                                                                                                                                                                                                                                                                                                                                                                                       28;
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                                                                                                                                                                                                                                                                                                                                                       DB 2;
                                                                                                                                                                                                                                                                                                                                                    27.1%; Score 171.5; DB 2 40.7%; Pred. No. 1.4e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 171.5; DB 2 Pred. No. 5.4e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-353 <FRA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               bone morphogenetic protein 2 - chicken (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                       12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   88
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63 RGQSPFTSIKSCCVPSKLRAMSMLYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27.1%;
ilarity 38.5%;
Conservative 18
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Best Local Similarity
Matches 42; Conserv
                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-102 <THO>
C; Superfamily: inhibin
                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Gene: Bmp-2
C;Superfamily: inhibin
                                                                                                                                                                                                                                                                                                                                                                                                       35;
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C:Species: Drosophila melanogaster
C:Accession: A26158
R:Padgett, R.W.; St. Johnston, R.D.; Gelbart, W.M.
Nature 325, 81-84, 1997
A;Title: A transcript from a Drosophila pattern gene predicts a protein homologous to the A; Accession: A26158; MUID:87090408
A; Accession: A26158
A; Molecule type: mRNA
A; Residues: 1-588 <PAD>
A; Residues: 1-588 <PAD>
A; Cross-references: GB:M30116; NID:9157291; PID:9157292
C; Genetics:
A; Gene: FlyBase:Gpp
A; Cross-references: FlyBase:FBgn0000490
C; Keywords: 91ycoprotein
F; 1-15/Domain: signal sequence #status predicted <SIG>F; 1-15/Domain: signal sequence #status predicted
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                                                                                                                                                                                 #sequence_revision 06-Mar-1992 #text_change 24-Nov-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15 CCVRPLYIDFRQDLGW-KWVHEPKGYYANFCSGPC--PYLRSAD-----TTHSTVLGLYN 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    46; Indels
                                                                                                                                              C; Species: Homo sapiens (man)
C; Date: 06-Mar-1992 #text_chang
C; Species: Homo sapiens (man)
C; Date: 06-Mar-1992 #text_chang
C; Accession: C39564
R; Lee, S.J.
Proc. Natl. Acad. Sci. U.S.A. 88, 4250-4254, 1991
A; Title: Expression of growth/differentiation factor 1 in the A; Reference number: A39364; MUID:91239545
A; Accession: C39564
A; Accession: C39564
A; Accession: C39564
A; Accession: C39564
A; Residues: preliminary
A; Molecule type: mRNA
A; Residues: 1-372 - CLEE>
A; Cross-references: GB:M62302; NID:9183050; PID:9183052
C; Superfamily: inhibin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              41; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            67 TLNPEASASPCCVPQDLEPLTILYYVGRTPKV-EQLSNMVVKSCKC 111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27.4%; Score 174; DB 2;
35.8%; Pred. No. 3.2e-10;
ive 17; Mismatches 41.
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35.8%; Pred. No. 8.3e-10;
iive 16; Mismatches 46
                                                                                                                              GDF-1 embryonic growth factor - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 35.88
Matches 39; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      38; Conservative
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Best Local Similarity
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bone morphogenetic protein 4 - fallow deer
C;Species: Dama dama (fallow deer)
C;Species: Dama dama (fallow deer)
C;Date: 15-Feb-1996 #sequence_revision 01-Mar-1996 #text_change 16-Feb-1997
C;Accession: 558791
R;Feng, J.Q.; Chen, D.; Esparza, J.; Harris, M.A.; Mundy, G.R.; Harris, S.E.
A;Title: Deer antler tissue contains two types of bone morphogenetic protein 4 mRNA the A;Reference number: $58791
A;Accession: $58791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C; Species: Rattus norvegicus (Norway rat)
C; Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 16-Jul-1999
C; Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 16-Jul-1999
C; Accession: S38343, #sequence of bone morphogenetic protein 4 cDNA from fetal rat cal A; Title: Cloning and sequence of bone morphogenetic protein 4 cDNA from fetal rat cal A; Reference number: S38343; MUID: 93385158
A; Status: preliminary
                                                                                                                                                                                                 | :|| ||:|| ||:|| ||:|| 302 RKKNKNCRRHSLYVDF-SDVGWNDWIVAPPGYQAFYCHGDCPFPLADHLNS--TNHAIVQ 358
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C;Superfamily: inhibin
                                                                                                                                            9 RNLEENCCVRPLYIDFRQDLGWK-WVHEPKGYYANFCSGPCPY----LRSADTTHSTVL 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9 RNLEENCCVRPLYIDFRQDLGWK-WVHEPKGYYANFCSGPCPY----LRSADTTHSTVL 62
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                                                                                                                                                                                                                                                                                                                                                                                   359 TLVNSVNSSIPKA----CCVPTELSAISML-YLDEYDKVVLKNYQEMVVEGCGC 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 359 TLVNSVNSSIPKA----CCVPTELSAISML-YLDEYDKVVLKNYQEMVVEGGGC 407
                                                                                                                                                                                                                                                                                                                              63 GLYNTLN---PEASASPCCVPQDLEPLTILYYVGRTPKV--EQLSNMVVKSCKC 111
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         Pred. No. 8e-10;
; Mismatches 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2;
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; Pred. No. 8e-10;
17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Score 170.5; DB
; Pred. No. 8e-10;
17; Mismatches
                                           17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  bone morphogenetic protein 4 - rat
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37.78;
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37.7%;
    37.78;
    Best Local Similarity 37.7% Matches 43; Conservative
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Best Local Similarity
Matches 43; Conserv
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Best Local Similarity
Matches 43; Conserv
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A; Residues: 1-408 <CHE>
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A; Residues: 1-408 <FEN>
C; Superfamily: inhibin
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C; Species: Gallus gallus (chicken)

C; Species: Gallus gallus (chicken)

C; Date: 13.5ep-1996 #sequence_revision 13.5ep-1996 #text_change 16-Jul-1999

C; Accession: 150608

R; Francis, P.H.; Richardson, M.K.; Brickell, P.M.; Tickle, C.

Bevelopment 120, 209-218, 1994

A; Title: Bone morphogenetic proteins and a signalling pathway that controls patterning A; Reference number: 150607; MUD:94163974

A; Accession: 150608

A; Astatus: preliminary; translated from GB/EMBL/DDBJ

A; Molecule type: mRNA

A; Residues: 1-405 < FRA>

A; Cross-references: EMBL:X75915; NID:9472929; PIDN:CAA53514.1; PID:9472930

C; Genetics:

A; Genetics:

A; Genetics:

A; Genetics:
A; Genetics:
A; Genetics:
A; Cross-references: EMBL:X75915; NID:9472939; PIDN:CAA53514.1; PID:9472930
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63 GLYNTLN---PEASASPCCVPQDLEPLTILYYVGRTPKV--EQLSNMVVKSCKC 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19;
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                                                                                                                                  Score 171; DB 2; L
Pred. No. 5.1e-11;
0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26.9%; Score 170.5; DB 2; 37.7%; Pred. No. 7.9e-10; ive 18; Mismatches 34;
                                                                                                                                                                                                                                                                                                                                                                     1 ALDINIXFRNLEENXXVRPLYIDFRQDLGWKWVH 34
                                                                                                                                                                                                                                                                                                                         1 ALDINYCFRNLEENCCVRPLYIDFRQDLGWKWVH 34
C; Keywords: growth factor; heterodimer
                                                                                                                                  Query Match 27.0%;
Best Local Similarity 91.2%;
Matches 31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 37.7%
Matches 43; Conservative
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Gaps

8;

Gaps

Length 408;

DB 1;

26.9%; Score 170.5;

Query Match

67

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inhibin beta-B2 chain - African clawed frog (fragment)
C;Species: Xenopus laevis (African clawed frog)
C;Date: 11-3nn-1991 #sequence_revision 11-Jan-1991 #text_change 15-Jun-1996
C;Accession: C36192
R;Thomsen, G.; Woolf, T.; Whitman, M.; Sokol, S.; Vaughan, J.; Vale, W.; Melton, D.A.
Cell 63, 485-493, 1990
A;Title: Activins are expressed early in Xenopus embryogenesis and can induce axial n A;Reference number: A36192; MUID:91029481
A;Accession: C36192
A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual
                                     15 CCVRPLYIDFRQDLGWK-WVHEPKGYYANFCSGPCP-YLR----SADTTHSTVLGLYNT-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Score 169; DB 2;
; Pred. No. 2.6e-10;
15; Mismatches 26
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Pred. No. 1.4e-09;
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38.2%; Pred. No. 1...
"'ve 13; Mismatches
                                                                                                                                                                                        64 GLNP-GTVNSCCIPTKLSTMSMLYF 87
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             68 -LNPEASASPCCVPQDLEPLTILYY 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Experimental source: hippocampus
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40.0%;
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Best Local Similarity 38.2%
Matches 39; Conservative
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Best Local Similarity 40.09
Matches 34; Conservative
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A;Cross-references: GDB:136392
C;Superfamily: inhibin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Superfamily: inhibin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Molecule type: DNA-A;Residues: 1-101 <TF
C;Superfamily: inhibi
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                                                                                  C; Species: Mus musculus (house mouse)
C; Species: Mus musculus (house mouse)
C; Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 16-Jul-1999
C; Accession: 149541; S29523; B34201
R; Feng, J.Q.; Chen, D.; Cooney, A.J.; Tsai, M.; Harris, M.A.; Tsai, S.Y.; Feng, M.; Mund A; Title: The mouse bone morphogenetic protein-4(BMP4) gene: Analysis of promoter utiliza A; Reference number: 149541; MUID:96081880
A; Accession: 149541
A; Statuus: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: GB:L47480; NID:g994733; PIDN:AAC37698.1; PID:g994734
R;Dickinson, M.E.; van der Meer-de Jong, R.; Hogan, B.L.M.
submitted to the EMBL Data Library, December 1990
A;Description: Nucleotide sequence of the mouse Bone Morphogenetic Protein-4 (BMP-4) CDN
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A.Accession: Barbara A.Accession:
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BJ6192
Linhibin beta-Bl chain - African clawed frog (fragment)
C;Species: Xenopus laevis (African clawed frog)
C;Date: 11-Jan-1991 #sequence_revision 11-Jan-1991 #text_change 15-Jun-1996
C;Date: 185192
R;Thomsen, G:; Woolf, T.; Whitman, M.; Sokol, S.; Vaughan, J.; Vale, W.; Melton, D.A.
Cell 63, 485-493, 1990
A;Title: Activins are expressed early in Xenopus embryogenesis and can induce axial me
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A, Status: preliminary; nucleic acid sequence not shown; not compared with conceptual
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                                                            bone morphogenetic protein 4 - mouse
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A; Residues: 253-420 <DI2>
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Best Local Similarity
Matches 35; Conserv
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A; Residues: 1-420 <RES>
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A;Introns: 11/1; 137/1
C;Superfamily: inhibin
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C;Superfamily: inhibin
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C)Accession: A45056
R;Oezkaynak, E.; Schnegelsberg, P.N.; Jin, D.F.; Clifford, G.M.; Warren, F.D.; Drier, J. Biol. Chem. 267, 25220-25227, 1992
A;Title: Osteogenic protein-2. A new member of the transforming growth factor-beta su A;Rcference number: A45056; MUID: 93094231
A;Accession: A45056
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Osteogenic protein 2 precursor - human
N:Alternate names: bone morphogenetic protein 8; OP-2
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 10-Jun_1993 #sequence_revision 18-Nov-1994 #text_change 16-Jul-1999
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                                                                                                                15 CCVRPLYIDFRQDLGWK-WVHEPKGYYANFCSGPCP-YLR----SADTTHSTVLGLYNT- 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: GB:M97016; NID:g189389; PIDN:AAB01360.1; PID:g189390
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9
Length 101;
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                                                        Indels
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C;Genetics:
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C.Species: Mus musculus (house mouse)
C.Species: Mus musculus (house mouse)
C.Date: 06-Mar-1992 #sequence_revision 06-Mar-1992 #text_change 24-Nov-1999
C.Accession: A39364; A35683
R.Lee, S.J.
Proc. Natl. Acad. Sci. U.S.A. 88, 4250-4254, 1991
A;Title: Expression of growth/differentiation factor 1 in the nervous system: conserv A; Reference number: A39364; MUID:91239545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (GDF-1) of the transforming growth factor-b
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C;Species: Mus musculus (house mouse)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 21-Jul-2000
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                                                                                                                                                                                                                                                                                                                    A; Molecule type: mRNA
A; Residues: 1-357 <LEES
A; Cross-references: GB:M62301; NID:g193458; PIDN:AAA37676.1; PID:g193460
R; Lee, S.J.
Mol. Endocrinol, 4, 1034-1040, 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: mRNA
Ksesidues: 1-144, C',146-357 <LE2>
A;Cross-references: GB:M57639; NID:g193456; PIDN:AAA37674.1; PID:g193457
C;Superfamily: inhibin
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R; Kurihara, T.; Kitamura, K.; Takaoka, K.; Nakazato, H.
Biochem. Biophys. Res. Commun. 192, 1049-1056, 1993
A; Title: Murine bone morphogenetic protein-4 gene: existence A; Reference number: JH0801; MUID: 93282803
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C;Species: Mus musculus (house mouse)
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35.5%; Pred. No. 2.8e-09;
iive 17; Mismatches 41
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Best Local Similarity 37.5%; Pred. No. 4.1e-09;
Matches 42; Conservative 17; Mismatches 34
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Best Local Similarity
Matches 38; Conserva
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A; Residues: 1-408 <KUR>
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C; Superfamily: int
C; Keywords: bone
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                                                                                                                                                   Applications of the protein 4 - African clawed frog
None morphogenetic protein 4 - African clawed frog
None morphogenetic protein 4 - African clawed frog
Species: Xenopus laevis (African clawed frog)
C;Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 16-Jul-1999
C;Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 16-Jul-1999
C;Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 16-Jul-1999
C;Development Apply
R;Dale: L; Howes, G; Price, B.M; Smith, J.C.
Development 115, 573-585, 1992
A;Title: Bone morphogenetic protein 4: a ventralizing factor in early Xenopus development A;Recession: A49147; MUID:93048819
A;Title: Bone morphogenetic protein 4: a ventralizing factor in early Xenopus development A;Recession: A49147; MUID:93048819
A;Title: Bone morphogenetic acid
A;Molecule type: nucleic acid
A;Molecule type: nucleic acid
A;Recession: A49147
A;Cross-references: GB:X64538; GB:S46999; NID:g64589; PIDN:CAA45836.1; PID:g64590
A;Cross-references: GB:X64538; GB:S46999; NID:g64589; NID:g64590; A;Experimental source: XTC cells
A;Note: sequence extracted from NCBI backbone (NCBIN:117127, NCBIP:117128)
C;Superfamily: inhibin
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JH0689
JH0689
Done morphogenetic protein 4 precursor - African clawed frog
C; Species: Kenopus laevis (African clawed frog)
C; Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Jul-1999
C; Accession: JH0689
R; Nishimatsu, S.; Suzuki, A.; Shoda, A.; Murakami, K.; Ueno, N.
Biochem. Biophys. Res. Commun. 186, 1487-1495, 1992
A; Title: Genes for bone morphogenetic proteins are differentially transcribed in early A; Reference number: JH0687; MUD:92378616
A; Residues: 1-401 KNIS>
A; Molecule type: mRNA
A; Residues: 1-401 KNIS>
A; Cross-references: GB:X63426; NID:964587; PIDN:CAA45020.1; PID:964588
A; Cross-references: cocyte
C; Superfamily: inhibin
C; Keywords: 91ycoprotein
C; Keywords: 91ycoprotein
F; 288-401/Product: bone morphogenetic protein 4 #status' predicted <MAT>
F; 141,204,238,343,358/Binding site: carbohydrate (Asn) (covalent) #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                         360 NAVPKACCAPTKLSATSVLYYDSSNNVILRKHRNMVVKACGC 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26.1%; Score 165.5; DB 2; 36.8%; Pred. No. 2.5e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26.1%; Score 165.5; DB 2 36.8%; Pred. No. 2.5e-09; iive 18; Mismatches 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 26.1%;
Best Local Similarity 36.8%;
Matches 42; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best_Local Similarity
Matches 42; Conserv
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Gaps

Query Match

295

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RESULT A39364

9

Gaps

Best Loca Matches

59

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C.Keywords: bone; glycoprotein
F:1-22/Domain: signal sequence #status predicted <SIG>
F:23-345/Domain: propeptide #status predicted <PRO>
F:346-472/Product: bone morphogenetic protein 3 #status predicted <MAT>
F:117,141,175,220,463/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C; Species: Rattus sp. (rat)
C; Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 16-Jul-1999
C; Accession: 153032
C; Accession: 153032
DNA Cell Biol. 14, 235-239, 1995
A; Title: Sequence and expression of bone morphogenetic protein 3 mRNA in prolonged A; Reference number: 153032; MUID: 95186061
A; Reference number: 153032
A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Homo sapiens (man)
C;Date: 16-Sep-1992 #sequence_revision 03-Aug-1995 #text_change 18-Jun-1999
C;Accession: D37278
R;Wozney, J.M.; Rosen, V.; Celeste, A.J.; Mitsock, L.M.; Whitters, M.J.; Kriz,
Science 242, 1528-1534, 1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Title: Novel regulators of bone formation: molecular clones and activities. A;Reference number: A37278; MUID:89072730
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               264 CGGALNGOCCKESFYVSFKA-LGWDDWIIAPRGYFANYCRGDCTGSFRTPDTFQTFHAHF 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14 NCCVRPLYIDFRQDLGW-KWVHEPKGYYANFCSGPC--PYLRS-ADTTHSTVLGLYNTLN 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Molecule type: mRNA
Xsesidues: 1-472 <WO4>
A;Cross-references: GB:M22491; NID:g179505; PIDN:AAA51836.1; PID:g179506
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                        7 CFRNLEENCCVRPLYIDFRQDLGW-KWVHEPKGYYANFCSGPCP-YLRSAD---TTHSTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15;
                                                                                                                                                                                                                                                                                                      9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 472;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           323 IEEYRKMGLMNGMRPCCAPIKFSSMSLIYYGDDGIIKRDLPKMVVDECGC 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62 IGLYNTLNPEASASPCCVPQDLEPLTILYYVGRTPKVEQLSNMVVKSCKC 111
                                                                                                                                                                                                                                                 Length 373;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         70 ----PEASASPCCVPQDLEPLTILYY-VGRTPKVEQLSNMVVKSCKC 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 158.5; DB 1;
Pred. No. 1.5e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   35;
                                                                                                                                                                                                                                              Score 159; DB 2;
Pred. No. 1.1e-08;
                                                                                                                                                                                                                                                                                                      14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          bone morphogenetic protein 3 precursor - human N;Alternate names: osteogenin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 bone morphogenetic protein 3 - rat (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: GDB:125206; OMIM:112263
A;Map position: 4p14-4q21
C;Superfamily: inhibin
                                                                   A;Cross-references: FlyBase:FBgn0024913
A;Start codon: GGT
A;Introns: 86/3
C;Superfamily: inhibin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25.0%;
34.3%;
                                                                                                                                                                                                                                              25.1%;
ilarity 31.8%;
Conservative 1
                 A; Cross-references: GB: AF054822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   37; Conservative
                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 35; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Accession: D37278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Gene: GDB: BMP3
                                            C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      transforming growth factor beta homolog Vgr-2 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 10-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 24-Nov-1999
C;Accession: A45402
R;Jones, C.M.; Simon-Chazottes, D.; Guenet, J.L.; Hogan, B.L.
R;Jones, C.M.; Simon-Chazottes, D.; Guenet, J.L.; Hogan, B.L.
A;Title: Isolation of Vgr-2, a novel member of the transforming growth factor-beta-relat
A;Reference number: A45402; MUID:93125570
                                                                                                                        the transforming growth factor-beta superfa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    activin - fruit fly (Drosophila sp.) (fragment)
C;Species: Drosophila sp.
C;Species: Drosophila sp.
C;Date: 18-Jun-1998 #sequence_revision 10-Jul-1998 #text_change 17-Nov-2000
C;Accession: PW0042
B;Kutty, G.; Kutty, R.K.; Samuel, W.; Duncan, T.; Jaworski, C.; Wiggert, B.
Biochem. Biophys. Res. Commun. 246, 644-649, 1998
A;Title: Identification of a new member of transforming growth factor-beta superfamily A;Reference number: PW0042; MUID: 98289585
A;Accession: PW0042
A;Molecule type: mRNA
A;Residues: 1-373 < KUT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7;
03-May-1994 #sequence_revision 03-May-1994 #text_change 24-Nov-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             264 NFCHRH------QLFINF-QDLGWHKWVIAPKGFMANYCHGECPFSMTTYLNSSN--Y 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NYCFRNLEENCCVRPLYIDFRQDLGW-KWVHEPKGYYANFCSGPCP----YLRSADITH 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NYCFRNLEENCCVRPLYIDFRQDLGW-KWVHEPKGYYANFCSGPCP----YLRSADTTH 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A Status: preliminary; not compared with conceptual translation A. Molecule type: nucleic acid A. Molecule type: nucleic acid A. Residues: 1-366 < JONN>
A. Cross-references: GB: S52658; NID: 9263309; PIDN: AAB24876.1; PID: 9263310
A. Kraperimental source: embryo
A. Note: sequence extracted from NCBI backbone (NCBIP: 122197)
C. Superfamily: inhibin
                                                                                                                                                                                                                                                                                          A;Cross-references: GB:L06443; NID:g293346; PIDN:AAA53034.1; PID:g567205
C;Superfamily: inhibin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          313 AFWQALMHMADPKVPKA-VCVPTKLSPISMLYQDSDKNVILRHYEDMVVDECGC 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STVLGLYNTLNPEASASPCCVPQDLEPLTILYY - VGRTPKVEQLSNMVVKSCKC 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STVLGLYNTLNPEASASPCCVPQDLEPLTILYY-VGRTPKVEQLSNMVVKSCKC 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19;
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                                                                                                                                                                                                                                                                                                                                                                                                                Length 366;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 2; Length 366;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25.3%; Score 160.5; DB 2; Length 3 35.1%; Pred. No. 7.4e-09; ive 20; Mismatches 35; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     34;
                                                                                                                                                                                                                                                                                                                                                                                                             25.6%; Score 162.5; DB 2; 35.1%; Pred. No. 4.6e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               21; Mismatches
                                                                                                                        oţ
C; Date: 03-May-1994 #sequence_revision 03-
C; Accession: A46607
R; McPherron, A.C.; Lee, S.J.
J. Biol. Chem. 268, 3444-3449, 1993
A; Title: GDF-3 and GDF-9: two new members
A; Reference number: A46607; MUID:93155193
A; Accession: A46607
A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 35.1%
Matches 40; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                     A; Molecule type: mRNA
A; Residues: 1-366 <MCP>
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R.W.;

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Gaps

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27 Page 5;

Gaps

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Table beta homolog ds1-1 - chicken
C;Species: Gallus gallus (chicken)
C;Species: Gallus gallus (chicken)
C;Species: Gallus gallus (chicken)
C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jul-2000
C;Accession: A40735
R;Basler, K.; Edlund, T.; Jessell, T.M.; Yamada, T.
C;Accession: A40735
A;Title: Control of cell pattern in the neural tube: regulation of cell differentiati
A;Reference number: A40735, MUID:93272310
A;Accession: A40735
A;Accessio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Jacobial transforming growth factor-beta homolog - human C; Species: Homo sapiens (man) C; Species: Homo sapiens (man) C; Species: Homo sapiens (man) C; Date: 20-Nov-1997 #sequence_revision 20-Nov-1997 #text_change 17-Mar-1999 C; Accession: JC5697 W.; Saeki, M.; Sekine, S.; Kato, S. J. Biochem. 122, 622-626, 1997 A; Title: Human cDNA encoding a novel TGF-beta superfamily protein highly expressed in A; Reference number: JC5697; MUID:98006316
                                                                                                                                                                                                                                                                                                                                                                                       260 NENERCORKGLYVDF-DILGWKQWVIAPEGFSAFYCSGDCSAPFSKEMNATSHAIVQSTL 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10 NLEENCCVRPLYIDFRQDLGWK-WVHEPKGYYANFCSGPC--PYLRSAD-TTHSTVLGLY 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9 RNLEENCCVR-PLYIDFRQDLGW-KWVHEPKGYYANFCSGPCPYLRSADTT---HSTVLG 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26 ODLGW-KWVHEPKGYYANFCSGPCPYLRSADTTHSTVLGLYNTLNPEASASPCCVPQDLE 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 309;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22.1%; Score 140; DB 2; Length 427; 31.8%; Pred. No. 1.1e-06; Live 21; Mismatches 46; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      64 LYNTLNPEASASPCCVPQDLEPLTILYY - - VGRTPKVEQLSNMVVKSCKC 111
                                                                                                                                                              Length 366
                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 319 HRVRPUSTIPAKCAPSSLGSYKILFVDQNKQVQIKRYRDMVVDECGC 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  66 NTLNPEASASPCCVPQDLEPLTILYY-VGRTPKVEQLSNMVVKSCKC 111
                                                                                                                                                                                                                                     45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21.4%; Score 135.5; DB 2; 27.6%; Pred. No. 2.2e-06; tive 15; Mismatches 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Comment: This protein plays a role in reproduction
                                                                                                                                                          Query Match 23.3%; Score 148; DB 2; Best Local Similarity 32.7%; Pred. No. 1.4e-07; Matches 35; Conservative 21; Mismatches 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             fibrosarcoma
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A;Residues: 1-309 <YOK>
A;Cross-references: DDBJ-AB000584
A;Experimental source: fibrosarcon
C;Comment: This protein plays a rc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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Matches 35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
   A;Note: F39G3.8
C;Superfamily: inhibin
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C.Date: 15-Oct_1999 #sequence_revision 15-Oct-1999 #text_change 17-Mar-2000
                                                                                                                                                                                                                                                                                                                                                                                                                          248 KGCCLYDLEIEF-EKIGWDWIVAPPRYNAYMCRGDCHYNAHHFNLAETGHSKIMRAAHKV 306
                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11; Gaps
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A;Molecule type: mRNA
A;Residues: 1-360 <RES>
A;Cross-references: GB:S77492; NID:g957225; PIDN:AAB33725.1; PID:g957226
C;Superfamily: inhibin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R; Bentley, D. 123431.
R; Bentley, D. 2000.
Submitted to the EMBL Data Library, December 1996
A; Description: The sequence of C. elegans, cosmid B0412.
A; Reference number: 220037
A; Accession: T25451
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Molecule type: DNA
A; Cross-references: EMBL: U80953; PIDN: AAB52554.1; GSPDB:GN00021
A; Experimental source: strain Bristol N2; clone B0412,
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    316 VVSGIPE----PCCVPEKMSSLSILFFDENKNVVLKVYPNMTVDSCAC 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         70 ----PEASASPCCVPQDLEPLTILYY-VGRTPKVEQLSNMVVKSCKC 111
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                                                                                                                                                                                                                             24.7%; Score 156.5; DB 2; 34.3%; Pred. No. 1.9e-08; iive 20; Mismatches 36;
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A; Introns: 43/3; 123/3; 184/2; 288/3
C; Superfamily: inhibin
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Best Local Similarity 34.3%
Matches 37; Conservative
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Done morphogenetic protein-3b precursor [similarity] - human
N.Alternate names: BMP-3b; GDF-10
S.Alternate names: BMP-3b; GDF-10
S.Species: Homo sapiens (man)
C.Species: Takeshita, N.; Konno, Y.; Nishizawa, T.; Matsuo, H.; Kangawa,
Biochem. Biophys. Res. Commun. 223, 304-310, 1996
A.Title: CDNA clouing and genomic structure of human bone morphogenetic protein-3b (B
A.Reference number: JC4838; MJID:96264636
A.Contents: femur
A.Accession: JC4838
A.Molecule type: mRNA
A.Residues: 1-478 <HIN>
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C;Comment: This protein induces endochondral bone formation, chemotaxis of monocytes,
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15 CCVRPLYIDFRQDLGW-KWVHEPKGYYANFCSGPCPY----LRSADTTHSTVLGLYNTL 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         F:1-33/Domain: signal sequence #status predicted <SIG>
F:34-368/Domain: propeptide #status predicted <PRO>
F:369-478/Product: bone morphogenetic protein-3b #status predicted <MAT>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21.1%; Score 133.5; DB 2; 30.3%; Pred. No. 5.5e-06; tive 21; Mismatches 36;
            | | :||::|| :|| 320 CAPVKTKPLSMLYVDNGRVLLEHKDMIVEEGG 353
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Best Local Similarity 30.3
Matches 33; Conservative
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C; Keywords: bone
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Done morphogenetic protein-3b precursor - rat

C.$Peciess: Rattus norvegicus (Norway rat)
C.$Peciess: Rattus norvegicus (Norway rat)
C.$Accession: JC4646

R.Takao, M.; Hino, J.; Takeshita, N.; Konno, Y.; Nishizawa, T.; Matsuo, H.; Kangawa, K.
Biochem. Biophys. Res. Commun. 219, 656-662, 1996
A;Title: Identification of rat bone morphogenetic protein-3b (BMP-3b), a new member of E
A;Reference number: JC4646; MuID:96193707
A;Accession: JC4646
A;Molecule type: mRNA
A;Residues: 1-476 <ARK>
A;Cross.references: DDBJ:D49494; NID:9699625; PIDN:BAA08454.1; PID:9699626
A;Experimental source: femur
C;Comment: This protein plays a role in the central nervous system as well as in new bor acellular matrix.
C;Superfamily: inhibin
C;Keywords: bone: glycoprotein
F;1-29/Domain: signal sequence #status predicted <SIG>F;30-366/Domain: propeptide #status predicted <SIG>F;30-476/Product: bone morphogenetic protein-3b #status predicted
F;14,152,277,467/Binding site: carbohydrate (Asn) (covalent) #status predicted
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Cispecies: Mus musculus (house mouse)
Cispecies: Mus musculus (house mouse)
Ciscession: S29718
Rizhou, X.; Sasaki, H.; Lowe, L.; Hogan, B.L.M.; Kuehn, M.R.
Rizhou, X.; Sasaki, H.; Lowe, L.; Hogan, B.L.M.; Kuehn, M.R.
A;Title: Nodal is a novel TGF-beta-like gene expressed in the mouse node dur A;Reference number: S29718; MUID:93156841
A;Reference number: S29718
A;Reference number: S29718
A;Reference number: S29718
A;Reference number: S29718
C;Supecule: 1-354 <ZHO>
A;Residues: 1-354 <ZHO>
A;Residues: 1-354 <ZHO>
A;Cross-references: EMBL:X70514; NID:926632074; FIDN:CAA49914.1; PID:9296605
C;Superfamily: inhibin
222 EDLGWADWVLSPREVQVTWCIGACPSQFRAANMHAQIKTSLHRLKPDTVPAPCCVPASYN 281
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IHBA_BOVIN
IHBA_HUMAN
60A_DROWI
60A_DROWI
IHBB_CHICK
IHBA_CHICK
BMP7_HUMAN
BMP7_HUMAN
                                                                             DVR1_BRARE
IHBA_SHEEP
GDFB_MOUSE
GDFB_HUMAN
GDF8_BOVIN
IHBA_MOUSE
IHBA_PIG
                                                                                                                                                                                                                                                                                                                                                                                                                       GDFB_RAT
BMP7_MOUSE
BMP2_RAT
                                             GDF8_MOUSE
GDF8_RAT
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IHBB_HUMAN
IHBB_BOVIN
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BMP2_RABIT
BMP2_DAMDA
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BMP5_MOUSE
BMP5_HUMAN
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BM8B_MOUSE
BMP4_CHICK
BMP4_DAMDA
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GDF5_HUMAN
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IHBC_HUMAN
IHBC_MOUSE
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GDF6_BOVIN
BM10_HUMAN
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BM8A_MOUSE
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GDF3_HUMAN
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             GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
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Maximum Match 100%
Listing first 100 summaries
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TGF2_PIG
TGF2_MOUSE
TGF1_MOUSE
TGF1_MOUSE
TGF1_RAT
TGF1_RAT
                                                                                                         October 30, 2001, 08:52:36
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TGF1_CHICK
TGF1_XENLA
GDF8_BRARE
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CHICK
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GDF8_CHICK
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Result

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299 ALDTNYCFRNLEENCCVRPLYIDFRQDLGWKWVHEPKGYYANFCSGPCPYLRSADTTHST 358

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                                                                                                                                                                                             Miller D.A., Lee A., Matsui Y., Chen E.Y., Moses H.L., Derynck R.; "Complementary DNA cloning of the murine transforming growth factor-beta 3 (TGF beta 3) precursor and the comparative expression of TGF beta 3 and TGF beta 1 messenger RNA in murine embryos and
                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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N-LINKED (GLCNAC. .) (POTENTIAL).

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                                                                                                                                                                                                                                                                                                          MEDLINE=91000714; PubMed=2206556;
Denhez F., Lafyatis R., Kondaiah P., Roberts A.B., Sporn M.B.;
"Cloning by polymerase chain reaction of a new mouse TGF-beta,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (POTENTIAL)
                        01-ANG-1990 (Rel. 15, Created)
01-ANG-1990 (Rel. 15, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
TRANSFORMING GROWTH FACTOR BETA 3 PRECURSOR (TGF-BETA 3)
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CELL ATTACHMENT SITE (POT
250F7048CA432BD6 CRC64;
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Pfam; PF00688; TGFD_propeptide; 1.
PRINTS; PR00438; GFCYSKNOT.
PROSITE; PS00250; TGF_BETA_1; 1.
Growth factor; Mitogen; Glycoprotein; Signal.
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  PRT;
                                                                                                                                                                                MEDLINE-90190650; PubMed-2628730;
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MGD; MGI:98727; Tgfb3.
InterPro; IPR001111; .
InterPro; IPR001839; -.
InterPro; IPR001809; -.
 STANDARD;
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PIR; A61039; A61039.
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TGF3_MOUSE
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the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=88263019; PubMed=3164476; MEDLINE=88263019; PubMed=3164476; ten Dijke P., Hansen P., Iwata K., Pieler C., Foulkes J.G.; "Identification of another member of the transforming growth factor type beta gene family.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "The crystal structure of TGF-beta 3 and comparison to TGF-beta 2: implications for receptor binding."; protein Sci. 5:1251-1271(1996).
-!- SUBUNIT: HOMODIMER, DISULETDE-LINKED.
-!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 301-412.
MEDLINE=96416253; PubMed=8819159;
Mittl P.R., Priestle J.P., Cox D.A., McMaster G., Cerletti N.,
Grutter M.G.;
TRANSFORMING GROWTH FACTOR BETA 3 PRECURSOR (TGF-BETA 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Proc. Natl. Acad. Sci. U.S.A. 85:4715-4719(1988).
                                                                                                                                                                                                                                                                                                                                   (Rel. 11, Last sequence update) (Rel. 38, Last annotation update)
                                                                                                                                                                                                                                         412 AA
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EMBL, X1449; CAA33362.1; -...
EMBL, X14885; CAA33024.1; ATL_INIT.
EMBL, X14886; CAA33024.1; JOINED.
EMBL, X14889; CAA33024.1; JOINED.
EMBL, X14889; CAA33024.1; JOINED.
EMBL, X14899; CAA33024.1; JOINED.
EMBL, X14891; CAA33024.1; JOINED.
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PF00688; TGFb_propeptide; 1.
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                                                                                                                                                                                                                                                                                                  01-JUL-1989 (Rel. 11, Created)
                                                                                                                                                                                                                                      STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human).
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1TGK; 12-MAR-97.
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190230;
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P10600;
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15-JUL-1999
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Gaps

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Score 633; DB 1; Length 410;

99.88;

Best Local Similarity 100. Matches 112; Conservative

Query Match

Pred. No. 1.6e-60;

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                                                                                                                                                                                                                                                                               Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                             Gaps
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N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
CELL ATTACHMENT SITE (POTENTIAL).
3CAD3548D3AEA178 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Cloning and expression of glucocorticoid-induced genes in fetal lung fibroblasts. Transforming growth factor-beta 3.";
J. Biol. Chem. 270:2722-2728(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN-WISTAR; TISSUE-Lung;
MEDLINE-95155340; PubMed-7852342;
Wang J., Kuliszewski M., Yee W., Sedlackova L., Xu J., Tseu I.,
Post M.;
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                                                          TRANSFORMING GROWTH FACTOR BETA 3.
                                                                                                                                                                                                                                                                                                                  61 VLGLYNTLNPEASASPCCVPQDLEPLTILYYVGRTPKVEQLSNMVVKSCKCS 112
                                                                                                                                                                                                                                                                                                                              361 VLGLYNTLNPEASASPCCVPQDLEPLTLYYVGRTPKVEQLSNMVVKSCKCS 412
                                                                                                                                                                                                                  99.8%; Score 633; DB 1; Length 412; 100.0%; Pred. No. 1.6e-60; ive 0; Mismatches 0; Indels
                     Growth factor; Mitogen; Glycoprotein; Signal; 3D-structure. 20 PROPEP 2 30 CHAIN 301 412 TRANSFORMING GROWTH FACTOR BET DISCULEID 316 TRANSFORMING GROWTH FACTOR BET DISCULLID 314 409
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"A role for TGF-beta in oligodendrocyte differentiation.";
Cell Biol. 121:1397-1407(1993).
-1- SUBUNIT: HOMODIMER, DISULFIDE-LINKED.
-1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                      01-FEB-1996 (Rel. 33, Last sequence update)
115-JUL-1999 (Rel. 38, Last annotation update)
TRANSFORMING GROWTH FACTOR BETA 3 PRECURSOR (TGF-BETA 3).
TGFB3 OR TGF-8
                                                                                                                    INTERCHAIN (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 159-213 FROM N.A. MEDLINE-93286190; Pubmed-8509457;
PRINTS; PR00438; GFCYSKNOT.
PROSITE; PS00250; TGF_BETA_1; 1.
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                                                                                                                                                                                 47328 MW;
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                                                                                                                                                                                                                                         Matches 112; Conservative
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412 AA;
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Q07258;
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Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 ALDINYCFRNLEENCCVRPLYIDFRQDLGWKWVHEPKGYYANFCSGPCPYLRSADTIHST
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N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

CELL ATTACHMENT SITE (POTENTIAL).
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Burt D.W., Dey B.R., Paton I.R.;
"Comparative analysis of human and chicken transforming growth
factor-beta 2 and -beta 3 promoters.";
J. Mol. Endocrinol. 7:175-183(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 412;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
TRANSFORMING GROWTH FACTOR BETA 3 PRECURSOR (TGF-BETA 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
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Santa-Coloma T.A., Cubert J., Sporn M.B., Roberts A.B.;
                                                                                                                                                                                                                                                                                                                                                                                                                  24FD7D899090AA9D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99.4%; Score 630; DB 1;
99.1%; Pred. No. 3.3e-60;
ive 1; Mismatches 0;
                                                                                                                                                                    Signal
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             HSSP, P10600, 17cK.
InterPor IPR001111; -.
InterPor IPR001111; -.
InterPor IPR001819; -.
Pfam: PF00019; TGF-beta; 1.
Pfam: PF00688; TGFD-propeptide; 1.
PRINTS; PR00438; GFCYSKNOT.
PROSTIE; PS00250; TGF_BETA_1: 1.
Growth factor; Mitogen; Glycoprotein; Sig
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S36042; S36042.
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412 AA;
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P16047;
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TGF2_CHICK
ID TGF2_CHICK
AC P30371;
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                                                                                                                                                                                                         between the Swiss Institute of Bloinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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INTERCHAIN (BY SIMILARITY).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

GELL ATTACHMENT SITE (POTENTIAL).

GELL ATTACHMENT SITE (POTENTIAL).

GR. E152E6B79D3F30F7 CRC64;
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"Identification and characterization of the chicken transforming
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TRANSFORMING GROWTH FACTOR BETA 3.
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P15503;
01-APR-1990 (Rel. 14, Created)
01-APR-11990 (Rel. 14, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
TRANSFORMING GROWTH FACTOR BETA 3 PRECURSOR (TGF-BETA 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99.2%; Score 629; DB 1;
99.1%; Pred. No. 4.2e-60;
iive 1; Mismatches 0;
                        th factor-beta 3 promoter.";
Endocrinol. 6:1285-1298(1992).
SUBUNIT: HOMODIMER, DISULFIDE-LINKED.
SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPRUUZ4UU,
PEām; PRO0019; TGF-beta; 1.
Pfam; PRO0688; TGFP_propeptide; 1.
PRINTS; PRO0438; GFCYSKNOT.
PROSITE; PSO0250; TGF_BETA_1; 1.
Growth factor; Mitogen; Glycoprotein; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Ovary;
MEDLINE-89091120; PubMed<sub>1</sub>3208746;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MW.
                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; M31154; AAA49089.1; -. EMBL; X58127; CAA41128.1; -. EMBL; X60055; CAA42653.1; -. EMBL; S46000; AAB23575.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Interpro; IPR001111; -. Interpro; IPR001839; -. Interpro; IPR002400; -.
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412
316
378
409
411
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HSSP; P10600; 1TGK.
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    412 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sus scrofa (Pig)
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Matches 111;
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PROPEP
CHAIN
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TD TGF3_AC
DT TOF3
AC
DT 01-AI
DT 15-JT
DE TRANK
GN TGFB:
OC EUKA:
OC MARMING

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           298 ALDINYCFRNLEENCCVRPLYIDFRQDLGWKWYHEPKGYYANFCSGPCPYLKSADTTHSS 357
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TRANSFORMING GROWTH FACTOR BETA 3.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
INTERCHAIN (BY SIMILARITY).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
CELL ATTACHMENT SITE (POTENTIAL).
GELL ATTACHMENT SITE (POTENTIAL).
GM: B4900235B5CC955E CRC64;
Derynck R., Lindquist B., Lee A., Wen D., Tamm J., Graycar J.L. Rhee L., Mason A.J., Miller D.A., Coffey R.J., Moses H.L., Chen E.Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
0
                                                               "A new type of transforming growth factor-beta, TGF-beta 3.";
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Pred. No. 3e-59;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-APR-1993 (Rel. 25, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
TRANSFORMING GROWTH FACTOR BETA 2 PRECURSOR (TGF-BETA 2).
                                                                                                 -: SUBUNIT: HOMODIMER, DISULFIDE-LINKED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Growth factor; Mitogen; Glycoprotein; Signal. SIGNAL
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                                                                                                                                                                                                                                                                                                                           EMBL; X14150; CAA32363.1; -. PIR; S01825; S01825. HSSP: P10600; 1TGK. InterPro; IPR001111; -. InterPro; IPR001839; -. InterPro; IPR002400; -. Pfam; PF00688; TGF_beta; 1. PRm; PR00488; TGF_beta; 1. PRm; PR00488; TGF_betoptide; 1. PRm; PR00488; GFCYSKNOT. PROSITE; PS00250; TGF_BETA_1; 1.
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SEQUENCE FROM N.A.
STRAIN-WHITE LEGHORN, TISSUE-BLOOD;
MEDLINE-92075163; Pubmed-1683775;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last seq
15-JUL-1999 (Rel. 38, Last anno
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98.2%;
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Best Local Similarity 98.2
Matches 110; Conservative
                                                                                  7:3737-3743(1988)
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259
409 /
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298
304
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341
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-!- SUBGUITT: HOWODIMEN, DISULFIDE-LINKED. HETERODIMERS OF TGF-BETA 1/2
AND OF TGF-BETA 2/3 HAVE BEEN FOUND IN BONE.
-!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
PIR, S15389, S15389.
HSSP, P08112; 1TFG.
InterPro; IPR01839; .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=92129307; PubMed=1733936;
Ogawa Y., Schmidt D.K., Dasch J.R., Chang R.J., Glaser C.B.;
"Purification and characterization of transforming growth factor-beta
2.3 and -beta 1.2 heterodimers from bovine bone.";
J. Biol. Chem. 267:2355-2328(1992).
-!- FUNCTION: TGP-BETA 2 HAS SUPPRESSIVE EFFECTS ON INTERLEUKIN-2
DEPENDENT T-CELL GROWTH.
                                                                                                                 Jin Y., Cox D.A., Knecht R., Raschdorf F., Cerletti N.;
"Separation, purification, and sequence identification of TGF-beta 1 and TGF-beta 2 from bovine milk.";
J. Protein Chem. 10:655-75(1991).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cox D.A., David A., Buerk R.R.; "Isolation and characterisation of milk growth factor, a transforming-growth-factor-beta 2-related polypeptide, from bovine
                                                                                                                                                                                                                                                                                                                                                                               "Cartilage-inducing factor-B is a unique protein structurally and functionally related to transforming growth factor-beta."; J. Biol. Chem. 262:1946-1949(1987).
                                                                                                                                                                                                                                                                                                       MEDLINE-87137406; PubMed-3469199;
Seyedin S.M., Segarini P.R., Rosen D.M., Thompson A.Y., Bentz H.,
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79.5%; Pred. No. 1.3e-50;
tive 14; Mismatches 9; Indels
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5142C7432C4EBC1C CRC64;
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BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=91224126; PubMed=2026157;
                                                                                        MEDLINE-92189724; PubMed-1799413;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRINTS; PR00438; GFCYSKNOT.
PROSITE; PS00250; TGF_BETA_1; 1.
Growth factor; Mitogen; Milk.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TGF2_HUMAN STANDARD;
P08112; Q15581;
01-AUG-1988 (Rel. 08, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12719 MW;
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78
109
111
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 1-19.
                                                                                                                                                                                                                                                     SEQUENCE OF 1-30.
                                                               TISSUE=Milk;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE-Milk;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE-Bone;
                                                                                                                                                                                                                                                                                                                                                               Graycar J.;
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                                      SEQUENCE
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ID TGF2_HU
AC P08112
DT 01-AUG
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                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Burt D.W., Paton I.R.;
"Molecular cloning and primary structure of the chicken transforming growth factor-beta 2 gene.";
DNA Cell Biol. 10:723-734(1991).
-I- FUNCTION: TGF-BETA 2 HAS SUPPRESSIVE EFFECTS ON INTERLEUKIN-2 DEPENDENT T-CELL GROWTH.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-WAY-1991 (Rel. 18, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
TRANSFORMING GROWTH FACTOR BETA 2 (TGF-BETA 2) (MILK GROWTH FACTOR)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bos taurus (Bovine).
Sukaryota Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinne; Bos.
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N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 412;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    93E759BF1BD958DC CRC64;
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79.5%; Pred. No. 1.9e-50;
Live 15; Mismatches 8;
                                                                                                                                                             SUBUNIT: HOMODIMER, DISULFIDE-LINKED.
SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
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EMBL; X59081; CAA41101.1; JOINED.
BMEL; X59080; CAA41101.1; JOINED.
PIR; A39489; A39489.
HSSP; PO8112; 1TFG.
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Matches 89; Conservative
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412 AA;
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CARBOHYD

CARBOHYD CARBOHYD SEQUENCE

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de Martin R., Haendler B., Hofer-Warbinek R., Gaugitsch H., Wrann M., Schluesener H., Seifert J.M., Bodmer S., Fontana A., Hofer E.; "Complementary DNA for human glioblastoma-derived T cell suppressor factor." a novel member of the transforming growth factor-beta gene family.";
01-AUG-1988 (Rel. 08, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
TRANSFORMING GROWTH FACTOR BETA 2 PRECURSOR (TGF-BETA 2)
(GLIOBLASTOMA-DERIVED T-CELL SUPPRESSOR FACTOR) (G-TSF) (BSC-1 CELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Daopin S., Piez K.A., Ogawa Y., Davies D.R.; "Crystal structure of transforming growth factor-beta 2: an unusual fold for the superfamily.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Amino acid sequence of the BSC-1 cell growth inhibitor (polyergin) deduced from the nucleotide sequence of the cDNA.";
Proc. Natl. Acad. Sci. U.S.A. 85:79-82(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SPECIES-Human; TISSUE-Lung; MEDLINE-22110032; PubMed-1764261; Noma T., Glick A.B., Geiser A.G., O'Reilly M.A., Miller J., Roberts A.B., Sporn M.B.; "Molecular cloning and structure of the human transforming growth
                                                                                                     Homo sapiens (Human), and Cercopithecus aethiops (Green monkey) (Grivet).

Carcopithecus aethiops (Green monkey) (Grivet).

Mananja; Metacos; Chordate, Craniata; Vertebrate; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SPECIES-Human;
MEDLINE-87308213; PubMed-3476488;
Marquardt H., Lioubin M.N., Ikeda T.;
"Complete amino acid sequence of human transforming growth factor type beta 2.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=92350287; PubMed=1641027;
Schlunegger M.P., Gruetter M.G.;
"An unusual feature revealed by the crystal structure at 2.2-A
resolution of human transforming growth factor-beta 2.";
Nature 358:430-434(1992).
-!- FUNCTION: TGF-BETA 2 HAS SUPPRESSIVE EFFECTS ON INTERLEUKIN-2
DEPENDENT T-CELL GROWTH.
                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDINE-BRANCH TO THE WEAP TO THE WARDING H., Ikeda T., Madisen L., Webb N.R., Rose T.M., Marquardt H., Ikeda T., Twardzik D.R., Seyedin S., Purchio A.F.; "Transforming growth factor-beta 2: cDNA cloning and sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SPECIES-C.aethiops;
MEDLINE-88124824; PubMed-3277172;
Hanks S., Armour R., Baldwin J.H., Maldonado F., Spiess J.,
                                                                         GROWTH INHIBITOR) (POLYERGIN) (CETERMIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS).
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                                                                                                                                                                                                                                         SPECIES-Human;
MEDLINE-88111555; PubMed-3322813;
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Growth Factors 4:247-255(1991).
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-!- SUBUNIT: HOMODIMER, DISULFIDE-LINKED

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PRINTS; PR00438; GFCYSKNOT.
PROSITE; PS00250; TGF\_BETA\_1; 1.
Growth factor; Mitogen; Glycoprotein; Signal; 3D-structure. 9; Indels 7D9D569E0F4A07D0 CRC64; N-LINKED (GLCNAC. ..)
N-LINKED (GLCNAC. ..)
N-LINKED (GLCNAC. ..)
F -> L (IN REF. 4). F -> L (IN REF. 4). MISSING (IN REF. 2) SIMILARITY: BELONGS TO THE TGF-BETA FAMILY. 14; Mismatches INTERCHAIN. POTENTIAL. 47747 MW; EMBL; Y00083; CAA68279.1; -. EMBL; M19154; AAA50405.1; -. EMBL; J03585; AAA35358.1; -. EMBL; M87843; AAA61162.1; -. InterPro; IPR001111; ...
InterPro; IPR001839; ...
InterPro; IPR002400; ...
Pfam; PR0019; TGF-beta; 1.
Pfam; PF00688; TGF-beta; 1. 89; Conservative PIR; A34005, A34005. PDB; 1TFG; 31-OCT-93. PDB; 2TGI; 31-JAN-94. S06216; S06216. A29478; A29478. A29798; A29798. Query Match Best Local Similarity Matches 89; Conserv 414 AA; DISULFID DISULFID DISULFID DISULFID CARBOHYD CARBOHYD CONFLICT HELIX DISULFID SEQUENCE CARBOHYD CONFLICT PROPEP CHAIN STRAND STRAND STRAND TURN STRAND HELIX STRAND STRAND SIGNAL STRAND STRAND STRAND HELIX HELIX TURN ŏ a

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INTERCHALN (BY SIMILARITY).
N'LINKED (GLCNAC. ...) (POTENTIAL).
N'LINKED (GLCNAC. ...) (POTENTIAL).
''TINKED (GLCNAC. ...) (POTENTIAL).
''TINKED (GLCNAC. ...) (POTENTIAL).
                                                                                                                                                                                                                                                           MEDLINE-87102890; PubMed-2879635; Cheifetz S., Weatherbee J.A., Tsang M.L.S., Anderson J.K., Mole J.E., Lucas R., Massague J.; "The transforming growth factor-beta system, a complex pattern of cross-reactive ligands and receptors."; cell 48:409-415(1987).

-i- FUNCTION: TGF-BETA 2. HAS SUPPRESSIVE EFFECTS ON INTERLEUKIN-2 DEPENDENT T-CELL GROWTH.
                                                                                                                                            Sus scrofa (Pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
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61 VLGLYNTLNPEASASPCCVPQDLEPLTILYYVGRTPKVEQLSNMVVKSCKCS 112
          TRANSFORMING GROWTH FACTOR BETA
                                                                                        01-MAR-1989 (Rel. 10, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
TRANSFORMING GROWTH FACTOR BETA 2 PRECURSOR (TGF-BETA 2)
                                                                                                                                                                                                                              Submitted (DEC-1992) to the EMBL/GenBank/DDBJ databases
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Pfam; PF00688; TGF-beta; 1.
PRINTS; PR00488; TGFZKNOT.
PROSTIE; PS00250; TGF_BTA_1; 1.
Growth factor; Mitogen; Glycoprotein; Signal.
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                                                                                                                                                                                                SEQUENCE OF 2-435 FROM N.A.
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InterPro; IPR001111; -.
InterPro; IPR001839; -.
InterPro; IPR002400; -.
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435
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ID TGF2_PIG
AC P09858;
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                                                                                                                                                                                                                     Zhou Y.;
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Gaps
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INTERCHAIN (BY SIMILARITY).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Derynck R.;

"Mutine transforming growth factor-beta 2 cDNA sequence and
expression in adult tissues and embryos.";

Mol. Endocrinol. 3:1108-1114(1989).
-!- FUNCTION: TGF-BETA 2 HAS SUPPRESSIVE EFFECTS ON INTERLEUKIN-2
DEPENDENT T-CELL GROWTH.
-!- SUBUNIT: HOWODIMER, DISULFIDE-LINKED.
-!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                    TRANSFORMING GROWTH FACTOR BETA
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                                                                                                                                                                                                                                                                                              01-AUG-1992 (Rel. 23, Created)
1-AUG-1992 (Rel. 23, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
TRANSFORMING GROWTH FACTOR BETA 2 PRECURSOR (TGF-BETA 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE-90014832; Pubmed-2797004;
Miller D.A., Lee A., Pelton R.W., Chen E.Y., Moses H.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10; Indels
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Pfam; PF00688; TGFD_propeptide; 1.
PRINTS; PR00438; GFCTSKNOT.
GROSTIES, P500250; TGF_BETA_1; 1.
Growth factor; Mitogen; Glycoprotein; Signal.
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Best Local Similarity 78.6
Matches 88; Conservative
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MGD, MGI:98726; Tgfb2.
InterPro; IPR001111, ...
InterPro; IPR001839; ...
InterPro; IPR002400; ...
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140
241
414 AA;
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303
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P27090;
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Gaps

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84.4%; Score 535; DB 1; Length 435; 79.5%; Pred. No. 5.3e-50; Live 14; Mismatches 9; Indels

Query Match 84.4 Best Local Similarity 79.5 Matches 89; Conservative

tgfb3p.rsp

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              9
                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE=90245678; PubMed=2336403;
Rebbert M.L., Bhatia-Dey N., Dawid I.B.;
"The sequence of TGF-Deta 2 from Xenopus laevis.";
Nucleic Acids Res. 18:2185-2185(1990).
-i- FUNCTION: TGF-BETA 2 HAS SUPPRESSIVE EFFECTS ON INTERLEUKIN-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TRANSFORMING GROWTH FACTOR BETA 2.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
INTERCHAIN (BY SIMILARITY).
INTERCHAIN (BY SIMILARITY).
N-LINKED (GLONAC. .) (POTENTIAL).
N-LINKED (GLONAC. .) (POTENTIAL).
N-LINKED (GLONAC. .) (POTENTIAL).
N-LINKED (GLONAC. .) (FOTENTIAL).
N-LINKED (GLONAC. .) (FOTENTIAL).
ALDINYCFRNLEENCCVRPLYIDFRQDLGWKWVHEPKGYYANFCSGPCPYLRSADTTHST
                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                          112
                                                                    61 VLGLYNTLNPEASASPCCVPQDLEPLTILYYVGRTPKVEQLSNMVVKSCKCS
                                                                                                                                                                                 01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
TRANSFORMING GROWTH FACTOR BETA 2 PRECURSOR (TGF-BETA 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROBLEM: PF00019; TGF-beta; 1.
Pfam: PF00019; TGF-beta; 1.
PRINTS; PR00438; GFCYSKNOT.
PROSITS; PR00438; GFCYSKNOT.
Signal; Micogen; Glycoprotein; Growth factor.
                                                                                                                                                         413 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBUNIT: HOMODIMER, DISULFIDE-LINKED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL.
                                                                                                                                                                                                                                                       Kenopus laevis (African clawed frog)
                                                                                                                                                         PRT;
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EMBL; X51817; CAA36117.1; ALT_INIT.
PIR; S09510; S09510.
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                                                                                                                                                         STANDARD;
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241
413 AA;
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                                                                                                                                                                                                                                                                                                   Xenopodinae;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 302 ALDAAYCFRNVQDNCCLRPLYIDFKKDLGWKWIHEPKGYNANFCAGACPYLWSSDTQHSR 361
                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Guron C., Sudarshan C., Raghow R.; Molecular organization of the gene encoding murine transforming growth factor beta 1."; Gene 165:325-326(1991.".
                                         VLGLYNTLNPEASASPCCVPQDLEPLTILYYVGRTPKVEQLSNMVVKSCKCS
                                                                                                                                                                                     15-JUL-1999 (Rel. 38, Last annotation update)
TRANSFORMING GROWTH FACTOR BETA 1 PRECURSOR (TGF-BETA 1).
                                                                                                                                                                                                                                                                                                               MEDLINE-86168129; PubMed-3007454; Derynck R., Järrett J.A., Chen B.Y., Goeddel D.V.; The murine transforming growth factor-beta precursor."; J. Biol. Chem. 261:4377-4379(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- SUBUNIT: HOMODIMER, DISULFIDE-LINKED.
-!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
                                                                                                                             390 AA
                                                                                                                                                                (Rel. 04, Last sequence update) (Rel. 38, Last annotation update)
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EMBL; L42465; AAB00138.1; -...
EMBL; L42456; AAB00138.1; JOINED.
EMBL; L42457; AAB00138.1; JOINED.
EMBL; L42458; AAB00138.1; JOINED.
EMBL; L42469; AAB00138.1; JOINED.
EMBL; L42461; AAB00138.1; JOINED.
EMBL; L42461; AAB00138.1; JOINED.
EMBL; AJ009862; CAA08900.1; -...
                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=96096545; PubMed=8522200;
                                                                                                                                                       20-MAR-1987 (Rel. 04, Created)
                                                                                                                             STANDARD;
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InterPro; IPR001111; -.
InterPro; IPR001839; -.
                                                                                                                                                                                                                              Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PIR; A01396; WFMS2.
HSSP; P01137; 1KLC.
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                                                                                                                                                                                                                                                                        NCBI_TaxID=10090;
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                                                                                                                                                                                   15-JUL-1999
                                                                                                                                                                      20-MAR-1987
                                                                                                                          TGF1_MOUSE P04202;
                                                                                               RESULT 12
TGF1_MOUSE
                                                                                                                                                                                                                 TGFB1
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Gaps

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Length 413;

81.4%; Score 516; DB 1; Length 41 76.8%; Pred. No. 5.4e-48; Live 14; Mismatches 12; Indels

86; Conservative

Matches

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Similarity

Query Match Local 1 ALDINYCFRNLEENCCVRPINIDFRQDLGWKWVHEPKGYYANFCSGPCPYLRSADTTHST 60

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HSSP; P01137; 1KLC
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"CDNA cloning by PCR of rat transforming growth factor beta-1.";
Nucleic Acids Res. 18:3059-3059(1990).

INCRINO: TGF-BETA IS A WULTIEVUKTIONAL PEPTIDE THAT CONTROL
PROLIFERATION, DIFFERENTIATION, AND OTHER FUNCTIONS IN MANY CELL
TYPES. MANY CELLS SYNTHESIZE TGF-BETA AND ESSENTIALLY ALL OF THEM
HAVE SPECIFIC RECEPTORS FOR THIS PEPTIDE. TGF-BETA REGULATES THE
ACTIONS OF MANY OTHER PEPTIDE GROWTH FACTORS AND DETERMINES
A POSITIVE OR NEGATIVE DIRECTION OF THEIR EFFECTS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    279 ALDINYCESSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSK 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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                                                                                                                                                                        TRANSFORMING GROWTH FACTOR BETA 1.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
INTERCHAIN (BY SIMILARITY).
N-LINKED (GLCNAC. . .) (POTEWIAL).
N-LINKED (GLCNAC. . .) (POTEWIAL).
CELL ATTACHMENT SITE (POTEWIAL).
CELL ATTACHMENT SITE (POTEWITAL).
WM: 4381A51B711D689E CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 79.3%; Score 503; DB 1; Length 390; Best Local Similarity 77.7%; Pred. No. 1.3e-46; Matches 87; Conservative 10; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-AUG-1990 (Rel. 15, Created)
1-AUG-1990 (Rel. 15, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
TRANSFORMING GROWTH FACTOR BETA 1 PRECURSOR (TGF-BETA 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBUNIT: HOMODIMER, DISULFIDE-LINKED.
SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
                                              Pfam; PFUUDDO; LOCKTRINGT.
PRINTS: PROOMSB; GFCYSROOT.
GROWTH factor; Mitogen; Glycoprotein; Signal.
23 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               390 AA
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InterPro; IPR002400; -.
Pfam; PF00019; TGF-beta; 1.
Pfam; PF00688; TGFb_propeptide; 1.
                                                                                                                                                                                                                                                                                                                                                                                                       44310 MW;
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3356
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390 AA;
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Gaps
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01-NOV-1990 (Rel. 16, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
TRANSFORMING GROWTH FACTOR BETA 1 PRECURSOR (TGF-BETA 1) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'Complementary deoxyribonucleic acid cloning of bovine transforming
                                                                                                                                                                     BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
INTERCHAIN (BY SIMILARITY).
N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bos taurus (Bovine).
Sukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthezra; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-91042552; PubMed-3153459;
van Obberghen-Schilling E., Kondaiah P., Ludwig R.L., Sporn M.B.,
                                                                                                                                                           TRANSFORMING GROWTH FACTOR BETA 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 390;
                                                                                                                                                                                                                                                                                                                                                                                           15; Indels
                                                                                                                                                                                                                                                                                                CELL ATTACHMENT SITE (POT
5E21108ED50D853C CRC64;
                                                                                                                                                                                                                                                                                                                                                            79.3%; Score 503; DB 1; 77.7%; Pred. No. 1.3e-46; iive 10; Mismatches 15;
                                          Pfam: PF00119; TGF-beta; 1.
Pfam: PF00688; TGF_propeptide; 1.
PRINTS; PR00488; GFC-SKNOT.
PROSTIE: P800250; TGF_BETA_1; 1.
Growth factor; Mitogen; Glycoprotein; Signal.
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Mol. Endocrinol. 1:693-698(1987).
                                                                                                                                                                                                                                                                                                                  ΨM.
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InterPro; IPR001111; -. InterPro; IPR001839; -. InterPro; IPR002400; -.
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ID TGF1_BOVIN
AC P18341;
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DISULFID
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Best Local
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  DISULFIDE-LINKED. HETERODIMERS OF TGF-BETA 1/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Ćĥordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
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N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).
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CELL ATTACHMENT SITE (POTENTIAL).
C2717A23D994E00E CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 315;
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01-0CT-1996 (Rel. 34, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
TRANSFORMING GROWTH FACTOR BETA 1 PRECURSOR (TGF-BETA 1).
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Pred. No. 2.1e-46;
                                               SIMILARITY: BELONGS TO THE TGF-BETA FAMILY
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NON TER 1 1 1 1 PROPEP <1 203
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Pfam; PF00688; TGFb_propeptide; 1.
PROSITE; PS00250; TGF_BETA_1; 1.
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76.8%;
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  SUBUNIT: HOMODIMER,
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InterPro; IPR001111; -.
InterPro; IPR001839; -.
                        HAVE BEEN FOUND IN
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315 AA;
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TGF1_CANFA
P54831;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseeisb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HAVE SPECIFIC RECEPTORS FOR THIS PEPTIDE, TGF-BETA REGULATES THE ACTIONS OF MANY OTHER PEPTIDE GROWTH FACTORS AND DETERMINES A POSITIVE OR NEGATIVE DIRECTION OF THEIR EFFECTS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 ALDINYCFRNLEENCCVRPLYIDFRQDLGWKWVHEPKGYYANFCSGPCPYLRSADTTHST 60
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MEDLINE-87246074; PubMed-3474130;
Shartples K., Plowman G.D., Rose T.M., Twardzik D.R., Purchio A.F.;
"Cloning and sequence analysis of simian transforming growth
factor-beta cDNA.";
DNA 6:239-244(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Cercopithecus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .) (POTENTIAL).
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N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
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TRANSFORMING GROWTH FACTOR BETA 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            78.9%; Score 500; DB 1; Length 390; 76.8%; Pred. No. 2.6e-46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAR-1989 (Rel. 10, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
TRANSFORMING GROWTH FACTOR BETA 1 PRECURSOR (TGF-BETA 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15; Indels
                                          SUBUNIT: HOMODIMER, DISULFIDE-LINKED.
SIMILARITY: BELONGS TO THE TGF-BETA FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cercopithecus aethiops (Green monkey) (Grivet).
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INTERCHAIN.
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InterPro; IPR001839; -.
InterPro; IPR002400; -.
Pfam; PF00019; TGF-beta; 1.
Pfam; PF00688; TGFb_propeptide; 1.
PRINTS; PR00438; GFCYSKNOT.
PROSITE; PS00250; TGF_BETA_1; 1.
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P09533;
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TGF1_CERAE
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"Intron-exon structure of the human transforming growth factor-beta
      RRITER SEED OF SEED OF
                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
INTERCHAIN (BY SIMILARITY).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
CELL ATTACHMENT SITE (POTENTIAL).
CELL ATTACHMENT SITE (POTENTIAL).
FUNCTION: MULTIFUNCTIONAL PEPTIDE THAT CONTROL PROLIFERATION, DIFFERRYIATION, AND OTHER FUNCTIONS IN MANY CELL TYPES. MANY CELLS SYNTHESIZE TGF-BETA AND ESSENTIALLY ALL OF THEM HAVE SPECIFIC RECEPTORS FOR THIS PEPTIDE. TGF-BETA REGULATES THE ACTIONS OF MANY OTHER PEPTIDE GROWTH FACTORS AND DETERMINES A SUBJULY ON NEGATIVE DIRECTION OF THEIR EFFECTS. SUBJULY: HOMODIMER, DISCULPIDE-LINKED. SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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201137; Q9UCG4;
21-JUL-1996 (Rel. 01, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
01-CCT-2000 (Rel. 40, Last annotation update)
TRANSFORMING GROWTH FACTOR BETA 1 PRECURSOR (TGF-BETA 1).
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Derynck R., Rhee L., Chen E.Y., van Tilburg A.;
                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR001839; ...
InterPro; IPR002400; -.
Pfam; PF00019; TGF-beta; 1.
Pfam; PF00689; TGF-propetide; 1.
PRINTS; PR00438; GFCYSKNOT.
PROSITE; PS00250; TGF_BETA_1; 1.
Growth factor; Mitogen; Glycoprotein; Signal.
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HSSP; P01137; IKLC.
InterPro; IPR001111; -.
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390 AA;
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Derynck R., Jarrett J.A., Chen E.Y., Eaton D.H., Bell J.R.,
Assoian R.K., Roberts A.B., Sporn M.B., Goeddel D.V.;
"Human transforming growth factor-beta complementary DNA sequence and
expression in normal and transformed cells.";
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Massague J., Like B.;
"Cellular receptors for type beta transforming growth factor. Ligand
binding and affinity labeling in human and rodent cell lines.";
J. Biol. Chem. 260:2636-2645(1985).
                                                                                                                                                                                                                                                                                                                                                                                       Urushizaki Y., Niitsu Y., Terui T., Koshida Y., Mahara K., Kohgo Y., Urushizaki I., Takahashi Y., Ito H.; "Cloning and expression of the gene for human transforming growth factor-beta in Escherichia coli."; Tumor Res. 22:41-55(1987).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Recombinant human transforming growth factor-beta 1: expression Chinese hamster ovary cells, isolation, and characterization."; Protein Expr. Purif. 4:130-140(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hinck A.P., Archer S.J., Qian S.W., Roberts A.B., Sporn M.B., Weatherbee J.A., Tsang M.L.-S., Lucas R., Zheng B.-L., Wenker J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Bladder carcinoma;
MEDLINE=93229900; PubMed=8471846;
Bourdrel L., Lin C.-H., Lauren S.L., Elmore R.H., Sugarman B.J.,
Hu S., Westcott K.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=93144319; PubMed=8424942;
Archer S.J., Bax A., Roberts A.B., Sporn M.B., Ogawa Y., Piez
Weatherbee J.A., Tsang M.L.-S., Lucas R., Zheng B.-L., Wenker
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Nucleic Acids Res. 15:3188-3189(1987).
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                                                            SEQUENCE FROM N.A.
MEDLINE-85296301; PubMed-3861940;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Biochemistry 32:1152-1163(1993).
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                                                                                                                                                                                                                                                                                                                                                                   IISSUE=Carcinoma;
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NCBI_TaxID=9823;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sus scrofa (Pig).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae, Sus.
                                                                                                                                                                                                                                                                                                                                                                        N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
CELL ATTACHMENT SITE (POTENTIAL).
L -> P (IN REF. 2).
R -> RR (IN REF. 2).
W; 75391614250288FE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                    (POTENTIAL).
                                                                                                                                                                                                                                                                                                                   TRANSFORMING GROWTH FACTOR BETA 1.
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InterPro; Irnv...
InterPro; IRR002400; -.
Pfam; PF00019; TGFb-bar; 1.
Pfam; PF00688; TGFb_Propeptide; 1.
PRINTS; PR00418; GFCYSKNOT.
PROSITE; PS00250; TGF_BETA_1; 1.
Growth factor; Mitogen; Glycoprotein; Signal; 3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 390;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGF1_PIG STANDARD; PRT; 390 AA. P07200; P08832; P01-APR-1998 (Rel. 07, Created) 01-APR-1988 (Rel. 07, Last sequence update) 15-JUL-1999 (Rel. 38, Last annotation update) TRANSFORMING GROWTH FACTOR BETA 1 PRECURSOR (TGF-BETA 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                          78.9%; Score 500; DB 1; 76.8%; Pred. No. 2.6e-46; ive 11; Mismatches 15.
                                                                                                                                                                                                                                                                                                                                              BY SIMILARITY.
BY SIMILARITY.
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                                                                                   EMBL; X05840; CAA29283.1; JOINED.
EMBL; X05844; CAA29283.1; JOINED.
EMBL; X05849; CAA29283.1; JOINED.
EMBL; X05849; CAA29283.1; JOINED.
EMBL; X05810; CAA29283.1; JOINED.
EMBL; X05812; CAA26580.1; JOINED.
EMBL; X02812; CAA26580.1; JOINED.
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Best Local Similarity 76.89
Matches 86; Conservative
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PIR; A22290; A22290.
PIR; A27513; A27513.
PDB; IKLA; 17-AUG-96.
PDB; IKLC; 17-AUG-96.
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390 AA;
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                                                                                                      Derynck R., Rhee L.; "Sequence of the porcine transforming growth factor-beta precursor."; Nucleic Acids Res. 15:3187-3187(1987).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-87102890; PubMed=2879635; Cheifetz S., Weatherbee J.A., Tsang M.L.S., Anderson J.K., Mole J.E., Lucas R., Massague J.;
Incas R., Massague J.;
"The transforming growth factor-beta system, a complex pattern of cross-reactive ligands and receptors.";
Cell 48:409-415(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- SUBUNIT: HOMODIMER, DISULFIDE-LINKED.
-!- SIMILARITY: BELONGS TO THE TGF-BERA FAMILY.
-!- CAUTION: REF. 3 SEQUENCE WHICH WAS SAID TO ORIGINATE FROM CHICKEN WHITE LEGHORN, SEEMS (REF. 4) TO ORIGINATE PROM PIG.
                                                                                                                                                                                                                           SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN=MINIATURE SWINE;
MEDLINE=89054010; PubMed=2461367;
Kondaiah P., van Obberghen-Schilling E., Ludwig R.L., Dhar R.,
Kondaiah P., Roberts A.B.;
Sporn M.B., Roberts A.B.;
"CDNA cloning of porcine transforming growth factor-beta 1 mRNAs."
"CDNA cloning of porcine transforming and polyadenylation.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE-88335639; PubMed=3166520;
Jakowlew S.B., Dillard P.J., Sporn M.B., Roberts A.B.;
"Nucleotide sequence of chicken transforming growth factor-beta 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TRANSFORMING GROWTH FACTOR BETA 1.
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Pfam; PF00688; TGF-beta; 1.
PRINTS; PR00438; GFCYSKNOT.
PROSITES, P800250; TGF_BRA_1; 1.
Growth factor; Mitogen; Glycoprotein; Signal.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleic Acids Res. 16:8730-8730(1988).
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                                TISSUE=Ovary;
MEDLINE=87174844; PubMed=3470708;
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PIR; A26356; A26356.
PIR; S01413; S01413.
HSSP; P01137; IKLC.
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SEQUENCE FROM N.A.
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STRAIN MEDLINE-95568698; PubMed=7749621;

Sutton R., Ward W.G., Raphael K.A., Cam G.R.;

Sutton R., Ward W.G., Raphael K.A., Cam G.R.;

Growth factor expression in skin during wool follicle development.";

Comp. Biochem. Physiol. 1108:697-705(1995).

-I-FUNCTION: TGF-BETA IS A MULTIFUNCTIONAL PEPTIDE THAT CONTROL

PROLIFERRATION, DIFFERRATIANION, AND OTHER FUNCTIONS IN MANY CELL

TYPES. MANY CELLS SYNTHESIZE TGF-BETA AND ESSENTIALLY ALL OF THEM
HANC SPECIFIC RECEPTORS FOR THIS PEPTIDE. TGF-BETA REGULATES THE

ACTIONS OF MANY OTHER PEPTIDE GROWTH FACTORS AND DEFERMINES

A POSITIVE OR NEGATIVE DIRECTION OF THEIR EFFECTS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-95121932; PubMed-7821809; Moodall C.J., McLaren L.J., Watt N.J.; "Sequence and chromosomal localisation of the gene encoding ovine latent transforming growth factor-beta 1.";
                                           BY SIMILARITY.
INTERCHAIN (BY SIMILARITY).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
CELL ATTACHMENT SITE (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                      Length 390;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
TRANSFORMING GROWTH FACTOR BETA 1 PRECURSOR (TGF-BETA 1).
                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                         LR -> PG (IN REF. 3).

L -> V (IN REF. 2 AND 3).

R -> G (IN REF. 3).

N -> NA (IN REF. 3).

N -> NA (IN REF. 3).
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76.8%; Pred. No. 2.6e-46;
ive 11; Mismatches 15;
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SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
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Matches 86; Conservative
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NCBI_TaxID=9940;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (TGF beta 1) CDNA.";
DNA Seq. 7:375-378(1997).
-!- FUNCTION: TGF-BETA IS A MULTIFUNCTIONAL PEPTIDE THAT CONTROL
-- PROLIFERRATION, DIPPERENTATION, AND OTHER FUNCTIONS IN MANY CELL
TYPES. MANY CELLS SYNTHESIZE TGF-BETA AND ESSENTIALLY ALL OF THEM
HAVE SPECIFIC RECEPTORS FOR THIS PEPTIDE. TGF-BETA REGULATES THE
ACTIONS OF MANY OTHER PEPTIDE GROWTH FACTORS AND DETERMINES
A POSITIVE OR NEGATIVE DIRECTION OF THEIR EFFECTS.
                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDINE-99185507; pubmed-9524819; Penha-Goncalves M.N., Onions D.E., Nicolson L.; Penha-Goncalves M.N., Onions D.E., Nicolson L.; "Cloning and sequencing of equine transforming growth factor-beta 1
                                                                                                                                                                                                 TRANSFORMING GROWTH FACTOR BETA 1.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
INTERCHAIN (BY SIMILARITY).
N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Equus caballus (Horse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
                                                                                                                                                                                                                                                                                                                       N-LINKED (GLCNAC. . .) (POTENTIAL).
CELL ATTACHMENT SITE (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                              Length 390;
                                                                                                                                                                                                                                                                                                                                                                                              78.9%; Score 500; DB 1; Length 39
76.8%; Pred. No. 2.6e-46;
iive 11; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
TRANSFORMING GROWTH FACTOR BETA 1 PRECURSOR (TGF-BETA 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     between the Swiss Institute of Bioinformatics and the
                                                                                                                                                                                                                                                                                                                                                   1C247299484D0E57 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBUNIT: HOMODIMER, DISULFIDE-LINKED. SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
                                                                                                                                                             Signal.
                                                                                                                                                                                        POTENTIAL.
                                                                                             Pfam: PF00019; TGF-beta; 1.
Pfam: PF00688; TGF-beta; 1.
PRINTS; PR00438; GFCYSKNOT.
PROSITE; PS00250; TGF_BETA_1; 1.
Growth factor; Mitogen; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                   44291 MW;
             EMBL; X76916; CAA54242.1;
                           L36038; AAA31526.1;
P01137; 1KLC.
                                                                                                                                                                                                                                                                                                                                                                                                                             86; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                      Interpro; IPR001111; -. Interpro; IPR001839; -. Interpro; IPR002400; -.
                                                                                                                                                                                      278
390
294
356
387
355
82
136
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                   390 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9796;
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285
293
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355
82
136
176
244
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019011;
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                                                                                                                                                                          SIGNAL
                            EMBL;
                                                                                                                                                                                                       CHAIN
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TGF1_HORSE
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DISULFID
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ID TGF1_C
AC P09531
DT 01-WAR
DT 15-JUI
DE TRANSF
DD (FRAGN
GN TGFBIL
OS GAllus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62
        qq
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Scarozza A.M., Ramsingh A.I., Wicher V., Wicher K.;
"Spontaneous cytokine gene expression in normal guinea pig blood and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Jeevan A., McMurray D.N., Yoshimura T.;
"Guinea pig transforming growth factor-beta in peritoneal exudates
after BCG vaccination.";
                                                                                                                                                                                                                                                                                                                                    TRANSFORMING GROWTH FACTOR BETA 1.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
INTERCHAIN (BY SIMILARITY).
N-LINKED (GLCNAC...) (POTENTIAL).
N-LINKED (GLCNAC...) (POTENTIAL).
N-LINKED (GLCNAC...) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cavia porcellus (Guinea pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    339 VLALYNQHNPGASAAPCCVPQVLEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 VLGLYNTLNPEASASPCCVPQDLEPLTILYYVGRTPKVEQLSNMVVKSCKCS 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 390;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 279-371 FROM N.A.
STRAIN-HARTLEY; TISSUE-Trachea;
Morishima Y., Uchida Y., Nomura A., Ishii Y., Sakamoto T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 499; DB 1; Length 39
Pred. No. 3.4e-46;
1: Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGF1_CAVPO STANDARD; PRT; 390 AA.
0921Y6; 0902B3; 09R148;
01-0CT-2000 (Rel. 40, Created)
01-0CT-2000 (Rel. 40, Last sequence update)
01-0CT-2000 (Rel. 40, Last annotation update)
TRANSFORMING GROWTH FACTOR BETA 1 PRECURSOR (TGF-BETA 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-LINKED (GLCNAC. . .) (P
A86D715F44549691 CRC64;
                                                                                                                                                                                                                                                                          Growth factor; Mitogen; Glycoprotein; Signal.
                                                                                                                                                                                                                                                                                                                          BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 265-382 FROM N.A.
MEDLINE-99144670; PubMed=10025978;
                                                                                                                                                                                            Pfam; PF00019; TGF-beta; 1.
Pfam; PF00688; TGF_propeptide; 1.
PRINTS; PR00438; GFCYSKNOT.
PROSITE; PS00250; TGF_BETA_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          43974 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  78.78;
76.88;
                                                                                                EMBL; X99438; CAA67801.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cytokine 10:851-859(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                       Interpro; IPR001111; ...
Interpro; IPR001839; ...
Interpro; IPR002400; -..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        390 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10141;
                                                                                                                                                                                                                                                                                                                     24
279
285
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293
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326
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                                                                                                                       P01137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         86;
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CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                            DISULFID
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TGF1_CAVPO
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15-JUL-1999 (Rel. 38, Last annotation update)
TRANSFORMING GROWTH FACTOR BETA 1 PRECURSOR (TGF-BETA 1) (TGF-BETA 4)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  280 LDTNYCFSSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKV 339
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N-LINED (GLONG...) (POTENTIAL).

N-LINKED (GLONG...) (POTENTIAL).

G-P (IN REP. 3).

F -> S (IN REF. 3).

C -> R (IN REF. 2).

C -> R (IN REF. 2).

C -> G (IN REF. 2).

A -> G (IN REF. 2).

C -> R (IN REF. 2).

A -> G (IN REF. 2).
                                                                         mitted (JUL-1199) to the EMBL/GenBank/DDBJ databases.
FUNCTION: MULTIFUNCTIONAL PEPTIDE THAT CONTROLS PROLIFERATION,
DIFFERENTIATION, AND OTHER FUNCTIONS IN MANY CELL TYPES. MANY
CELLS SYNTHESIZE TGF-BETA 1 AND ESSENTIALLY ALL OF THEM HAVE
SPECIFIC RECEPTORS FOR THIS PEPTIDE. TGF-BETA 1 REGULATES THE
ACTIONS OF MANY OTHER PEPTIDE GROWTH FACTORS AND DETERMINES A
POSITIVE OR NEGATIVE DIRECTION OF THEIR EFFECTS.
SUBUNIT: HOMODIMER, DISULFEDE-LINKED (BY SIMILARITY).
Sekizawa K.;
"Guinea-pig transforming growth factor-beta expression in injured
tracheal epithelium.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 LDTNYCFRNLEENCCVRPLYIDFRQDLGWKWVHEPKGYYANFCSGPCPYLRSADTTHSTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL. TRANSFORMING GROWTH FACTOR BETA 1.
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Pred. No. 5.1e-45;
1; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00019; TGF-beta; 1.
PROSITE; PS00250; TGF_BETA; 1.
Growth factor; Mitogen; Glycoprotein; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             77.0%; Score 400, 75.7%; Pred. No. 5.1e-
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2294
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Best Local Similarity
Matches 84; Conserv
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P09531;
                                                                                  Submitted
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321 KVLALYNQHNPGASAAPCCVPQTLDPLPIIYYVGRNVRVEQLSNMVVRACKCS 373

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                                                                                                                                                                                                                                                                                                                                  -!- FUNCTION: TGF-BETA IS À MULTIFUNCTIONAL PEPTIDE THAT CONTROL PROLIFERATION, DIFFERENTIATION, AND OTHER FUNCTIONS IN MANY CELL TYPES. MANY CELLS SYNTHESIZE TGF-BETA AND ESSENTIALLY ALL OF THEM HAVE SPECIFIC RECEPTORS FOR THIS PEPTIDE. TGF-BETA REGULATES THE
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                   Burt D.W., Jakowlew S.B.;
Correction: a new interpretation of a chicken transforming growth
factor-beta 4 complementary DNA.";
Mol. Endocrinol. 6:989-992(1992).
                                                                                                             MEDLINE-89112198; PubMed-2464131;
Jakowlew S.B., Dillard P.J., Sporn M.B., Roberts A.B.;
"Complementary deoxyribonucleic acid cloning of a messenger ribonucleic acid encoding transforming growth factor beta 4 from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CELL ATTACHMENT SITE (POTENTIAL).
9903F3479C8552E5 CRC64:
                                                                                                                                                                                                                                                                                                                                                                                                     ACTIONS OF MANY OTHER PEPTIDE GROWTH FACTORS AND DETERMINES A POSITIVE OR NEGATIVE DIRECTION OF THEIR EFFECTS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-LINKED (GLCNAC. .) (POTENTIAL)
N-LINKED (GLCNAC. .) (POTENTIAL)
N-LINKED (GLCNAC. .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TRANSFORMING GROWTH FACTOR BETA 1.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
INTERCHAIN (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBUNIT: HOMODIMER, DISULFIDE-LINKED. SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Promit PF00019; TGF-beta: 1.
Pfam; PF00688; TGFD_propeptide; 1.
PROSITE; PS00250; TGF_BETA_1; 1.
Growth factor; Mitogen; Glycoprotein; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL.
                                                                                                                                                                                 chicken embryo chondrocytes.";
Mol. Endocrinol. 2:1186-1195(1988).
                                                                                                                                                                                                                                                    MEDLINE=92357039; Pubmed=1353860;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          42634 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; M31160; AAB05637.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PIR; A34941, A34941.
PIR; S03110; S03110.
HSSP; P01137; IKLC.
InterPro; IPR001111; -.
InterPro; IPR001839; -.
                                                                                                   LEGHORN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        153
224
373 AA;
                                                                                  SEQUENCE FROM N.A.
                                              NCBI_TaxID=9031;
                                                                                                 STRAIN-WHITE
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ï Gaps 2 LDTNYCF--RNLEENCCVRPLYIDFRQDLGWKWVHEPKGYYANFCSGPCPYLRSADTTHS 59 5, Query Match 72.7%; Score 461; DB 1; Length 373; Best Local Similarity 71.7%; Pred. No. 3.8e-42; Matches 81; Conservative 13; Mismatches 17; Indels

TVLGLYNTLNPEASASPCCVPQDLEPLTLLYYVGRTPKVEQLSNMVVKSCKCS 112 09

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                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                    01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
15-UUL-1999 (Rel. 38, Last annotation update)
TRANSFORMING GROWTH FACTOR BETA 1 PRECURSOR (TGF-BETA 1) (TGF-BETA 5).
                                                                                                                                                                                                                                     Kondaiah P., Sands M.J., Smith J.M., Fields A., Roberts A.B., Sporn M.B., Melton D.A.; "Identification of a novel transforming growth factor-beta (TGF-beta
                                                                                                                                                                                                                                                                                                                                             Vempati U.D., Kondaiah P.;
Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases.
--- FUNCTION: IMPORTANT ROLE IN CERTAIN ASPECTS OF DIFFERENTIATION.
--- SUBUNIT: HOWODIMER, DISULFIDE-LINKED.
--- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
                                                                                                                  Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INTERCHAIN (BY SIMILARITY).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

CELL ATTACHMENT SITE (POTENTIAL).

1034621C917AAE15 CRC64;
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Pred. No. 8.9e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00019; TGF-beta; 1,
Pfam; PF00688; TGFb_propeptide; 1.
PRINTS; PR00438; GFCYSKNOT.
PROSITE; PS00250; TGF_BETA_1; 1.
Growth factor; Mitogen; Glycoprotein; Signal.
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BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                             382 AA
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                             PRT;
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EMBL; AF009335; AAB6441.1; -.
EMBL; AF009331; AAB6441.1; JOINED.
                                                                                                                                                                                                                                                                                                   Biol. Chem. 265:1089-1093(1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AF009332; AAB64441.1; JOINED.
EMBL; AF009333; AAB64441.1; JOINED.
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                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE=90110090; PubMed=2295601;
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72.0%;
                                                                                                                                                                                                                                                                                     5) mRNA in Xenopus laevis.
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                             STANDARD;
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3382
286
348
379
347
                                                                                                                                                                   Xenopus.
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382 AA;
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Best Local Similarity
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                                                                                                                                                                              NCBI_TaxID=8355;
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277
285
285
314
347
                                                                                                                                                                Xenopodinae;
                           TGF1_XENLA
P16176;
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                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE-Skeletal muscle;
MEDLINE-98024153; PubMed=9356471;
MCPherron A.C., Lee S.-J.;
Mouble muscling in cattle due to mutations in the myostatin gene.";
Proc. Natl. Acad. Sci. U.S.A. 94:12457-12461(1997).
-: FUNCTION: ACTS SPECIFICALLY AS A NEGATIVE REGULATOR OF SKELETAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Brachydanio rerio (2ebrafish) (Zebra danio).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Buteleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Rasborinae; Danio.
                                                     6 YCFRNLEENCCVRPLYIDFRQDLGWKWVHEPKGYYANFCSGPCPYLRSADTTHSTVLGLY
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LLIKKED (GLCNAC. .) (POTENTIAL)
N-LINKED (GLCNAC. ..) (FOTENTIAL)
6302BCGC8656276 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
GROWTH/DIFFERENTIATION FACTOR 8 PRECURSOR (GDF-8) (MYOSTATIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              œ
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BY SIMILARITY.
BY SIMILARITY.
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-i- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
      21; Indels
                                                                                                                                                                                                                   66 NTLNPEASASPCCVPQDLEPLTILYYVGRTPKVEQLSNMVVKSCKCS
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Pfam; PF00688; TGFb_propeptide; 1.
PROSITE; PS00250; TGF_BETA_1; 1.
Growth factor; Cytokine; Glycoprotein; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                       374 AA
      Mismatches
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77; Conservative
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374 AA;
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                                                                                                                                                                                                                                                                                                                                 RESULT 24
GDF8_BRARE
DC 04222;
DT 30-MAY-2000
DT 30-MAY-2000
DT 30-MAY-2000
DT 01-OT-2000
DT 01-OT-2000
DE GROWTH/DIFFE
GNOWTH/DIFFE
CC ENTINE-SREIGH
RA MEDLINE-9802
RA MEDLINE-SREIGH
CC 1- SIMILARI
CC 1- SIMIL
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Best Local Sim:
Matches 44;
Matches
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                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INTERCHAIN (BY SIMILARITY).
N-LINKED (GLCNAC. .) (POTENTIAL).
7B49B90ACAB926EA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6
                                                                                                                                                                                         15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
01-OCT-2000 (Rel., 40, Last annotation update)
GROWTH/DIFFERENTIATION FACTOR 8 PRECURSOR (GDF-8) (MYOSTATIN).
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64 LYNTLNPEASASPCCVPQDLEPLTILYYVGRTPKV-EQLSNMVVKSCKCS 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL.
GROWTH/DIFFERENTIATION FACTOR
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- SUBUNIT: HOMODIMER, DISULFIDE-LINKED (BY SIMILARITY).
                          70 PEASASPCCVPQDLEPLTILYYVGRTPKV-EQLSNMVVKSCKCS 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; Irnovasa; ...
InterPro; Irnovasa; ...
Piam; PP00019; TGF-beta; 1.
Pfam; PF00688; TGF-Propeptide; 1.
PROSITE; PS00250; TGF-BETA_1; 1.
Growth factor; Cytokine; Glycoprotein; Signal.
                                                                                                                                                      375
                                                                                                                                                                                                                                                                                                     Papio hamadryas (Hamadryas baboon).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      42; Conservative
                                                                                                                                                    STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                  Cercopithecinae; Papio.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9557;
                                                                                                                                                                                                                                                                                 GDF8 OR MSTN.
                                                                                                                                                  GDF8_PAPHA
018828;
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ID IHBE_MOUSE
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CARBOHYD
SEQUENCE
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                                             325
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Fang J., Wang S.Q., Smiley E., Bonadio J.;
Fang J., Wang S.Q., Smiley E., Bonadio J.;
"Genes coding for mouse activin beta C and beta E are closely linked and exhibit a liver-specific expression pattern in adult tissues.";
Biochem. Biophys. Res. Commun. 231:655-661(1997).
-!- FUNCTION: INHIBINS ARE GONADAL GIXCOPEPTIDES THAT INHIBIT THE SECRETION OF FOLLITROPIN BY THE PITUITARY GLAND. ON THE OTHER HAND ACTIVINS ACTIVINS ACTIVINS REGULATE GROWTH AND DIFFERENTIATION OF FOLLITROPIN. ACTIVINS REGULATE EXPLANDAL CARCINOMA CELLS, INDUCE EXTHROPOIESIS, STIMULATE INSULIN SECRETION, AND PROMOTE NEURAL CELL SURVIVAL. ACTIVINS ARE ALSO IMPORTANT IN EMBRYONIC AXIAL
                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                  Fang J., Yin W., Smiley E., Wang S.Q., Bonadio J.; "Molecular cloning of the mouse activin beta E subunit gene."; Biochem. Biophys. Res. Commun. 228:669-674(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBUNIT: DIMERIC, LINKED BY ONE OR MORE DISULFIDE BONDS
                15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
INHIBIN BETA E CHAIN PRECURSOR (ACTIVIN BETA-E CHAIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
                                                                                                                                                                                                     MEDLINE=97096313; PubMed=8941337;
                                                                                                                                                                                                                                                                                              MEDLINE=97224404; PubMed=9070865;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; U96386; AAB53801.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR001318; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MGD; MGI:109269; Inhbe.
                                                                                            Mus musculus (Mouse)
                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                       NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DEVELOPMENT.
                                                                                                                                                                                        TISSUE-Liver
                                                                                                                                                                                                                                                                                 MAPPING
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InterPro; IPR002400; -.
Pfam; PF00019; TGF-beta; 1.
PRINTS; PR00438; GFCYSKNOT.
PRINTS; PR00672; INHIBINBC.
PROSITE; PS00250; TGF\_BETA\_1; 1.
Follitropin inhibitor; Contraceptive; Hormone; Glycoprotein; Signal. F37C76C8061D8AD9 CRC64; INTERCHAIN (BY SIMILARITY). POTENTIAL. INHIBIN BETA E CHAIN. BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY. SIMILARITY. POTENTIAL. N-LINKED 39057 MW; 236 350 248 315 347 349 198 350 AA; DISULFID DISULFID DISULFID DISULFID DISULFID SEQUENCE PROPEP SIGNAL CHAIN

9 CCVRPLYIDFRQDLGWK-WVHEPKGYYANFCSGPC-PYLRS----ADTTHSTVLGLYNTL 68 10; 32.8%; Score 208; DB 1; Length 350; 42.5%; Pred. No. 4.5e-15; Indels 4.5e-15; ches 33; ; Pred. No. 4.5e 18; Mismatches Best Local Similarity 42.5% Matches 45; Conservative Query Match 15

NPEASASPCCVPQDLEPLTILY--YVGRTPKVEQLSNMVVKSCKCS 112 69

247 CCRRDHYVDF-QELGWRDWILQPEGYQLNYCSGQCPPHLAGSPGIAASFHSAVFSLLKAN 305

q ò

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Length 350;

Score 208; DB 1; Pred. No. 4.5e-15;

32.8%;

Best Local Similarity

Query Match

306 NPWPAGSSCCVPTARRPLSLLYLDHNGNVVKTD-VPDMVVEACGCS 350

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the European Bioinformatics Institute. There are no restrictions on its
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modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                      Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                      STRAIN-SPRAGUE-DAWLEY; TISSUE-Liver, and Lung; O'BFYAN M.K., Sebirer K., Hedger M.P., Hearn M.T.W., de Kretser D.M.; O'BFYAN M.K., Sebirer K., Hedger M.P., Hearn M.T.W., de Kretser D.M.; "The cloning and requlation of the rat activin bE subunit."; submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00019; TGF-beta; 1.
PRINTS; PR00438; GFCYSKNOT.
PRINTS; PR00672; INHIBINBC.
PROSITE; PS00250; TGF_BETA_1; 1.
FOllitropin inhibitor; Contraceptive; Hormone; Glycoprotein; Signal.
SIGNAL
                                                                                                                                     Eukaryota; Métazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INTERCHAIN (BY SIMILARITY).
N-LINKED (GLCNAC. .) (POTENTIAL).
EH -> DY (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                -1- SUBUNIT: DIMERIC, LINKED BY ONE OR MORE DISULFIDE BONDS (BY SIMILARITY).
-1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EH -> DY (IN REF. 2).
0CEBF6E108E926E3 CRC64;
                                                                                           INHIBIN BETA E CHAIN PRECURSOR (ACTIVIN BETA'E CHAIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INHIBIN BETA E CHAIN.
BY SINILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                  Last sequence update)
Last annotation update)
                          AA
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                       THBE_RAT STANDARD; E 088959; Q9R285; L15-JUL-1999 (Rel. 38, Created) 15-JUL-1999 (Rel. 38, Last sequol-ocT-2000 (Rel. 40, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AF089825; AAC36741.1; -. EMBL; AF140032; AAD30133.1; -.
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                                                                                                                         Rattus norvegicus (Rat).
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350
248
315
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      350 AA;
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                                                                                                                                                                 NCBI_TaxID=10116;
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240
247
276
280
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RESULT.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3;
                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                   15 CCVRPLYIDFRQDLGWK-WVHEPKGYYANFCSGPC-PYLRS----ADTTHSTVLGLYNTL 68
                                                                                                                                                                                                                                                                                                                          McPherron A.C., Lee S.-J.;
"Double musciling in cattle due to mutations in the myostatin gene.";
"Proc. Natl. Acad. Sci. U.S.A. 94:12457-12461(1997).
-i- FUNCTION: ACTS SPECIFICALLY AS A NEGATIVE REGULATOR OF SKELETAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EENCCVRPLYIDFRQDLGWKWVHEPKGYYANFCSGPCPYLRSADTTHSTVLGLYNTLNPE 71
                                                                                                                                                                                                                      Ovis aries (Sheep).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
  10;
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N.LINKED (GLCNAC. .) (POTENTIAL)

N.LINKED (GLCNAC. .) (POTENTIAL)

IC36F3833BB11241 CR664;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5;
                                                                                                                                                                 15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
GROWTH/DIFFERENTIATION FACTOR 8 PRECURSOR (GDF-8) (MYOSTATIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GROWTH/DIFFERENTIATION FACTOR BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                               -i- SUBUNIT: HOWODIMER, DISULFIDE-LINKED (BY SIMILARITY).
  Indels
                                                                            NPEASASPCCVPQDLEPLTILY - - YVGRTPKVEQLSNMVVKSCKCS 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        72 ASASPCCVPQDLEPLTILYYVGRTPKV-EQLSNMVVKSCKCS 112
 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  32.7%; Score 207.5; DB 1
39.2%; Pred. No. 5.5e-15;
ive 16; Mismatches 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00019; TGF-beta; 1.
Pfam; PF00688; TGF-propeptide; 1.
PROSITE; PS00250; TGF_BETA_1; 1.
Growth factor; Cytokine; Glycoprotein; Signal.
                                                                                                                                              Ä
18; Mismatches
                                                                                                                                             375
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                                                                                                                                                                                                                                                                                                              MEDLINE-98024153; PubMed-9356471;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AF019622; AAB86689.1; -. InterPro; IPR001111; -. InterPro; IPR001839; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   42827 MW;
Conservative
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                                                                                                                                                                                                                                                         Bovidae; Caprinae; Ovis.
                                                                                                                                                                                                                                                                                                     TISSUE-Skeletal muscle;
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340
372
374
339
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                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                       MUSCLE GROWTH
                                                                                                                                                                                                                                                                    NCBI_TaxID=9940;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24
267
281
309
313
339
                                                                                                                                                                                                              GDF8 OR MSTN.
45;
                                                                                                                                            GDF8_SHEEP
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Matches
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                                                                                                                                                                                  01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
BONE MORPHOGENETIC PROTEIN 6 PRECURSOR (BMP-6) (VG-1-RELATED PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95 SDYNSSELKTACKKHELYVSF-QDLGWQDWIIAPKGYAANYCDGECSFPLNAHMNATNHA 153
                                                                                                                                                                                                                                                                                                                        Rattus norvegious (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 TNYCFRNLEENCCVRPLYIDFRQDLGWK-WVHEPKGYYANFCSGPCPYLRSAD---TTHS 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-93085758; PubMed=1453478; MEDLINE-93085758; PubMed=1453478; Squermann U., Meyermann R., Schluesener H.J.; Squermann U., Meyermann R., Schluesener H.J.; Cloning of a novel TGF-beta related cytokine, the vgr, from rat Drain: cloning of and comparison to homologous human cytokines."; J. Neurosci. Res. 33:142-147(1992).
-: FUNCTION: INDUCES CARTILAGE AND BONE FORMATION (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INTERCHAIN (BY SIMILARITY).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

D5D83C3898213F51 CRC64;
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9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 32.5%; Score 206; DB 1; Length 207, 37.2%; Pred. No. 4.3e-15; Live 22; Mismatches 43; Indels
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BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00019; TGF-beta; 1.
PROSITE; PS00250; TGF_BETA_1; 1.
Growth factor; Cytokine; Bone; Cartilage; Glycoprotein.
AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              426
                                                                                                                                          207
                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23225 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; X58830; CAA41634.1; -. PIR; S37618. HSSP; P18075; IBMP. InterPro; IPR001839; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        75
207
172
204
206
206
171
171
80
98
                                                                                                                                                                                                                                                                             (VGR-1) (FRAGMENT).
BMP6 OR BMP-6 OR VGR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             76
106
135
139
171
80
98
148
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                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                42;
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DISULFID
DISULFID
                                                                                                                                          BMP6_RAT
Q04906;
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IHBA_HORSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CHAIN
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2
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-1- FUNCTION: INHIBIN IS A GONADAL GLYCOPEPTIDE THAT INHIBITS THE SECRETION OF FOLLITROPIN BY THE PITUITARY GLAND. ON THE OTHER HAND ACTIVIN ACTIVINA CTIVINA STATE SECRETION OF FOLLITROPIN. ACTIVIN IS ALSO IMPORPART IN EMBRYONIC AXIAL DEVELOPMENT.

-1- SUBUNIT: DIMERIC, LINKED BY ONE OR MORE DISULFIDE BONDS.

INHIBIN A IS A DIMER OF ALPHA AND BETA-B.

ACTIVIN A IS A DIMER OF BETA-A.

ACTIVIN AB IS A DIMER OF BETA-A.

ACTIVIN AB IS A DIMER OF BETA-A.

-1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               321 CCKKQFFVSFK-DIGWNDWIIAPSGYHANYCEGECPSHIAGTSGSSLSFHSTVINQYRLR 379
                                                                                                                                                                      Yoshida S., Yamanouchi K., Hasegawa T., Ikeda A., Suzuki M.,
Chang K., Matsuyama S., Nishihara M., Takahashi M.;
"Molecular cloning of cDNA for equine ovarian inhibin/activin beta A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HSSP; P18075; 1BMP.
InterPro; IPR000491; -.
InterPro; IPR001839; -.
InterPro; IPR001839; -.
InterPro; IPR002400; -.
Pfam. PF00019; TGF-beta; 1.
Pfam; PF00688; TGF-beta; 1.
PRINTS; PR00488; GFCVSKNOT.
PRINTS; PR00450; INITBINBA.
PROSTTE; PS00250; TGF_BETA, 1; 1.
POLILITOPIN inhibitor; Contraceptive; Hormone; Glycoprotein; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15 CCVRPLYIDFRQDLGWK-WVHEPKGYYANFCSGPCP----YLRSADTTHSTVLGLYNTL 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INHIBIN BETA A CHAIN.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
INTERGIAIN (BY SIMILARITY).
INTERGIAIN (GLCNAC. . .) (POTENTIAL).
W. E481060B836BA77D CRC64;
                                                                                   Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1; Length 426;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            36; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GHNPFANLKSCCVPTKLRPMSMLYYDDGQNIIKKDIQNMIVEECGCS 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       --NPEASASPCCVPQDLEPLTILYY-VGRTPKVEQLSNMVVKSCKCS 112
                     01-OCT-1996 (Rel. 34, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
INHIBIN BETA A CHAIN PRECURSOR (ACTIVIN BETA-A CHAIN).
                                                                                  Eúkaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9e-15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    32.5%; Score 206; DB
38.3%; Pred. No. 9e-1
ive 20; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL.
                                                                                                                                                            MEDLINE=96031670; PubMed=7548399;
              Created)
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426
322
391
423
390
         01-OCT-1996 (Rel. 34, 01-OCT-1996 (Rel. 34, 01-OCT-2000 (Rel. 40,
                                                                      caballus (Horse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              426 AA;
                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                            NCBI_TaxID=9796;
                                                                                                                                                   TISSUE=Ovary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                              subunit.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIGNAL
                                                            INHBA.
                                                                         Eguus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRINTS, PROMOTO, TGF-beta; 1.

R Pfam; PF00019; TGF-beta; 1.

R PRINTS, PR00438; TGF-beta; 1.

R PROSTE; PR00438; TGF_BETA_1; 1.

R PROSTE; PR00436; TGF_BETA_1; 1.

R PROSTE; PS00250; TGF_BETA_1; 1.

T CHAIN 382 513 BONE MORPHOGENETIC PROTEIN 6.

DISULFID 441 510 BY SIMILARITY.

T DISULFID 445 512 BY SIMILARITY.

T CARBOHYD 241 241 N-LINKED (GLCNAC. .) (POTENTIAL).

T CARBOHYD 269 269 N-LINKED (GLCNAC. .) (POTENTIAL).

T CARBOHYD 454 404 N-LINKED (GLCNAC. .) (POTENTIAL).

T CARBOHYD 454 454 N-LINKED (GLCNAC. .) (POTENTIAL).
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BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

INTERCHAIN (BY SIMILARITY).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Celeste A.J., Iannazzi J.A., Taylor R.C., Hewick R.M., Rosen V., Wang E.A., Wozney J.M.;

"Identification of transforming growth factor beta family members present in bone-inductive protein purified from bovine bone.";

Proc. Natl. Acad. Sci. U.S.A. 87:9843-9847(1990).

-i. FUNCTION: INDUCES CARTILAGE AND BONE FORMATION.
                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60 TVLGLYNTLNPEASASPCCVPQDLEPLTILYYVGRTPKV-EQLSNMVVKSCKC 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1; Length 513;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            43; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -! - SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      32.5%; Score 206; DB 1;
37.2%; Pred. No. 1.1e-14;
tive 22; Mismatches 43;
                                                           01-AUG-1991 (Rel. 19, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
01-CCT-2000 (Rel. 40, Last annotation update)
BONE MORPHOGENETIC PROTEIN 6 PRECURSOR (BMP-6),
   513 AA
   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Bone;
MEDLINE=91088608; Pubmed=2263636;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL, M60315; AAA36737.1; -. PIR; B39263; B39263. HSSP; P18075; 1BMP. MIM; 112266; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         57225
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   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Interpro; IPR001111; -. Interpro; IPR001839; -. Interpro; IPR002400; -.
                                                                                                                                                                                                                          Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606;
BMP6_HUMAN
P22004:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=89282810; PubMed=2734307;
MEDLINE=89282810; PubMed=2734307;
Lyons K., Graycar J.L., Lee A., Hashmi S., Lindquist P.B., Chen E.Y., Hogan B.L.M., Derynck R.;
"Vgr-1, a manmalian gene related to Xenopus Vg-1, is a member of the transforming growth factor beta gene superfamily.";
Proc. Natl. Acad. Sci. U.S.A. 86:4554-4558(1989).
-! FUNCTION: INDUCES CARTILAGE AND BONE FORMATION (BY SIMILARITY).
-! TISSUE SPECIFICITY: EXPRESSED IN THE LUNGS. LOW LEVELS SEEN IN THE KIDNEY.
                                                                 01-FEB-1991 (Rel. 17, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
BONE MORPHOGENETIC PROTEIN 6 PRECURSOR (BMP-6) (VG-1-RELATED PROTEIN)
                                                                                                                                                                                                                                                  Gitelman S.E., Kobrin M.S., Ye J.Q., Lopez A.R., Lee A., Derynck R., "Recombinant Vgr-1/BMD-6-expressing tumors induce fibrosis and endochondral bone formation in vivo.";
J. Cell Biol. 126:1595-1609(1994).
                                                                                                                                               Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                         Gitelman S.E., Kobrin M., Lee A., Fet V., Lyons K., Hogan B.L.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam: PF00019; TGF-beta: 1.
Pfam: PF00688; TGFD_propeptide: 1.
PRINTS; PR00438; GFCYSKNOT.
PROSITE; PS00250; TGF_BETA_1: 1.
Signal: Growth factor: Cytokine; Bone; Cartilage; Glycoprotein.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                     "Structure and sequence of the mouse Bmp6 gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 THE ALDNEY.
-1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY
                                               510 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL, U73520; AAB18235.1; -:
EMBL, U73515; AAB18235.1; -:
EMBL, U73515; AAB18235.1; JOINED.
EMBL, U73517; AAB18235.1; JOINED.
EMBL, U73519; AAB18235.1; JOINED.
EMBL, U73519; AAB18235.1; JOINED.
EMBL, U74566; AAA40548.1; -:
EMSL, J04566; AAA40548.1; -:
HSSP; P18075; IBMP.
                                                                                                                                                                                                                          TISSUE=Embryo;
MEDLINE-94375533; PubMed-8089189;
                                                                                                                                                                                                                                                                                                                                MEDLINE-9722480; PubMed-9069123;
                                                                                                                                                                                                                                                                                                                                                                                   Mamm. Genome 8:212-214(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; X80992; CAA56917.1; -.
                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MGD; MGI:88182; Bmp6.
InterPro; IPR001111; -
InterPro; IPR001839; -
InterPro; IPR002400; -
                                                                                                                                   BMP6 OR BMP-6 OR VGR1.
                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                      NCBI_TaxID=10090;
                                           BMP6_MOUSE
P20722;
                                                                                                                                                                                                                                                                                                                                                         Derynck R.;
                 RESULT 32
BMP6_MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                               4 TNYCFRNLEENCCVRPLYIDFRQDLGWK-WVHEPKGYYANFCSGPCPYLRSAD---TTHS 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    McPherron A.C., Lee S.-J.;
"Double muscaling in cattle due to mutations in the myostatin gene.";
"Proc. Natl. Acad. Sci. U.S.A. 94:12457-12461(1997).
-i- FUNCTION: ACTS SPECIFICALLY AS A NEGATIVE REGULATOR OF SKELETAL
BONE MORPHOGENETIC PROTEIN 6.
BY SIMILARITY.
BY SIMILARITY.
INTERCHAIN 'EW SIMILARITY).
N-LINKED (GLCNAC...) (POTENTIAL).
E -> M (IN REF. 3).
E -> P (IN REF. 3).
L -> P (IN REF. 3).
L -> P (IN REF. 3).
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9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        457 IVQTLVHLMNPEYVPKPCCAPTKLNAISVLYFDDNSNVILKKYRNMVVRACGC 509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-JUL-1999 (Rel. 38, Last sequence update).
30-MAY-2000 (Rel. 39, Last annotation update)
GROWTH/DIFFERENTIATION FACTOR 8 PRECURSOR (GDF-8) (MYOSTATIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GROWTH/DIFFERENTIATION FACTOR 8.
                                                                                                                                                                                                                                                                                                                                 Score 205; DB 1; Length 510;
Pred. No. 1.4e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -i- SUBUNIT: HOMODIMER, DISULFIDE-LINKED (BY SIMILARITY).
-i- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                             43; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPRU01053,
Pfam; PF00019; TGF-beta; 1.
Pfam; PF00688; TGF-berpeptide; 1.
PROSITE; PS00250; TGF_BETA_1; 1.
Growth factor; Cytokine; Glycoprotein; Signal.
23 POTEMITAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN-WHITE LEGHORN; TISSUE-Skeletal muscle;
MEDLINE-98024153; PubMed-9356471;
                                                                                                                                                                                                                                                                                                              32.3%; SCUL.

y 37.2%; Pred. NO. 1...
''' 22; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           375 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AF019621; AAB86688.1; -.
InterPro; IPR001111; -.
InterPro; IPR001839; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (Rel. 38, Created)
(Rel. 38, Last sequ
                                                                                                                                                                                                                                                                        MW.
  510
507
509
509
474
238
266
383
461
73
73
73
73
73
73
73
                                                                                                                                                                                                                                                                                                                                                                         42; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MUSCLE GROWTH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gallus.
NCBI_TaxID=9031;
      3379
4438
4442
2238
2266
266
401
73
73
86
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267
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-JUL-1999
15-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GDF8_CHICK
    CHAIN
DISULFID
                                                                                                                                                                   CARBOHYD
CARBOHYD
                                                                                                                                                                                                                              CONFLICT
                                                                                                      CARBOHYD
                                            DISULFID
                                                                   DISULFID
                                                                                      DISULFID
                                                                                                                              CARBOHYD
                                                                                                                                                   CARBOHYD
                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                             CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIGNAL
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tqfb3p.rsp

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                                                                                                                                        4;
                                                                                                                                                                                          278 ESRCCRYPLTVDF-EAFGWDWIIAPKRYKANYCSGECEFVFLOKYPHTH----LVHOAN 331
                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          McPherron A.C., Lee S.-J.;
"Double muscaling in cattle due to mutations in the myostatin gene.";
"Proc. Natl. Acad. Sci. U.S.A. 94:12457-12461(1997).
-i- FUNCTION: ACTS SPECIFICALLY AS A NEGATIVE REGULATOR OF SKELETAL
                                                                                                                                                               EENCCVRPLYIDFRQDLGWKWVHEPKGYYANFCSGPCP--YLRSADTTHSTVLGLYNTLN 69
                                                                                                                                                                                                                                                                                                                                                                                                                                Euteleostomi;
                                                     LINKED (GLCNAC. . .) (POTENTIAL). DA732DB9426E4D4F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-LINKED (GLCNAC. . .) (POTENTIAL).
EBFF6129725E6AFA CRC64;
                                                                                                                                       6
                                                                                                                                                                                                                                                                                                                                          15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
01-CCT-2000 (Rel. 40, Last annotation update)
GROWTH/DIFFERENTIATION FACTOR 8 PRECURSOR (GDF-8) (MYOSTATIN)
                                                                                                            Length 375;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL.
GROWTH/DIFFERENTIATION FACTOR 8.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
INTERCHAIN (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ω.
                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MUSCLE GROWTH.
-!- SUBUNIT: HOMODIMER, DISULFIDE-LINKED (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
INTERCHAIN (BY SIMILARITY).
N-LINKED (GLCNAC. . .) (POTH
                                                                                                                                       Indels
                                                                                                                                                                                                                                    70 PEASASPCCVPQDLEPLTILYYVGRTPKV-EQLSNMVVKSCKCS 112
                                                                                                                                       36;
                                                                                                            DB 1;
                                                                                                           ; Score 204.5; DB 1; Pred. No. 1.1e-14; 15; Mismatches 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Growth factor; Cytokine; Glycoprotein; Signal.
                                                                                                                                                                                                                                                                                                                  375 AA
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                                                                                                                                                                                                                                                                                                                   PRT;
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Pfam; PF00688; TGFD_propeptide; 1.
PROSITE; PS00250; TGF_BETA_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
TISSUE-Skeletal muscle;
MEDLINE-98024153; PubMed-9356471;
                                                                     MW.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AF019627; AAB86694.1; -.
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                                                                                                           32.3%;
39.4%;
                                                                   42707
                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR001111; -. InterPro; IPR001839; -.
 340
372
374
339
71
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375
340
372
374
339
                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human)
                                                                                             Query Match
Best Local Similarity
Thes 41; Conserve
 281
309
313
339
71
375 AA;
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339
71
375 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                   GDF8 OR MSTN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               601788;
                                                                                                                                                                                                                                                                                                                  GDF8_HUMAN
DISULFID
DISULFID
DISULFID
                                       DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CARBOHYD
SEQUENCE
                                                                   SEQUENCE
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                                                                                                                                                                                                                                                                                       RESULT 34
GDF8_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CHAIN
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 SEFFF
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                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Meleagrididae; Meleagris.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                             12 EENCCVRPLYIDFRQDLGWKWVHEPKGYYANFCSGPCP--YLRSADTTHSTVLGLYNTLN 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the myostatin gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        McPherron A.C., Lee S.-J.;
"Double musciling in cattle due to mutations in the myostatin gene.";
"Proc. Natl. Acad. Sci. US.A. 94:12457-12461(1997).
-i- FUNCTION: ACTS SPECIFICALLY AS A NEGATIVE REGULATOR OF SKELETAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL.
GROWTH/DIFFERENTIATION FACTOR 8.
BY SIMILARITY.
BY SIMILARITY.
INTERCHAIN (BY SIMILARITY).
INTERCHAIN (BY SIMILARITY).
N-LINKED (GLCNAC. . .) (POTENTIAL).
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30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
GROWTH/DIFFERENTIATION FACTOR 8 PRECURSOR (GDF-8) (MYOSTATIN).
 Length 375;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 375;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBUNIT: HOMODIMER, DISULFIDE-LINKED (BY SIMILARITY). SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                       332 PRGSAGPCCTPTKMSPINMLYFNGKEOIIYGKIPAMVVDRCGCS 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         70 PEASASPCCVPQDLEPLTILYYVGRTPKV-EQLSNMVVKSCKCS 112
                                                                                                                          70 PEASASPCCVPQDLEPLTILYYVGRTPKV-EQLSNMVVKSCKCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1;
 DB 1;
32.3%; Score 204.5; DB 1
39.4%; Pred. No. 1.1e-14;
ive 15; Mismatches 39
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROBLEM: PF00019; TGF-beta; 1.
Pfam; PF000688; TGF-propeptide; 1.
PROSITE; PS00250; TGF_BETA_1; 1.
Growth factor; Cytokine; Glycoprotein; Signal.
                                                                                                                                                                                                                                   375 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  32.3%; Score 204.5;
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Interpro; IPR001111; -.
Interpro; IPR001839; -.
                                                                                                                                                                                                                                                                                                                                        Meleagris gallopavo (Common turkey).
                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE-Skeletal muscle;
MEDLINE-98024153; PubMed-9356471;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  42784 MW;
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                                Conservative
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                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   374
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              Best_Local Similarity
Matches 41; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MUSCLE GROWTH
                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    281
309
313
339
                                                                                                                                                                                                                                                                                                                               GDF8 OR MSTN
                                                                                                                                                                                                                                    GDF8_MELGA
   Query Match
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Tue Oct 30 12:56:54 2001
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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN=DURCC, HAMPSHIRE, MEISHAN, & YORKSHIRE; TISSUE=Skeletal muscle;
Voelker G.R., Conroy J.C., Wheeler M.B.;
"Porcine myostatin cDNA sequences: Duroc, Hampshire, Meishan and
Yorkshire pigs.";
Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-98024153; PubMed-9356471;
MCPherron A.C., Lee S.-J.;
"Double muscling in cattle due to mutations in the myostatin gene.";
Proc. Natl. Acad. Sci. U.S.A. 94:12457-12461(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dancau I., Silversides D.W.;
Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
-! FUNCTION: ACTS SPECIFICALLY AS A NEGATIVE REGULATOR OF SKELETAL
                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae, Sus,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BY SIMILARITY.

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BY SIMILARITY.

BY SIMILARITY.

N-LINERCHAIN (BY SIMILARITY).

N-LINKED (GLCNAC. . .) (POTENTIAL).

0F658685EFDA3418 CRC64;
                                                                                                                                                                                                           15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
GROWTH/DIFFERENTIATION FACTOR 8 PRECURSOR (GDF-8) (MYOSTATIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GROWTH/DIFFERENTIATION FACTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -i- SUBUNIT: HOMODIMER, DISULFIDE-LINKED (BY SIMILARITY).
-i- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
Cytokine; Glycoprotein; Signal.
                                                                                                                                                                    ΑA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 1-10 AND 36-375 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00019; TGF-beta; 1.
Pfam; PF00688; TGFb_propeptide; 1.
PROSITE; PS00250; TGF_BETA_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AF019623; AAB86690.1; -. EMBL; AF188635; AAF02770.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AF188637; AAF02772.1; -. EMBL; AF188638; AAF02773.1; -. EMBL; AF033855; AAC08035.1; -. EMBL; AF093798; AAC62489.1; -. InterPro; IPR001111; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AF188636; AAF02771.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      42791 MW;
                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
TISSUE=Skeletal muscle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 266
375
340
372
374
339
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267
281
309
313
339
71
375 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PR001839
                                                                                                                                                                                                                                                                                                                                                       Sus scrofa (Pig).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MUSCLE GROWTH
                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Growth factor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE ** Muscle;
                                                                                                                                                                                                                                                                                                                        GDF8 OR MSTN.
                                                                                                                                                         GDF8_PIG
018831;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                    RESULT 36
GDF8_PIG
DT GDF8_PIG
DT GDF8_PIG
DT GDF8_PIG
DT GDF8_PIG
DT GDF8_PIG
DF GDF GDF8_PIG
DF GDF8_PIG
DF GDF8_PIG
DF GDF8_PIG
DF GDF8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- SUBUNIT: HOMODIMER, DISULFIDE-LINKED (BY SIMILARITY).
-!- TISSUE SPECIFICITY: EXPRESSED SPECIFICALLY IN DEVELOPING AND ADULT SKELETAL MUSCLE. WEAK EXPRESSION IN ADIPOSE TISSUE.
-!- DEVELOPMENTAL STAGE: FIRST DETECTED AT DAY 9.5 POST-COITUM IN ONE-THIRD OF DEVELOPING SOMITES. AT DAY 10.5, EXPRESSED IN THE MYOTOME COMPARTMENT OF SOMITES. AT LATER STAGES OF DEVELOPMENT, DETECTED IN A WIDE RANGE OF DEVELOPING MUSCLES. EXPRESSION CONTINUES IN ADULTHOOD.
                                                                             12 BENCCVRPLYIDFRQDLGWKWVHEPKGYYANFCSGPCP--YLRSADTTHSTVLGLYNTLN 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nature 387:83-90(1997).
-!- FUNCTION: ACTS SPECIFICALLY AS A NEGATIVE REGULATOR OF SKELETAL
                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-LINKED (GLCNAC. . .) (PÓTENTIAL). 3E19814DD62C08BE CRC64;
                                                                                                                                                                                                                                                               01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
GROWTH/DIFFERENTIATION FACTOR 8 PRECURSOR (GDF-8) (MYOSTATIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       McPherron A.C., Lawler A.M., Lee S.-J.;
"Regulation of skeletal muscle mass in mice by a new TGF-beta
   Length 375;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GROWTH/DIFFERENTIATION FACTOR 8.
                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
INTERCHAIN (BY SIMILARITY).
                                                                                                                       70 PEASASPCCVPQDLEPLTILYYVGRTPKV-EQLSNMVVKSCKCS 112
                                                                                                                                          39;
; Score 204.5; DB 1; Pred. No. 1.1e-14; 15; Mismatches 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00119; TGF-beta; 1.
Pfam; PF00688; TGF-propeptide; 1.
PROSITE; PS00250; TGF_BETA_1; 1.
Growth factor; Cytokine; Glycoprotein; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-CD-1; TISSUE-Skeletal muscle; MEDLINE-97284412; Pubmed-9139826;
                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ΜM
 32.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; U84005; AAC53167.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         376
341
373
373
340
72
42921 1
                              Conservative
                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MGD; MGI:95691; Mstn.
InterPro; IPR001111; -.
InterPro; IPR001839; -.
                                                                                                                                                                                                                                                                                                                                              (Wouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         superfamily member."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            268
282
310
314
340
72
376 AA;
                Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P18075; 1BMP.
                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MUSCLE GROWTH
                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                              GDF8 OR MSTN.
                                                                                                                                                                                                                                                                                                                                                Mus musculus
                                41;
                                                                                                                                                                                                                                   GDF8_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DISULFID
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                                                                                                                                                                                                                                                   008689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HSSb;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CHAIN
                             Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4
                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                          12 EENCCVRPLYIDFRQDLGWKWVHEPKGYYANFCSGPCP--YLRSADTTHSTVLGLYNTLN 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Double muscling in cattle due to mutations in the myostatin gene."; Proc. Natl. Acad. Sci. U.S.A. 94:12457-12461(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EENCCVRPLYIDFRQDLGWKWVHEPKGYYANFCSGPCP--YLRSADTTHSTVLGLYNTLN 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   933043D8C8C3294B CRC64;
                                 6
                                                                                                                                                                                                                                   035312;
15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
GROWTH/DIFFERENTIATION FACTOR 8 PRECURSOR (GDF-8) (MYOSTATIN).
    Length 376;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 32.3%; Score 204.5; DB 1; Length 376; 39.4%; Pred. No. 1.1e-14; ive 15; Mismatches 39; Indels 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL. GROWTH/DIFFERENTIATION FACTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MUSCLE GROWTH.
-!- SUBUNIT: HOMODIMER, DISULFIDE-LINKED (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
INTERCHAIN (BY SIMILARITY).
N-LINKED (GLCNAC. . .) (POTE)
                                 Indels
                                                                                                                    70 PEASASPCCVPQDLEPLTILYYVGRTPKV-EQLSNMVVKSCKCS 112
                                                                                                                                    DB 1;
                Pred. No. 1.1e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00019; TGF-beta; 1.
Pfam; PF00688; TGF_bropeptide; 1.
PS0021E; PS00250; TGF_BFR_1; 1.
Growth factor; Cytokine; Glycoprotein; Signal.
                                                                                                                                                                                                                          376 AA
                                 15; Mismatches
   32.3%; Score 204.5; 39.4%; Pred. No. 1.16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL.
                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Skeletal muscle;
MEDLINE=98024153; PubMed=9356471;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AF019624; AAB86691.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        72 N-
42829 MW;
Query Match
Best Local Similarity 39.4%
Matches 41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               41; Conservative
                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                               McPherron A.C., Lee S.-J
                                                                                                                                                                                                                                                                                                                              Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR001111; -. InterPro; IPR001839; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     376 AA;
                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                               GDF8 OR MSTN.
                                                                                                                                                                                                                       GDF8_RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DISULFID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CHAIN
                                                                                       279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DEVELOPMENTAL STAGE: CONCENTRATED IN THE STREAMING CYTOPLASM IN JUST'S PERTITIORED DURING CLEAVAGE AMONG ALL BLASTOMERES. ABSENT IN THE YOLK CELL DURING CLEVAGE, BLASTULA AND GASTRULA STAGES. DISTRIBUTED HOMOGENEOUSLY AMONG ALL CELLS OF THE
                                                                                                                                                                                                                                                                                                                                                                 Helde K.A., Grunwald D.J.; "The DVR-1 (Vg1) transcript of zebrafish is maternally supplied and
                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
INTERCHAIN (BY SIMILARITY).
N'LINKED (GLCNAC. .) (POTENTIAL).
N'LINKED (GLCNAC. .) (POTENTIAL).
N'LINKED (GLCNAC. .) (POTENTIAL).
N'LINKED (GLCNAC. .) (POTENTIAL).
W; OEDSB9850EBFB222 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                           Dev. Biol. 159:418-426(1993).

-1- FUNCTION: SERVES TO FACILITATE THE DIFFERENTIATION OF EITHER MESODERN OR BY PROVIDING PREMISSIVE ENVIRONMENT.

-1- SUBUNIT: HOMODIMER (PROBABLE).

-1- TISSUE SPECIFICITY: ABUNDANT IN OVARIES AND EGGS, AND EQUALLY DISTREBUTED AMONG ALL BLASTOMERES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 355;
70 PEASASPCCVPQDLEPLTILYYVGRTPKV-EQLSNMVVKSCKCS 112
                333 PRGSAGPCCTPTKMSPINMLYFNGKEQIIYGKIPAMVVDRCGCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1;
                                                                                                                                       01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
DVR-1 PROTEIN PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00019; TGF-beta; 1.
Pfam; PF00689; TGF-beta; 1.
PRINTS; PR00489; GFC-SKNOT.
GROSTIE; P500250; TGF-BETA 1; 1.
Growth factor; Mitogen; Glycoprotein; Signal.
                                                                                                                                                                                                                                                                 Cypriniformes; Cyprinidae; Rasborinae; Danio
NCBI_TaxID=7955;
                                                                                                                                                                                                                        Brachydanio rerio (Zebrafish) (Zebra danio).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DVR-1 PROTEIN.
                                                                                                           355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 204;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL. POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                distributed throughout the embryo.";
                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                    TISSUE=Embryo;
MEDLINE=94009920; PubMed=8405668;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZFIN; ZDB-GENE-980526-389; vgl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     40201 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; U00931; AAC27347.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   32.2%;
                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR001839; -. InterPro; IPR002400; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      355
320
320
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354
319
179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    296
355 AA;
                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      241
254
283
287
                                                                                                                                                                                                      VG1 OR DVR-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GASTRULA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HSSP; P18075
                                                                                                        DVR1_BRARE P35621;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CARBOHYD
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                                                                                              DVR1_BRARE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        between the Swiss Institute of Bioinformatics and the EMBL outstatist the Buropean Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commercements and the statement is not removed.
                                                                                                          15 CCVRPLYIDFRODLGWK-WVHEPKGYYANFCSGPCPYLRSAD---TTHSTVLGLYNTLNP 70
                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Interpro; IPR001839; ...
Interpro; IPR0018199; ...
Interpro; IPR001919; TGF-beta; 1.
Pfam; PF00168; TGF-beta; 1.
PRINTS; PR006438; GFCYSKNOT.
PRINTS; PR00670; INIIBINBA.
PROSITE; PS00250; TGF_BETA_1; 1.
PROSITE; PS00250; TGF_BETA_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chordata; Craniata; Vertebrata; Euteleostomi;
Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                       ;
9
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INHIBIN BETA A CHAIN.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
INTERCHAIN (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fleming J.S., Galloway S.M., Crawford R.J., Tisdall D.J.,
                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
INHIBIN BETA A CHAIN PRECURSOR (ACTIVIN BETA-A CHAIN).
                                                                                                                                                                         71 EASASPCCVPQDLEPLTILYYVGRTPKV-EQLSNMVVKSCKC 111
                                                                                                                                                                                                         Pred. No. 1.2e-14;
8; Mismatches 37;
                                                                                                                                                                                                                                                                                                                                                         ¥.
40.2%; Preq. .v..
                                                                                                                                                                                                                                                                                                                                                       425
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=95217464; PubMed=7702862;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; L19218; AAC41621.1; -.
                                  41; Conservative
                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR000491; -.
InterPro; IPR0011111; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bovidae; Caprinae; Ovis
NCBI_TaxID=9940;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        309
425
321
390
422
424
389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ovis aries (Sheep).
         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Greenwood P.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HSSP; P18075
                                                                                                                                                                                                                                                                                                                                                    IHBA_SHEEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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       Best Local
Matches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DISULFID
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                                                                                                                                                                                                                                                                                                  RESULT 40
IHBA_SHEEP
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This SWISS-PROT entry is copyright. It is produced through a collaboration
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01-0CT-2000 (Rel. 40, Last sequence update)
01-0CT-2000 (Rel. 40, Last sequence update)
01-0CT-2000 (Rel. 40, Last annotation update)
GROWTH/DIFFERENTIATION FACTOR 11 PRECURSOR (BONE MORPHOGENETIC PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nakashima M., Toyono T., Akamine A., Joyner A.;
"Expression of growth/differentiation factor 11, a new member of the BMP/TGFDeta superfamily during mouse embryogenesis.";
Mech. Dev. 80:185-189(1999).
-!- FUNCTION: SECRETED SIGNAL THAT ACTS GLOBALLY TO SPECIFY POSITIONAL IDENTITY ALONG THE ANTERIOR/POSTERIOR AXIS DURING DEVELOPMENT.
PLAY CRITICAL ROLES IN PATTERNING BOTH MESODERMAL AND NEURAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUES AND IN ESTABLISHING THE SKELETAL PATTERN.
-!- SUBGNIT: HOWODIMER, DISULFIDE-LINKED (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: SECRETED (PROBABLE).
-!- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN THE DEVELOPING LIMB BUD,
INITIALLY DETECTED IN THE DISTAL MESENCHYME, AND LATER LOCALIZING
TO REGIONS AROUND THE DEVELOPING BONES. IS ALSO EXPRESSED IN ADULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tail
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             McPherron A.C., Lawler A.M., Lee S.-J.; "Regulation of anterior/posterior patterning of the axial skeleton by growth/differentiation factor 11.";
                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DEVELOPMENTAL STAGE: FIRST STRONGLY EXPRESSED IN RESTRICTED DOMAINS AT 8.5 DAYS POST COITUS (DPC) WHERE IT IS HIGHEST IN THE TAIL BUD. AT 10.5 DPC, EXPRESSED IN THE BRANCHIAL ARCHES, LIMB BUD, TAIL BUD AND POSTERIOR DORSAL NEURAL TUBE. LATER, EXPRESSED IN TEMINALLY-DIFFERENTATED ODONTOBLASTS, THE NASAL EPITHELIUM, SIMILARITY: BELONGS TO THE TEFAIN.
                                                                                                                                           15 CCVRPLYIDFRQDLGWK-WVHEPKGYYANFCSGPCP----YLRSADTTHSTVLGLYNTL 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      novel BMP expressed in developing mouse limb, spinal cord, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Я,
N-LINKED (GLCNAC. . .) (POTENTIAL). C910F7F64FF82F67 CRC64;
                                                                                                           10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gamer L.W., Wolfman N.M., Celeste A.J., Hattersley G., Hewick
                                                                        Length 425;
                                                                                                         36; Indels
                                                                                                                                                                                                                                      69 -- NPEASASPCCVPQDLEPLTILYY - VGRTPKVEQLSNMVVKSCKCS 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     bud is a potent mesoderm inducer in Xenopus embryos."; Dev. Biol. 208:222-232(1999).
                                                                    Score 204; DB 1;
Pred. No. 1.5e-14;
                                                                                                                                                                                                                                                                                                                                               ¥.
                                                                                                         20; Mismatches
                                                                                                                                                                                                                                                                                                                                               405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               [1]
SEQUENCE FROM N.A.
MEDLINE=99177155; Pubmed=10075854;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     [3]
SEQUENCE OF 75-405 FROM N.A.
SEQUENCE OF 75-405 FROM N.A.
MEDLINE=99173787; PubMed=10072786;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=129/SVJ;
MEDLINE=99318097; PubMed=10391213;
              47565 MW;
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                                                                    32.2%;
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                                                                                                         41; Conservative
                                                                                                                                                                                                                                                                                                                                             STANDARD;
              425 AA;
                                                                                       Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              [2]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GDF11 OR BMP11
                                                                                                                                                                                                                                                                                                                                             GDFB_MOUSE
CARBOHYD
                SEQUENCE
                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rosen V
                                                                                                                                                                                                                                                                                                          RESULT 41
GDFB_MOUSE
                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1
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Bovidae; Bovinae; Bos.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                             PROPEP
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GDF8_BOVIN
                                                                                                                                                                                                                                                                                                                                    SIGNAL
                                                                                                                                                                                                                                                                                                                                                       CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       δ
between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                   5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GDFB_HUMAN STANDARD; PRT; 407 AA.
095390; Q9UID1; Q9UID2;
01-007-2000 (Rel. 40, created)
01-007-2000 (Rel. 40, Last sequence update)
01-007-2000 (Rel. 40, Last annotation update)
GROWTH/DIFFERENTIATION FACTOR 11 PRECURSOR (BONE MORPHOGENETIC PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "A novel BMP expressed in developing mouse limb, spinal cord, and tail
                                                                                                                                                                                                                                                                                                                                                                                                                                          60 TVLGLYNTLNPEASASPCCVPQDLEPLTILYY-----VGRTPKVEQLSNMVVKSCKCS 112
                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                    9 RNL------EENCCVRPLYIDFRQDLGWKWVHEPKGYYANFCSGPCPYLRSADTTHS 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gamer L.W., Wolfman N.M., Celeste A.J., Hattersley G., Hewick R.,
                                                                                                                                                                                                                                                                                                      . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                   26;
                                                                                                                                                                                                                        BY SIMILARITY.
GROWTH/DIFFERENTIATION FACTOR 11.
                                                                                                                                                                                                                                                                                                                                                                Length 405;
                                                                                                                                                                                                                                           POLY-ALA.
POLY-GLX.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
INTERCHAIN (BY SIMILARITY).
N-LINKED (GLCNAC. . .) (POTER F - S (IN REF. 3).
T -> N (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                   39; Indels
                                                                                                                                                                                                                                                                                                               -> G (IN REF. 3).
-> N (IN REF. 2).
A74E382710A14781 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   bud is a potent mesoderm inducer in Xenopus embryos.";
                                                                                                                                                                                                                                                                                                                                                              32.0%; Score 203; DB 1; 36.7%; Pred. No. 1.8e-14;
                                                                                                                                                                                                      Growth factor; Cytokine; Glycoprotein; Signal.
                                                                                                                                                                                                                                                                                                                                                                                 11; Mismatches
                                                                                                                                                                                                                 POTENTIAL.
                                                                          Pfam: PF00019; TGF-beta; 1.
Pfam: PF00688; TGFb_propeptide; 1.
PROSITE; PS00250; TGF_BETA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Fetal brain;
MEDLINE=99177155; PubMed=10075854;
                                                                  EMBL; AF100906; AAC72853.1; -.
                                                                                                                                                                                                                                                                                                                                    ΜW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Dev. Biol. 208:222-232(1999).
                                                                                                                                                                                                                                                                                                                                  44946
                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                    MGD; MGI:1338027; Gdf11.
HSSP; P18075; 1BMP.
                                                                                                                                            HSSP; P18075; 1BMP.
InterPro; IPR001111; -.
InterPro; IPR001839; -.
                                                                                                                                                                                                                                                                370
402
404
369
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405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11).
GDF11 OR BMP11.
                                                                                                                                                                                                                                                                                                                                                                                  44;
                                                                                                                                                                                                                                                                                                                CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                   DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rosen V.;
                                                                                                                                                                                                                                                                DISULFID
                                                                                                                                                                                                                                                                           DISULFID
                                                                                                                                                                                                                                                                                                       CARBOHYD
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                                                                                                                                                                                                                                              DOMAIN
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                                                                                                                                                                                                                 SIGNAL
                                                                                                                  EMBL;
                                                                                                                                                                                                                                    CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 42
GDFB_HUMAN
                                                                             EMBL;
                                                                                       EMBL;
                                                                                               EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 60 TVLGLYNTLNPEASASPCCVPQDLEPLTILYY-----VGRTPKVEQLSNMVVKSCKCS 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---HLVQQANPRGSAGPCCTPTKMSPINMLYFNDKQQIIYGKIP-----GMVVDRCGCS 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9 RNL-----EENCCVRPLYIDFRQDLGWKWVHEPKGYYANFCSGPCPYLRSADTTHS 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                McPherron A.C., Lawler A.M., Lee S.-J.;

"Regulation of anterior/posterior patterning of the axial skeleton by growth/ddifferentiation factor 11.";

Nat. Genet. 22:260-264(1999).

-I. FUNCTION: SECRETED SIGNAL THAT ACTS GLOBALLY TO SPECIFY POSITION IDENTITY ALONG THE ANTERIOR/POSTERIOR AXIS DURING DEVELOPMENT.

PLAY CRITICAL ROLES IN PATTERNING BOTH MESODERMAL AND NEURAL TISSUES AND IN ESTABLISHING THE SKELETAL PATTERN.

-I. SUBGUIT: HOMODIMER, DISGUEDE-LINKED (BY SIMILARITY).

-I. SUBGELLULAR LOCATION: SECRETED (PROBABLE).

-I. SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GDF8 OR MSTN OR MH.

Bos taurus (Bovine).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POLY-ALA.
POLY-GLY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
N'INTECHAIN (BY SIMILARITY).
N'INKED (GLCNAC. . . ) (POTENTIAL).
W, EBFF48E3635BA8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GDF8_BOVIN STANDARD; PRT; 375 AA.
018836; 018829;
15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
GROWTH/DIFFERENTIATION FACTOR 8 PRECURSOR (GDF-8) (MYOSTATIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL.
BY SIMILARITY.
GROWTH/DIFFERENTIATION FACTOR 11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     32.0%; Score 203; DB 1; Length 407; 36.7%; Pred. No. 1.8e-14; Live 11; Mismatches 39; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00019; TGF-beta; 1.
Pfam; PF00688; TGFb_propeptide; 1.
PS0021E; PS00250; TGF_BETA; 1.
Growth factor; Cytokine; Glycoprotein; Signal.
[2]
SEQUENCE FROM N.A.
MEDLINE=99318097; PubMed=10391213;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AF100907; AAC72852.1; -. EMBL; AF028333; AAF21630.1; -. EMBL; AF028334; AAF21631.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              45090 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MIM; 603936; -.
HSSP; P18075; 1BMP.
InterPro; IPR001111; -.
InterPro; IPR001839; -.
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372
404
406
371
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407 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                     DEVELOPMENTAL STAGE: WIDELY EXPRESSED THROUGHOUT DEVELOPMENT.
LOW LEVELS ARE FOUND UP TO DAY 29 EMBRYOS. LEVELS INCREASE FROM
DAY 31 UP UNTIL LATE GESTATION.
DISEASE: DEFECTS IN GDF8 ARE THE CAUSE OF THE DOUBLE-MUSCLE
PHENOTYPE OR MUSCULAR HYPERTROPHY (MH), AN AUTOSOMAL RECESSIVE
DISEASE FREQUENTLY FOUND IN THE BELGIAN BLUE AND PIEDMONTESE
CATTLE BREEDS. THIS DISEASE IS CHARACTERIZED BY AN INCREASED
MUNDER OF MUSCLE FIBERS (HYPERPLASIA), RESULTING IN AN INCREASE IN
SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
                                                                                                                                                                                                                                                                                                                           SUBUNIT: HOMODIMER, DISULFIDE-LINKED (BY SIMILARITY).
TISSUE SPECIFICITY: SPECIFICALLY EXPRESSED IN DEVELOPING AND ADULT
SKELETAL MUSCLE. HIGHEST LEVELS FOUND IN THE HINDLIME MUSCLES
M.SEMIMEMBRANOSUS AND M.BICEPS FEMORIS; LOW LEVELS IN OTHER
                                                                                                                                                                                                                                                      "Double muscling in cattle due to mutations in the myostatin gene.";
Proc. Natl. Acad. Sci. U.S.A. 94:12457-12461(1997).
-!- FUNCTION: ACTS SPECIFICALLY AS A NEGATIVE REGULATOR OF SKELETAL
                                                                                       Kambadur R., Sharma M., Smith T.P.L., Bass J.J.;
"Mutations in myostatin (GDF8) in double-muscled Belgian Blue and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
INTERCHAIN (BY SIMILARITY).
N-LINKED (GLCNAC. .) (POTENTIAL).
F -> L (IN MH; PIEDMONTESE BREED).
C -> Y (IN MH; PIEDMONTESE BREED).
T -> M (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00019; TGF-beta; 1.
Pfam; PF00688; TGF-propeptide; 1.
PROSITE: PS00250; TGF_BETA_1; 1.
Growth factor; Cytokine; Glycoprotein; Signal; Disease mutation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GROWTH/DIFFERENTIATION FACTOR 8.
                                                                                                                                                                                   SEQUENCE FROM N.A., AND VARIANTS MH LEU-94 AND TYR-313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E1B791AD92D4A9E6 CRC64;
                                                      STRAIN-FRIESIAN; TISSUE-Muscle, and Embryo; MEDLINE-97458167; PubMed-9314496;
                                     SEQUENCE FROM N.A., AND VARIANT MH TYR-313
                                                                                                                                                                                                  STRAIN-HOLSTEIN; TISSUE-Skeletal muscle;
MEDLINE-98024153; PubMed-9356471;
MCPherron A.C., Lee S.-J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL. POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AF019761; AAB81508.1; -. EMBL; AF019620; AAB86687.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          42520 MW;
                                                                                                                                               Genome Res. 7:910-916(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HSSP; P18075; IBMP.
InterPro; IPR001111; -.
InterPro; IPR001839; -.
                                                                                                                              Piedmontese cattle.";
                                                                                                                                                                                                                                                                                                                                                                                                        HINDLIMB MUSCLES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14
375 AA;
                                                                                                                                                                                                                                                                                                              MUSCLE GROWTH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CHAIN
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Albano P.M., Groome N., Smith J.C.;
"Activins are expressed in preimplantation mouse embryos and in ES
and EC cells and are regulated on their differentiation.";
Development 117.711-723(1993).
-!- FUNCTION: INHIBIN IS A GONADAL GLYCOPEPTIDE THAT INHIBITS THE
SECRETION OF FOLLITROPIN BY THE PITUITARY GLAND. ON THE OTHER HAND
ACTIVIN ACTIVIN ACTIVATES THE SECRETION OF FOLLITROPIN. ACTIVIN IS ALSO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; MINOSON MINO
                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INTERCHAIN (BY SIMILARITY).
N-LINKED (GLCNAC. .) (POTENTIAL).
80C251B8754A7213 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IMPORTANT IN EMBRYONIC ACKALLING C. COLLINGER IN THE MANAGE DESCRIPTION OF WORE DISULFIDE BONDS.

-!- SUBUNIT: DIMERIC, LINKED BY ONE OR WORE DISULFIDE BONDS. INHIBIN A IS A DIMER OF ALPHA AND BETA-B.

ACTIVIN A IS A DIMER OF BETA-A.

ACTIVIN AB IS A DIMER OF BETA-A AND BETA-B.

-!- TISSUE SPECIFICITY: UTERUS, OVARY, AND LIVER.

-!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
                                                                                                                                                                                                                                                                                                01-FEB-1994 (Rel. 28, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
INHIBIN BETA A CHAIN PRECURSOR (ACTIVIN BETA-A CHAIN).
                              70 PEASASPCCVPQDLEPLTILYYVGRTPKV-EQLSNMVVKSCKCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INHIBIN BETA A CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                              424 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE-93321614; PubMed-8330535;
                                                                                                                                                                                                                                                                  (Rel. 28, Created)
(Rel. 28, Last sequ
(Rel. 40, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; X69619; CAA49325.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HSSP; P18075; 1BMP.
MGD; MGI:96570; Inhba.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIR; S31440; S31440.
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424 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID-10090;
                                                                                                                                                                                                                                                                  01-FEB-1994
                                                                                                                                                                                                                                                                                          01-FEB-1994
01-OCT-2000
                                                                                                                                                                                                        IHBA_MOUSE
004998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DISULFID
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31.5%; Score 200; DB 1; Length 424;

47392 MW;

SEQUENCE

4

Gaps

6

40; Indels

DB 1; Length 375;

31.8%; Score 201.5; DB 1 39.4%; Pred. No. 2.4e-14;

14; Mismatches

41; Conservative

12 Matches

ð g

Similarity

Query Match Local EENCCVRPLYIDFRQDLGWKWVHEPKGYYANFCSGPCP--YLRSADTTHSTVLGLYNTLN 69

Query Match

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NA FIT FIT FIT SO
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A MAKANUKE T., Asashima M., Eto Y., Titani K., Sugino H.;
A MIizumi T., Mashiro T., Sugino K., Titani K., Sugino H.;
T "Isolation and characterization of native activin B.";
U. J. Biol. Chem. 267:16385-16389(1992).
C -!- FUNCTION: INHIBIN IS A GONADAL GLYCOPEPTIDE THAT INHIBITS THE SECRETION OF FOLLITROPIN. ACTIVIN IS ALSO
ACTIVIN ACTIVIN ACTIVIN SATIVED BY ONE DIGULETIDE BONDS.
INHIBIN A IS A DIMER OF ALPHA AND BETA-B.
C --- SUBUNITY: DIMERSIC, LINEAD BY ONE DIGULETIDE BONDS.
INHIBIN A IS A DIMER OF BETA-A.
C ACTIVIN A IS A DIMER OF BETA-A.
C --- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
                       5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                       Mason A.J., Hayflick J.S., Ling N., Esch F., Ueno N., Ying S.-Y., Guillemin R., Niall H., Seeburg P.H.; "Complementary DNA sequences of ovarian follicular fluid inhibin show precursor structure and homology with transforming growth
                                                           CCVRPLYIDFRODLGWK-WVHEPKGYYANFCSGPCP----YLRSADTTHSTVLGLYNTL 68
                                                                                                                                                                                                                                                                                    Euteleostomi;
Sus.
                       Indels
                                                                                              -- NPEASASPCCVPQDLEPLTILYY-VGRTPKVEQLSNMVVKSCKCS 112
                                                                                                           378 GHSPFANLKSCCVPTKLRPMSMLYYDDGQNIIKKDIQNMIVEEGGCS 424
                                                                                                                                                                                                         23-OCT-1986 (Rel. 02, Created)
23-OCT-1986 (Rel. 02, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
INHIBIN BETA A CHAIN PRECURSOR (ACTIVIN BETA-A CHAIN).
                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae;
. 3.9e-14;
                                                                                                                                                                                   424 AA
     37.4%; Preu. ....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00019; TGF-beta; 1.
Pfam; PF00688; TGFb_propeptide; 1.
PRINTS; PR00438; GFCYSKNOT.
PRINTS; PR00670; INITBINBA.
                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
TISSUE-Follicular fluid;
MEDLINE-86092207; PubMed-2417121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Follicular fluid;
MEDLINE=92355604; PubMed=1644823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; X03266; CAA27020.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HSSP; P18075; 1BMP.
InterPro; IPR000491; -.
InterPro; IPR001111; -.
InterPro; IPR001839; -.
InterPro; IPR002400; -.
                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                     Nature 318:659-663(1985).
                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WFPGBA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 309-323
         Best Local Similarity Matches 40; Conserv
                                                                                                                                                                                                                                                                        Sus scrofa (Piq).
                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                            factor-beta.
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                                                                                                                                                                                  IHBA_PIG
P03970:
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                                                                                                                                                                                                                                                            INHBA
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                                                                                              69
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Macduif T.K., Meunier H., Jones P.B.C., Hsueh A.J.W., Mayo K.E.;

Mocduif T.K., Meunier H., Jones P.B.C., Hsueh A.J.W., Mayo K.E.;

"Rat inhibin: molecular cloning of alpha- and beta-subunit
complementary deoxyribonucleic acids and expression in the ovary.";

Mol. Endocrinol. 1:561-568(1987).

"In FUNCTION: INHIBIN IS A GONADAL GLYCOPEPTIDE THAT INHIBITS THE
COMPLEMENT IN HIBIN IS A GONADAL GLYCOPEPTIDE THAT INHIBITS THE
COMPLEMENT IN EMBRYONIC AXIAL DEVELOPMENT.

"INPORTANT IN EMBRYONIC AXIAL DEVELOPMENT.

"INFORTANT IN EMBRYONIC AXIAL DEVELOPMENT.

"INTIBIN A IS A DIMER OF ALPHA AND BETA-A.

INHIBIN B IS A DIMER OF ALPHA AND BETA-B.

ACTIVIN AB IS A DIMER OF BETA-A.

ACTIVIN AB IS A DIMER OF BETA-A.

COMPLEMENT.

"INHIBITAL SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
PROSITE; PS00250; TGF_BETA_1; 1.
Follitropin inhibitor; Contraceptive; Hormone; Glycoprotein; Signal.
SIGNAL 1 20
POTENTIAL.
PROPEP 21 308
CHAIN 309 424 INHIBIN BETA A CHAIN.
DISULED 312 320 BY SIMILARITY.
DISULED 319 389 BY SIMILARITY.
DISULED 348 421 BY SIMILARITY.
DISULED 352 423 BY SIMILARITY.
DISULED 352 423 BY SIMILARITY.
DISULED 352 423 BY SIMILARITY.
DISULED 358 388 INTERCHAIN (BY SIMILARITY).
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                                                                                                                                                                       BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
INTERCHIN (BY SIMILARITY).
N'LINKED (GLCNAC. .) (POTENTIAL).
W, 436BC62226FDAF52 CRC64;
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01-NOV-1990 (Rel. 16, Last sequence update)
01-NOT-2000 (Rel. 40, Last annotation update)
INHIBIN BETA A CHAIN PRECURSOR (ACTIVIN BETA-A CHAIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                               31.5%; Score 200; DB 1; 37.4%; Pred. No. 3.9e-14; tive 21; Mismatches 36;
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MEDLINE=91042598; Pubmed=3153478;
                                                                                                                                                                                                                                                                                                                                                                      MW;
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InterPro; IPR000491;
InterPro; IPR001111;
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InterPro; IPR002400;
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Matches 40; Conserv
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MEDLINE-86205842; PubMed-3458167;
MEDLINE-86205842; PubMed-3458167;
MEDLINE-86205842; PubMed-3458167;
Grage R.G., Rain J.M., Brown R.W., McInerney B.V., Cobon G.S.,
Gregson R.P., Robertson D.M., Morgan F.J., Hearn M.T.W., Findlay J.K.,
Wettenhall R.E.H., Burger H.G., de Kretser D.M.;
Gloning and sequence analysis of cDNa species coding for the two
subunits of inhibin from bovine follicular fluid.";
Proc. Natl. Acad. Sci. U.S.A. 83:3091-3095 [1986].
-! FUNCTION: INHIBIN IS A GONADAL GLYCOPEPTIDE THAT INHIBITS THE
SECRETION OF FOLLITROPIN BY THE PITUITARY GLAND. ON THE OTHER HAND
ACTIVIN ACTIVATES THE SECRETION OF FOLLITROPIN. ACTIVIN IS ALSO
IMPORTANT IN EMBRYONIC AXIAL DEVELOPMENT.
-: SUBBRYONIC AXIAL DEVELOPMENT.
-: SUBBRYONIC AXIAL DEVELOPMENT.
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Thompson D.A., Cronin C.N., Martin F.;
"Genomic cloning and sequence analyses of the bovine alpha-, beta A-and beta B-inhibin/activin genes. Identification of transcription factor AP-2-binding sites in the 5'-flanking regions by DNase I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CCVRPLYIDFRQDLGWK-WVHEPKGYYANFCSGPCP----YLRSADTTHSTVLGLYNTL 68
                                                                                                                                                                                                                                                                        Hormone; Glycoprotein; Signal.
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BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
INTERCHAIN (BY SIMILARITY.
INTERCHAIN (BY SIMILARITY).
N-LINKED (GLCNAC. . .) (POTENTIAL).
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
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01-OCT-1996 (Rel. 34, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
INHIBIN BETA A CHAIN PRECURSOR (ACTIVIN BETA-A CHAIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31.5%; Score 200; DB 1;
37.4%; Pred. No. 3.9e-14;
live 21; Mismatches 36;
J 12:56:54

J 12:56:54

A Pfam; PF00019; TGF-beta; 1.

DR Pfam; PF00688; TGFb_propeptide; 1.

DR PRINTS; PR00438; GFCYSKNOT.

DR PRINTS; PR00570; INHIBINBA.

DR PROSITE; PS00250; TGF_BETA_1; 1.

TO POLILITOPIN inhibitor; Contraceptive; Hormone; SIGNAL

J 20

POTENTIAL.

PROPEP 21 308

AIN 309 424 INHIBIN BFT

TEFID 312 320 BY SIMIT

TO 319 389 BY ST

348 421 BV

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INHIBIN B IS A DIMER OF ALPHA AND BETA-B.
ACTIVIN A IS A DIMER OF BETA-A.
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P07995;
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                                                                 SWISS-PROT entry is copyright. It is produced through a collaboration en the Swiss Institute of Bioinformatics and the EMBL outstation -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
N. INTERCHAIN (BY SIMILARITY).
N. LINKED (GICNAC...) (POTENTIAL).
W; 2D8799D7197CDA37 CRC64;
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Sukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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P08476; Q14599;
01-AUG-1988 (Rel. 08, Created)
01-MR-1989 (Rel. 10, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
INHIBIN BETA A CHAIN PRECURSOR (ACTIVIN BETA-A CHAIN) (ERYTHROID DIFFERENTIATION PROTEIN) (EDF).
                                                                                                                                                                                                                                                 R EMBL; U16239; AAB60627.1; -.
R EMBL; U16238; AAB60627.1; -.
R EMBL; U16238; AAB60627.1; -.
R PIR; B25/32; B25/32.
R HSSP; P18075; 1BMP.
R InterPro; IPR001491; -.
R InterPro; IPR001491; -.
R InterPro; IPR001839; -.
R Pfam; PF00019; TGF-beta; 1.
R Pfam; PF00688; TGFb_Dropeptide; 1.
R Pfam; PF00688; TGFb_Dropeptide; 1.
R PRIMTS; PR00670; INHIBINBA.
R PRIMTS; PR00670; INHIBINBA.
R PRIMTS; PR006250; TGF_BETA_1; 1.
R PCOLILITOPIN inhibitor; Contraceptive; Hormone; Glycoprotein;
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ACTIVIN AB IS A DIMER OF BETA-A AND BETA-B.
SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
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INHIBIN BETA A CHAIN.
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SEQUENCE FROM N.A.
MaDLINE-86186863; PubMed-3754442;
Mason A.J., Niall H.D., Seeburg P.H.;
"Structure of two human ovarian inhibins.";
Biochem. Biophys. Res. Commun. 135:957-964(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21; Mismatches
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Matches 40; Conserv
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425 P
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SEQUENCE
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IHBA_HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BEGG H., Walter M., Northemann W.;
Submitted (MAY-1993) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: INHIBIN IS A GONDAL GIVCOBETIDE THAT INHIBITS THE
SECRETION OF FOLLITROPIN BY THE PITUITARY GLAND. ON THE OTHER HAND
ACTIVIN ACTIVATES THE SECRETION OF FOLLITROPIN. ACTIVIN IS ALSO
IMPORTANT IN EMBRYONIC AXIAL DEVELOPMENT.
-!- SUBGNIT: DIMBRIC, LINKED BY ONE OR MORE DISULFIDE BONDS.
INHIBIN A IS A DIMER OF ALPHA AND BETA-A.
ACTIVIN A IS A DIMER OF BETA-A.
ACTIVIN A IS A DIMER OF ESTA-A.
-- ACTIVIN A BIS A DIMER OF BETA-A.
-- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
                                                            Murata M., Eto Y., Shibai H., Sakai M., Muramatsu M.;
"Erythroid differentiation factor is encoded by the same mRNA as that of the inhibin beta A chain.";
Proc. Natl. Acad. Sci. U.S. 85:2434-2438(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Stewart A.G., Milborrow H.M., Ring J.M., Crowther C.E., Forage R.G., "Human inhibin genes. Genomic characterisation and sequencing."; FEBS Lett. 206:329-334(1986).
                                                                                                                                                                                                                                                        Tanimoto K., Handa S.I., Ueno N., Murakami K., Fukamizu A.; "Structure and sequence analysis of the human activin beta A subunit
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Pfam; PF00019; TGF-beta; 1.
Pfam; PF00688; TGFD_propeptide; 1.
PRINTS; PR00438; GFCYSKNOT.
PRINTS; PR00570; INHIBINBA.
PROSTTE; PS00250; TGF_BETA_1; 1.
PROSTTE; PS00250; TGF_BETA_1; 1.
PROSTTE; PS00250; TGF_PSTA_1; 1.
PROSTTE; PS00250; TGF_PSTA_1; 1.
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BY SIMILARITY.
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BY SIMILARITY.
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                                                                                                                                                                                                 SEQUENCE FROM N.A. MEDLINE=92135888; PubMed=1777673;
                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 311-426 FROM N.A. MEDLINE-87005283; PubMed=3758355;
SEQUENCE FROM N.A.
MEDLINE-88190086; Pubmed=3267209;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 311-426 FROM N.A.
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                                                                                                                                                                                                                                                                                                                                            DNA Seq. 2:103-110(1991).
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                                                                                                                                                                                                                                                                                                            01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
60A PROTEIN PRECIRSOR (GLASS BOTTOM BOAT PROTEIN).
GBB OR 60A OR TGFB-60A.
Drosophila virilis (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                     Gaps
                                                                                                                                                     CCVRPLYIDFRQDLGWK-WVHEPKGYYANFCSGPCP----YLRSADTTHSTVLGLYNTL 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60A PROTEIN.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
INTERCHAIN (BY SIMILARITY).
N'LINKED (GLCNAC. . .) (POTENTIAL).
N'LINKED (GLCNAC. . .) (POTENTIAL).
                           .) (POTENTIAL)
                                                                                                                          10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Isolation and sequence of the Drosophila virilis 60 A gene, a transforming growth factor-beta superfamily member related to vertebrate bone morphogenetic proteins.";
Blochim. Blophys. Acta 1307:273-279(1996).
-!- SUBUNIT: HOMODIMER, DISULFIDE-LINKED (BY SIMILARITY).
-! SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
                                                                                               DB 1; Length 426;
                                                                                              31.5%; Score 200; DB 1; Length 42 37.4%; Pred. No. 4e-14; Live 21; Mismatches 36; Indels
BY SIMILARITY.
INTERCHAIN (BY SIMILARITY).
N-LINKED (GLCNAC. . .) (FOTE
RMR -> AC (IN REF. 5).
4; 201CDEDF99CE6919 CRC64;
                                                                                                                                                                                                           --NPEASASPCCVPQDLEPLTILYY-VGRTPKVEQLSNMVVKSCKCS 112
                                                                                                                                                                                                                                     380 GHSPFANLKSCCVPTKLRPMSMLYDDGQNIIKKDIQNMIVEECGCS 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPkUvu*vv, ...
Pfam; PF00019; TGF-beta; 1.
Pfam; PF00688; TGFb_propeptide; 1.
PRINTS; PR00438; GFCYSKNOT.
PROSITE; PS00250; TGF_BETA_1; 1.
Growth factor; Cytokine; Glycoprotein; Signal.
                                                                                                                                                                                                                                                                                                           436 AA
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MEDLINE=96305349; PubMed=8688461;
Du W., Doctor J.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FlyBase; FBgn0015681; Dvir\gbb.
                                                        MM;
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InterPro; IPR001839; -.
InterPro; IPR002400; -.
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 354
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426 AA;
                                                                                                             Similarity
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Q24735:
 DISULFID
                                            CONFLICT
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Best Local S
                             CARBOHYD
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AMEDINE-20196006; PubMed=10731132;

ADDINE-20196006; PubMed=10731132;

ADDINE-2019606; ADDINE-201960; Chang Q., Chen L.X.,

ADDINE-2019606; ADDINE-201960; Chang Q., Chen L.X.,

ADDINE-2019606; ADDINE-201960; Chen L. ADDINE-201960;

ADDINE-2019606; ADDINE-201960; ADDINE-2019606; AD
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P27091; 09WIL14;
P27091; 09WIL14;
P27091; 09WIL14;
P27092 (Rel. 23, Created)
O1-AUG-1992 (Rel. 23, Last sequence update)
O1-CCT-2000 (Rel. 40, Last annotation update)
O1-CCT-2000 (Rel. 40, Last annotation update)
GOA PROTEIN PRECURSON (GLASS BOTTOM BOAT PROTEIN).
GBB OR GOA OR CG5562.
Drosophila melanogaster (Fruit fly).
BUKaryota; Merazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Perryota; Merazoa; Arthropoda; Tracheata; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                            Doctor J.S., Jackson P.D., Rashka K.E., Visalli M., Hoffmann F.M.; "Sequence, biochemical characterization, and developmental expression of a new member of the TGF-beta superfamily in Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=92021021; PubMed=1924384; Whatton K.A., Thomsen G.H., Gelbart W.M.; Ubrosophila 60A gene, another transforming growth factor beta family member, is closely related to human bone morphogenetic proteins."; Proc. Natl. Acad. Sci. U.S.A. 88:9214-9218(1991).
                                                                                                                                                                                                                                                     NYCFRNLEEN----CCVRPLYIDFRQDLGW-KWVHEPKGYYANFCSGPCPYLRSAD---TT 57
                                                                                                                                                                                                                                                                                                                                                 58 HSTVLGLYNTLNPEASASPCCVPQDLEPLTILYYVG-RTPKVEQLSNMVVKSCKC 111
                                                                                                                                                                                                                                                                                                                                                                             N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
                                                                                                                                                      Length 436;
                                                                                                                                                                                                       43; Indels
                                                          -LINKED (GLCNAC. . .) (P
C744B4AE58796692 CRC64;
                                                                                                                                                      DB 1;
                                                                                                                                                 30.8%; Score 195.5; DB 1
39.1%; Pred. No. 1.2e-13;
iive 18; Mismatches 43
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                                                                          49999 MW;
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                                                                                                                                                                                                    Conservative
  217
229
377
217
229
377
436 AA;
                                                                                                                                                                           Similarity
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                                             CARBOHYD
  CARBOHYD
                         CARBOHYD
                                                                                                                                                 Query Match
Best Local 3
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Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., Anttei B., McIntosh T.C., McLeod M.P., McPherson D., Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A., Mont S.M., Moy M., Murphy E., Murphy L., Muzny D.M., Nelson D.L., Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M., Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., Reinert K., Remindton K., Sauders R.D.C., Scheeler F., Shu H., Shue B.C., Siden Kiamos I., Simpson M., Skupski M.P., Smith T., Spiel E., Spradling A.C., Stapleton M., Strong R., Sun E., Spirskas R., Tector C., Turner R., Venter E., Wang A., Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J., Williams S.M., Woodage T., Worley K.C., Mu D., Yang S., Yao Q.A., A. Y., Yeh R.-F., Zaveri J.S., Zhan M., Zhou S., Zhu S., Zhu X., Smith H.O., Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
The genome sequence of Drosophila melanogaster.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    353 SCQMQTLYIDFK-DLGWHDWIIAPEGYGAFYCSGECNFPLNAHMNATNHAIVQTLVHLLE 411
                                                                                                                                                                                                                                                                                                   -i- SUBUNIT: HOMODIMER, DISULFIDE-LINKED.
-i- DEVELOPMENTAL STAGE: EXPRESSED THROUGHOUT DEVELOPMENT WITH PEAKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14 NCCVRPLYIDFRQDLGW-KWVHEPKGYYANFCSGPCPYLRSAD---TTHSTVLGLYNTLN 69
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60A PROTEIN.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
INTERCHAIN (BY SIMILARITY).
INTERCHAIN (BY SIMILARITY).
N-LINKED (GLCNAC. .) (POTENTIAL).
...TINKED (GLCNAC. .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                       OF TRANSCRIPTION DURING EARLY EMBRYOGENESIS, IN PUPAE, AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30.8%; Score 195; DB 1; Length 455; 39.8%; Pred. No. 1.5e-13; Live 19; Mismatches 37; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-LINKED (GLCNAC. . ) (PC
C8FA795556341F94 CRC64;
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Pfam: PF00019; TGF-beta: 1.
Pfam: PF00088; TGFD_propeptide; 1.
PRINTS; PR00438; GFCYSKNOT.
PROSITE; PS00250; TGF_BETA_1; 1.
Growth factor; Cytokine; Glycoprotein; Signal.
36
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MM;
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PIR, A41233; A41233.
PIR; A43918; A43918.
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FlyBase; FBgn0024234; gbb.
InterPro; IPR001111; -.
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452
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Matches 41; Conser
                                                                                                                                                                                                                                                                                                                                                         ADULT MALES.
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354
383
387
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DISULFID
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CARBOHYD
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RESULT

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Gallus
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IHBA_CHICK
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                                                                                                                                                                                                                                                                                                                                                -1. FUNCTION: INHIBITS IS A GONADAL GLYCOPEPTIDE THAT INHIBITS THE SECRETION OF FOLLITROPIN BY THE PITUITARY GLAND. ON THE OTHER HAND ACTIVIN ACTIVATES THE SECRETION OF FOLLITROPIN. ACTIVIN IS ALSO IMPORTANT IN EMBRY CAIL AND DEVELOPMENT.
-1. SUBUNT: DIMERIC, LINED BY ONE OR MORE DISULFIDE BONDS.
INHIBIN A IS A DIMER OF ALPHA AND BETA-B.
ACTIVIN A IS A DIMER OF BETA-A.
ACTIVIN AB IS A DIMER OF BETA-A.
-1. SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
                                                                                                                                                                                                                                                                             SEQUENCE OF 311-381 FROM N.A.
MEDLINE=91029482; PubMed=2225063;
Mitrani E., Ziv T., Thomsen G., Shimoni Y., Melton D.A., Bril A.;
"Activin can induce the formation of axial structures and is expressed in the hypoblast of the chick.";
                                                                                                                                                                                   Klinger H., Halaschek-Wiener J., Wohlrab B.K., Kuchler K., Wohlrab F.;
Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                pram; PF00019; TGF-bets; 1.
Pfam; PF00688; TGF-bets; 1.
PRINTS; PR00438; GGTSKNOT.
PROSITE; PS00250; TGF_BETA_1: 1.
Follitropin inhibitor; Contraceptive; Hormone; Glycoprotein; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INHIBIN BETA B CHAIN.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
INTERCHAIN (BY SIMILARITY).
N-LINKED (GLCNAC. .) (POTENTIAL).
P -> PG (IN REF. 2).
W; 060017BF33F7AF6C CRC64;
                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN-WHITE LEGHORN; TISSUE-Ovary;
Hecht D.J., Davis A.J., Ryan I.M., Johnson P.A.;
Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
                   P27093; 073796;
01-AUG-1992 (Rel. 23, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
INHIBIN BETA B CHAIN PRECURSOR (ACTIVIN BETA-B CHAIN).
           391 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL. POTENTIAL.
           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL, AF055478; AAC14187.1; -.
EMBL, M61166; AAA48568.1; -.
EMBL, M57408; AAA48509.1; -.
HSSP; P18075; 1BMP.
InterPro; IPR001111; -.
InterPro; IPR001839; -.
InterPro; IPR002400; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; Z71594; CAA96248.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                43608 MW;
         STANDARD;
                                                                                           Gallus gallus (Chicken).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25
276
391
288
356
388
390
355
77
                                                                                                                                                                                                                                                                                                                                        Cell 63:495-501(1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              280
287
316
320
355
77
30 AA;
                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                       NCBI_TaxID=9031;
                                                                                                                                                                         TISSUE=Follicle;
           [HBB_CHICK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DISULFID
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                                                                                                                            Gallus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIGNAL
IHBB_CHICK
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                                                                    7;
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-!- SUBUNIT: DIMERIC, LINKED BY ONE OR WORE DISULFIDE BONDS.
INHIBIN A IS A DIMER OF ALPHA AND BETA-A.
ACTIVIN AB IS A DIMER OF BETA-A.
ACTIVIN AB IS A DIMER OF BETA-A. AND BETA-B.
                                                                                                                                                                                                 287 CCRQQFYIDFRL-IGWNDWIIAPSGYYGNYCEGSCPAYLAGVPGSASSFHTAVVNQYRMR 345
                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                   15 CCVRPLYIDFRQDLGWK-WVHEPKGYYANFCSGPCP-YLR----SADTTHSTVLGLYNT- 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          chen C.C., Johnson P.A.; "Molecular cloning of inhibin/activin beta A-subunit complementary deoxyribonucleic acid and expression of inhibin/activin alpha- and beta A-subunits in the domestic hen."; Biol. Reprod. 54:429-435(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mitrani E., Ziv T., Thomsen G., Shimoni Y., Melton D.A., Bril A.; expetivin can induce the formation of axial structures and is expressed in the hypoblast of the chick."; cell 63:495-501(1990).
                                                                 11;
   Length 391;
                                                                    Indels
                                                                                                                                                                                                                                                                      68 -LNPEASASPCCVPQDLEPLTILYYVGRTPKVEQ-LSNMVVKSCKCS 112
                                                                                                                                                                                                                                                                                                        Submitted (MAY-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  THEA_CHICK STANDARD; PRT; 424 AA.
P27092; 090697;
01-AUG-1992 (Rel. 23, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-COT-2000 (Rel. 40, Last annotation update)
INHIBIN BETA A CHAIN PRECURSOR (ACTIVIN BETA-A CHAIN).
                                                                 35;
   DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
30.2%; Score 191.5; DB 38.3%; Pred. No. 3e-13;
                        38.38; Pred. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN-WHITE LEGHORN;
MEDLINE-96380183; PubMed-8788196;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE-Hypoblast;
MEDLINE-91029482; Pubmed-2225063;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 317-349 FROM N.A.
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                                                                    41; Conservative
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                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9031;
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   Query Match
Best Local S
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DISULFID
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                                                                                                                                                                                                                                                                                  SIGNAL
                                                                                                                                                                                                                                                                                                  CHAIN
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                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDINE-89305504; PubMed-2519512; Dale L., Matthews G., Tabe L., Colman A.; Davelopmental expression of the protein product of Vg1, a localized maternal mRNA in the frog Xenopus laevis."; EMBO J. 8:1057-1065(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Weeks D.L., Melton D.A.;
"A maternal mRNA localized to the vegetal hemisphere in Xenopus eggs codes for a growth factor related to TGF-beta.";
Cell 51:861-867(1987).
                                                                                                                                                                                                                                                                                                                                     CCVRPLYIDFRQDLGWK-WVHEPKGYYANFCSGPCP----YLRSADTTHSTVLGLYNTL 68
                                                                                                PROSITE; PS00250, TGF_BETA_1; FALSE_NEG.
Follitropin inhibitor; Contraceptive; Hormone; Glycoprotein; Signal.
SIGNAL 1 20 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus.
                                                                                                                                                                                              . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAR-1989 (Rel. 10, Created)
01-MAR-1989 (Rel. 10, Last sequence update)
01-JUN-1994 (Rel. 29, Last annotation update)
DVR-1 PROTEIN PRECURSOR (VEGETAL HEMISPHERE VG1 PROTEIN) (VG-1).
                                                                                                                                                                                                                                                                                                                     10;
                                                                                                                                                                                                                                                                                                  Length 424;
                                                                                                                                                                                                                                                                                                30.1%; Score 191; DB 1; Length 42. 36.4%; Pred. No. 3.6e-13; ive 21; Mismatches 37; Indels
                                                                                                                                                                                                                                                                                                                                                                         -- NPEASASPCCVPQDLEPLTILYY-VGRTPKVEQLSNMVVKSCKCS 112
                                                                                                                                                                                                                                                                                                                                                                                   378 GHSPFANLKSCCVPTKLRPMSMLYYDDGQNIIKKDIQNMIVEECGCS 424
                                                                                                                                                                                      SIMILARITY)
                                                                                                                                                                                                                                                                      96E158FE119E1D69 CRC64;
                                                                                                                              BY SIMILARITY. INHIBIN BETA A CHAIN.
                                                                                                                                               BY SIMILARITY.
BY SIMILARITY.
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INTERCHAIN (BY S.
N-LINKED (GLCNAC,
A -> T (IN REF.
C -> K (IN REF.
E -> K (IN REF.
E -> G (IN REF.
                                                                                                                                                                                             (GLCNAC
                                                                                                                                                                                                                                                                                                                                                                                                                                         360 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Xenopus laevis (African clawed frog)
                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                             Pfam; PF00019; TGF-beta; 1.
Pfam; PF00688; TGFD-propeptide; 1.
PRINTS: PR00438; GFCYSKNOT.
PRINTS; PR00670; INHIBINBA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE=88052889; PubMed=3479264;
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Σ
                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 36.4%,
"-hes 39; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CARBOHYDRATE-LINKAGE SITES.
                                                                                                                                                                                                                                                                       47574
EMBL; M57407; AAA03080.1;
                 HSSP; P18075; 1BMP.
InterPro; IPR000491; -
InterPro; IPR001111; -
InterPro; IPR001839; -
InterPro; IPR002400; -
                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                       424
320
389
421
421
165
165
87
         PIR; B36193; B36193.
                                                                                                                                                                                                                                                                      424 AA;
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P09534;
                                                                                                                                                                   DISULFID
                                                                                                                                                                                                               CONFLICT
                                                                                                                                                DISULFID
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                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                              PROPEP
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-i- FUNCTION: SERVES TO FACILITATE THE DIFFERENTIATION OF EITHER MESODERM OR ENDODERM EITHER AS A COFACTOR IN AN INSTRUCTIVE SIGNAL OR BY PROVIDING PERMISSIVE ENVIRONMENT.

-i- SUBUNIT: HOWODIMER (PROBABLE).

-i- TISSUE SPECIFICITY: VEGETAL REGION OF THE EGG.

-i- DEVELOPMENTAL STAGE: ABUNDANT IN OCCYTES AND PRESENT THROUGHOUT CLEAVAGE AND GASTROLA STAGE. NOT READLIY DETECTED AT A STAGE WHEN SOMITOGENESIS IS NEARLY COMPLETE IN 24 HR EMBRYOS. STEADY STATE LEVEL DECREASES IN A CONTINUOUS FASHION WITH DEVELOPMENTAL AGE.

-i- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-OCT-2000 (Rel. 40, Last annotation update)
BONE MORPHOGENETIC PROTEIN 7 PRECURSOR (BMP-7) (OSTEOGENIC PROTEIN 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    . 9
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; Pred. No. 3.9e-13;
19; Mismatches 39; Indels
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N-LINKED (GLCNAC. . .).
N-LINKED (GLCNAC. . .).
N-LINKED (GLCNAC. . .).
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SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
TISSUE-Placenta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30.0%; Score 190; 37.3%; Pred. No. 3
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(Rel. 16, Last sequ
(Rel. 40, Last anno
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human).
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01-OCT-2000
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P18075;
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317 NVAENSSSDQRQACKKHELYVSFR-DLGWQDWIIAPEGYAAYYCEGECAFPLNSYMNATN 375

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                                                                                                                                                                                                                     X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF 293-431.
MEDLINE=96149402; PubMed=8570652;
Griffith D.L., Keck P.C., Sampath T.K., Rueger D.C., Carlson W.D.;
"Three-dimensional structure of recombinant human osteogenic protein
1: structural paradigm for the transforming growth factor beta
                                                                                                                                                                                                                                                                                                                                                                                               -!- SUBUNIT: HOMODIMER, DISULFIDE-LINKED.
-!- TISSUE SPECIFICITY: EXPRESSED IN THE KIDNEYS AND BLADDER. LOWER LEVELS SEEN IN THE BEAIN.
-!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
                                               "OP-1 cDNA encodes an osteogenic protein in the TGF-beta family."; {\tt EMBO} J. 9:2085-2093(1990).
                                                                                                                                        Wang E.A., Wozney J.M.; "Identification of transforming growth factor beta family members
                                                                                                                            Celeste A.J., Iannazzi J.A., Taylor R.C., Hewick R.M., Rosen V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IRR001111; -.
InterPro; IRR001111; -.
InterPro; IRR001839; -.
InterPro; IRR002400; -.
Pfam; PR001019; TGF-beta; 1.
Pfam; PR00181; GFCYSKNOT.
PROSITE; PS00250; TGF_BETA_1; 1.
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N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                 Proc. Natl. Acad. Sci. U.S.A. 93:878-883(1996).
-!- FUNCTION: INDUCES CARTILAGE AND BONE FORMATION. MAY BE THE OSTEOINDUCTIVE FACTOR RESPONSIBLE FOR THE PHENOMENON OF EPITHELIAL OSTEOGENESIS. PLAYS A ROLE IN CALCIUM REGULATION
                Oezkaynak E., Rueger D.C., Drier E.A., Corbett C., Ridge R.J.,
Sampath T.K., Oppermann H.;
                                                                                                                                                                        present in bone-inductive protein purified from bovine bone.";
Proc. Natl. Acad. Sci. U.S.A. 87:9843-9847(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL.
POTENTIAL.
BONE MORPHOGENETIC PROTEIN 7.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INTERCHAIN.
                                                                                                            MEDLINE-91088608; PubMed-2263636;
MEDLINE=90291971; PubMed=2357959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              49313 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; X51801; CAA36100.1; -. EMBL; M60116; AAA36738.1; -. PIR; S10529; S10529. PIR; C39263; C39263. PDB; 1BMP; 23-JUL-97.
                                                                                                                                                                                                                                                                                                                                                                                  AND BONE HOMEOSTASIS.
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                                                                                             SEQUENCE FROM N.A.
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29.8%; Score 189; DB 1; Length 431; y 34.8%; Pred. No. 6.1e-13; rvative 22; Mismatches 39; Indels

Conservative

Local Similarity nes 40; Conserv

Best Loca Matches

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Query Match

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                                                                                Nishimatsu S., Suzuki A., Shoda A., Murakami K., Ueno N.; "Genes for bone morphogenetic proteins are differentially transcribed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BY SIMILARITY.

BY SIMILARITY.

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N-LINKED (GLCNAC. . .) (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).

KRR -> NVV (IN REF. 2).

D -> E (IN REF. 2).
                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
               |: | | :: ||| | | | | | :::||: : : : ||||::| | | HAIVQTILVHFINPETVPKPCCAPTQLNAISVLYFDDSSNVILKKYRNMVVRACGC 430
                                                                                                                                                                                                                                                                                                                                                                                                                       Hawley S.H.B., Wunnenberg-Stapleton K., Hashimoto C.,
Laurent M.N., Watabe T., Blumberg B.W., Cho K.W.Y.;
Submitted (DEC-1995) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: INDUCES CARTILAGE AND BONE FORMATION. MAY BE THE
OSTEOINDUCTIVE FACTOR RESPONSIBLE FOR THE PHENOMENON OF
EPITHELIAL OSTEOGENESIS. PLAYS A ROLE IN CALCIUM REGULATION
AND BONE HOMEOSTASIS.
-!- SUBUNIT: HOMODIMER, DISULFIDE-LINKED.
-!- SUBUNIT: HOMODIMER, DISULFIDE-LINKED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bone; Cartilage; Glycoprotein.
58 HSTVLGLYNTLNPEASASPCCVPQDLEPLTILYYVGRTPKV-EQLSNMVVKSCKC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BONE MORPHOGENETIC PROTEIN 7.
                                                                                                                                                                                                                                                                                                                                                                  in early amphibian embryos.";
Biochem. Biophys. Res. Commun. 186:1487-1495(1992)
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InterPro; IPR001111; -.
InterPro; IPR001839; -.
InterPro; IPR001899; -.
Pfam; PF00019; TGF-Deta; 1.
PRINTS; PR00438; TGFD-Dropeptide; 1.
PROSITE; PS00250; TGF_BETA_1; 1.
Signal; Growth factor; Cytokine; Bonk StGNAL 1.
                                                                                                                                                                                                                     Xenopus laevis (African clawed frog).
                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. MEDLINE=92378616; Pubmed=1510675;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; X63427; CAA45021.1; -. EMBL; U38559; AAA82616.1; -.
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426
3391
423
390
1177
307
319
355
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NCBI_TaxID=8355;
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HSSP; P18075; 1BMP.
                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                       (OP-1) (XBMP7).
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283
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Follitropin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE-Ovarian follicular fluid,
MEDLINE-86092207; PubMed=2477121;
MEDLINE-86092207; PubMed=24477121;
MASON A.J., Hayflick J.S., Ling N., Esch F., Ueno N., Ying S.-Y.,
Guillemin R., Niall H., Seeburg P.H.;
"Complementary DNA sequences of ovarian follicular fluid inhibin show
precursor structure and homology with transforming growth
                                                                         Gaps
                                                                                                                9 RNLEENCCVRPLYIDFRQDLGWK-WVHEPKGYYANFCSGPCPYLRSA---DTTHSTVLGL 64
                                                                                                                                                                                                                                                                                                                                                        Sus scrofa (Pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
                                                                                                                                                                                                                                                                                                    01-NOV-1986 (Rel. 03, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
INHIBIN BETA B CHAIN PRECURSOR (ACTIVIN BETA-B CHAIN) (FRAGMENT)
                                                                          .
9
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SUBUNIT: DIMERIC, LINKED BY ONE OR MORE DISULFIDE BONDS.
INHIBIN A IS A DIMER OF ALPHA AND BETA-A.
INHIBIN B IS A DIMER OF ALPHA AND BETA-B.
ACTIVIN A IS A DIMER OF BETA-A.
ACTIVIN AB IS A DIMER OF BETA-A.
SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
                                          Length 426;
                                                                                                                                                                         378 VHFINPETVPKPCCAPTQLNGISVLYFDDSANVILKKYKNMVVQACGC 425
                                                                                                                                                         65 YNTLNPEASASPCCVPQDLEPLTILYYVGRTPKV-EQLSNMVVKSCKC 111
                                                                       41; Indels
  6401D5151AC97117 CRC64;
                                       29.5%; Score 187; DB 1;
35.2%; Pred. No. 9.8e-13;
11ve 23; Mismatches 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam: PF00019; TGF-beta; 1.
Pfam; PF00688; TGFb_propeptide; 1.
PROSITE; PS00250; TGF_BETA_1; 1.
                                                                                                                                                                                                                                                                                    01-NOV-1986 (Rel. 03, Created)
01-NOV-1986 (Rel. 03, Last seq
15-JUL-1998 (Rel. 36, Last anno
 48965 MW;
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                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nature 318:659-663(1985).
                                                                                                                                                                                                                                                            STANDARD;
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InterPro; IPR001111; -.
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426 AA;
                                                        Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9823;
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                                                                      38;
SEQUENCE
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**A MEDLINE-86186863; PubMed=754442;

**A MEDLINE-86186863; PubMed=754442;

**MEDLINE-86186863; PubMed=754442;

**MEDLINE-86186863; PubMed=754442;

**MEDLINE-86186863; PubMed=754442;

**Biochem. Biophys. Res. Commun. 135:957-964(1986).

**Extructure of two human ovarian inhibins.";

**Biochem. Biophys. Res. Commun. 135:957-964(1986).

**Extraction of Follitropin by THE PITUITARY GLAND. ON THE OTHER HAND ACTIVIN ACTIVATES THE SECRETION OF FOLLITROPIN. ACTIVIN IS ALSO IMPORPANT IN EMBRYONIC AXIAL DEVELOPMENT.

**INHIBIN A IS A DIMER OF ALPHA AND BETA-B.**

**ACTIVIN A IS A DIMER OF BETA-A.**

**ACTIVIN AB IS A DIMER OF BETA-B.**

**ACTIVIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15 CCVRPLYIDFRQDLGWK-WVHEPKGYYANFCSGPCP-YLR----SADTTHSTVLGLYNT-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                 INTERCHAIN (BY SIMILARITY).
N-LINKED (GLCNAC. .) (POTENTIAL).
C571EA91ADA5DE77 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-90114200; PubMed-2575216;
Mason A.J., Berkemeier L.M., Schmelzer C.H., Schwall R.H.;
"Activin B: precursor sequences, genomic structure and in vitro
                                                                                                                                                                                                                                                                                                                                                                                                                                        11;
                                                                                                                                                                                                                                                                                                                                                                             Length 349;
     Contraceptive; Hormone; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                     35; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         68 -LNPEASASPCCVPQDLEPLTILYYVGRTPKVEQ-LSNMVVKSCKCS 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-WAR-1989 (Rel. 10, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
01-0CT-1996 (Rel. 34, Last annotation update)
INHIBIN BETA B CHAIN PRECURSOR (ACTIVIN BETA-B CHAIN).
                                                                                    INHIBIN BETA B CHAIN.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                          29.4%; Score 186.5; DB 1; 37.4%; Pred. No. 9e-13; ive 21; Mismatches 35;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mol. Endocrinol. 3:939-948(1989).
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N
39354 MW;
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inhibitor;
                                                                                                                                                                                                                                                           35
349 AA;
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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseelsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      303 CCROOFFIDFRL-IGWNDWIIAPTGYYGNYCEGSCPAYLAGVPGSASSFHTAVVNQYRMR 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Thompson D.A., Cronin C.N., Martin F.; "Genomic Loloning and sequence analyses of the bovine alpha-, beta A-and beta B-inhibin/Activin genes. Identification of transcription factor AP-2-binding sites in the 5'-flanking regions by DNase I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15 CCVRPLYIDFRQDLGWK-WVHEPKGYYANFCSGPCP-YLR----SADTTHSTVLGLYNT- 67
                                                                                                                                                                                                                                                                                                    Contraceptive; Hormone; Glycoprotein; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eur. J. Biochem. 226:751-764(1994).
-!- FUNCTION: INHIBIN IS A GONADAL GLYCOPEPTIDE THAT INHIBITS THE
                                                                                                                                                                                                                                                                                                                                                                                                               INTERCHAIN (BY SIMILARITY).
N-LINKED (GLCNAC. . .) (POTENTIAL).
S -> A (IN REF. 2).
90316C83597BA684 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 29.4%; Score 186.5; DB 1; Length 407; Best Local Similarity 37.4%; Pred. No. 1.1e-12; Matches 40; Conservative 21; Mismatches 35; Indels 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    362 GLNP-GTVNSCCIPTKLSTMSMLYFDDEYNIVKRDVPNMIVEECGCA 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    68 -LNPEASASPCCVPQDLEPLTILYYVGRTPKVEQ-LSNMVVKSCKCS 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
INHIBIN BETA B CHAIN PRECURSOR (ACTIVIN BETA-B CHAIN).
                                                                                                                                                                                                                                                                                                                                             INHIBIN BETA B CHAIN.
                                                                                                                                                                                                                                                                                                                                                          BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                 POTENTIAL.
                                                                                                                                                                                             InterPro; IPR001839; -.
InterPro; IPR002400; -.
Pfam; PF00019; TGF-beta; 1.
Pfam; PF00688; TGFb_propeptide; 1.
PRINTS; PR00438; GFCYSKNOT.
PROSITE; PS00250; TGF_BETA,1.
POSITE; PS00250; TGF_BETA,1.
                                                                   MEDLINE-95112839; PubMed-7813465;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              45121 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                    InterPro; IPR000381; -. InterPro; IPR0011111; -.
                                                                                                                                                                                                                                                                                                                 28
292
407
372
404
406
371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                              93
47
407 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9913;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE-Liver;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7;
SECRETION OF FOLLITROPIN BY THE PITUITARY GLAND. ON THE OTHER HAND ACTIVIN ACTIVATES THE SECRETION OF FOLLITROPIN. ACTIVIN IS ALSO IMPORTANT IN EMBRYONIC AXIAL DEVELOPMENT.
SUBBUNIT: DIMERIC, LINKED BY ONE OR MORE DISULFIDE BONDS.
INHIBIN A IS A DIMER OF ALPHA AND BETA-A.
INHIBIN B IS A DIMER OF BETA-A.
ACTIVIN A IS A DIMER OF BETA-A.
SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR001833; -.
InterPro; IPR002400; -.
Pfam; PF00019; TGF-bets; 1.
Prints; PR00438; GFCYSKNOT.
PRINTS; PR00438; GFCYSKNOT.
PRINTS; PR00571; INHIBINB.
PROSTE; PS00250; TGF_BETA_1; 1.
Pollitropin inhibitor; Contraceptive; Hormone; Glycoprotein; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15 CCVRPLYIDFRQDLGWK-WVHEPKGYYANFCSGPCP-YLR----SADTTHSTVLGLYNT-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IHBB_MOUSE STANDARD; PRT; 255 AA.
004999; Q61277;
01-FEB-1994 (Rel. 28, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
INHIBIN BETA B CHAIN PRECURSOR (ACTIVIN BETA-B CHAIN) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EF497DB30D2897DF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 408;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. 1.1e-12;
1: Mismatches 35; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                68 -LNPEASASPCCVPQDLEPLTILYYVGRTPKVEQ-LSNMVVKSCKCS 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 363 GLNP-GTVNSCCIPTKLSTMSMLYFDDEYNIVKRDVPNMIVEECGCA 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29.4%; Score 186.5; DB 1; 37.4%; Pred. No. 1.1e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INHIBIN BETA B CHA:
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
INTERCHAIN (BY SIM.
INTERCHAIN (BY SIM.
N-LINKED (GLCNAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21; Mismatches
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STRAIN-CBA X NMR1; TISSUE-Testis;
MEDLINE-95344997; PubMed-7619733;
                                                                                                                                                                                                                                                                                          EMBL; U16241; AAB60628.1; -.
EMBL; U16240; AAB60628.1; JOINED.
HSSP; P18075; 1BMP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                44897 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              40; Conservative
                                                                                                                                                                                                                                                                                                                                              InterPro; IPR000381; -. InterPro; IPR001111; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              408 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DISULFID
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                                                                                                                                                                                                                            Nakashina M., Toyono T., Akamine A., Joyner A.;
Nakashina M., Toyono T., Akamine A., Joyner A.;
Expression of growth/differentiation factor 11, a new member of the BMP/TGPbeta superfamily during mouse embryogenesis.";
Mech. Dev. 80:185-189(199).
-!- FUNCTION: SECRETED SIGNAL THAT ACTS GLOBALLY TO SPECIFY POSITIONAL IDENTITY ALONG THE ANTERIOR/POSTERIOR AXIS DURING BEVELOPMENT.
PLAY CRITICAL ROLES IN PATTERNING BOTH MESODERMAL AND NEURAL.
TISSUES AND IN ESTABLISHING THE SKELETAL PATTERN (BY SIMILARITY).
-!- SUBGUNIT: HOWODIMER, DISULFIDE-LINKED (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: SECRETED (PROBABLE).
   01-OCT-2000 (Rel. 40, Last annotation update)
GROWTH/DIFFERENTIATION FACTOR 11 PRECURSOR (BONE MORPHOGENETIC PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1991 (Rel. 20, Created)
01-NOV-1991 (Rel. 20, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
BONE MORPHOGENETIC PROTEIN 7 PRECURSOR (BMP-7) (OSTEOGENIC PROTEIN 1)
(OP-1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9 RNL------EENCCVRPLYIDFRQDLGWKWVHEPKGYYANFCSGPCPYLRSADTTHS 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BY SIMILARITY.
INTERCHAIN (BY SIMILARITY).
N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GROWTH/DIFFERENTIATION FACTOR 11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29.1%; Score 184.5; DB 1; Length 345; 39.1%; Pred. No. 1.5e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     242 BY SIMILARITY.
>345 GROWTH/DIFFERENTIATION FACTO
159 POLY-GLY.
316 BY SIMILARITY.
315 INPERCHAIN (BY SIMILARITY).
318 N-LINKED (GLCNAC. . .) (POTE
345 AA, 8105B93FED6B0443 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        430 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               301 ---HLVQQANPRGSAGPCCTPTKMSPINMLYF 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        60 TVLGLYNTLNPEASASPCCVPQDLEPLTILYY 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pfam; PF00019; TGF-beta; 1.
Pfam; PF00688; TGFb_propeptide; 1.
PROSITE; PS00250; TGF_BETA; 1.
Growth factor; Cytokine; Glycoprotein.
                                                                                                                                                                       SEQUENCE FROM N.A.
TISSUE-Dental pulp;
MEDLINE=99173787; Pubmed=10072786;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AF092733; AAD05266.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          36; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR001111; -. InterPro; IPR001839; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         345 AA;
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Matches 36; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P18075; 1BMP
                                                                                                                                     NCBI_TaxID=10116;
                                         11) (FRAGMENT).
GDF11 OR BMP11.
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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BMP7_MOUSE
1D BMP7_MC
1D 2013159;
DT 01-NOV-
DE 00-1),
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                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15 CCVRPLYIDFRQDLGWK-WVHEPKGYYANFCSGPCP-YLR----SADITHSTVLGLYNT- 67
                                                                                                                                               Albano P.M., Groome N., Smith J.C.; "Activins are expressed in preimplantation mouse embryos and in ES and EC cells and are regulated on their differentiation."; Development 117:711-723(1993).
                                   Activin disrupts epithelial branching morphogenesis in developing
O., Tuuri T., Eramaa M., Sainio K., Hilden K., Saxen L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1; Length 255;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR001839; -. Pfam; PF00019; TGF-beta; 1. PROSITE; PS00250; TGF-BETA_1; 1. Follitropin inhibitor; Contraceptive; Hormone; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               36; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BY SIMILARITY.
INTERCHAIN (BY SIMILARITY).
H -> D (IN REF. 2).
2524B21DC648D9A9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INHIBIN BETA B CHAIN.
BY STMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-OCT-2000 (Rel. 40, Created)
01-OCT-2000 (Rel. 40, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29.1%; Score 184.5; 37.4%; Pred. No. 1.16
                                                                                                            SEQUENCE OF 134-255 FROM N.A. MEDLINE-93321614; PubMed-8330535;
                                                       glandular organs of the mouse.";
Mech. Dev. 50:229-245(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29178 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; X83376; CAA58290.1; -. EMBL; X69620; CAA49326.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 37.4 Matches 40; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            255
152
220
252
252
254
219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIR; S31441; S31441.
HSSP; P18075; 1BMP.
MGD; MGI:96571; Inhbb.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             135
255 AA;
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151
180
184
219
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ID GDFB_RAT

AC Q9Z217;

DT 01-OCT-200

DT 01-OCT-200
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PROPEP
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CHAIN

RESULT 60

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3;

Gaps

13;

34; Indels

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394 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 44383 MW;
                                                                                                                                                                                                                                                                                                                                          EMBL; 225868; CAA81088.1; -. HSSP; P18075; 1BMP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 28.85
Best Local Similarity 37.77
Matches 43; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              393
393
392
357
1133
1161
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20
280
280
322
322
357
161
193
333
393 AA;
                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                           NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10090;
                                                                                                      TISSUE-Bone;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BMP2_MOUSE
P21274;
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POTENTIAL.

BONE MORPHOGENETIC PROFEIN 7.

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

N-LINED (GLCNAC. ..) (POTENTIAL).

N-LINKED (GLCNAC. ..) (POTENTIAL).

N-LINKED (GLCNAC. ..) (POTENTIAL).

N-LINKED (GLCNAC. ..) (POTENTIAL).

N-LINKED (GLCNAC. ..) (POTENTIAL).
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                                                                                                 MEDLINE-91354237; PubMed-1715687;
Oezkaynak E., Schnegelsberg P.N.J., Oppermann H.;
"Murine osteogenic protein (OP-1): high levels of mRNA in kidney.";
Biochem. Biophys. Res. Commun. 179:116-123(1991).
-1- FUNCTION: INDUCES CARTILAGE AND BONE FORMATION. MAY BE THE
OSTEOINDUCTIVE FACTOR RESPONSIBLE FOR THE PHENOMENON OF
EPITHELIAL OSTEOGENESIS. PLAYS A ROLE IN CALCIUM REGULATION
                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00250; TGF_BETA_1; 1.
Signal; Growth factor; Cytokine; Bone; Cartilage; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28.9%; Score 183; DB 1; Length 430; 35.3%; Pred. No. 2.7e-12; Live 22; Mismatches 38; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P49001;
01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
01-CCT-2000 (Rel. 40, Last annotation update)
BONE MORPHOGENETIC PROTEIN 2 PRECURSOR (BMP-2A).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     486C36DD97754047 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    71 EASASPCCVPQDLEPLTILYYVGRTPKV-EQLSNMVVKSCKC 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : |||| | :::||; : : ||||::| |
DTVPKPCCAPTQLNAISVLYFDDSSNVILKKYRNMVVRACGC
                                                                                                                                                                                                      AND BONE HOMEOSTASIS.
SUBUNIT: HOMODIMER, DISULFIDE-LINKED.
SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          393 AA
                                                                                                                                                                                                                                                                                                                                                                                                                               MGD; MGT:103302; Bmp7.
InterPro; IPR001111; -
InterPro; IPR001839; -
InterPro; IPR002400; -
Pfam; PF00019; TGF-beta; 1.
Pfam; PF00488; TGF-beropetide; 1.
PRNITS; PR00438; GFCYSKNOT.
PROSITE; PS00250; TGF_BETA_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   49283 MW;
                                                                                                                                                                                                                                                                                                                                                                                      EMBL; X56906; CAA40222.1; -. PIR; JQ1184; JQ1184.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 35.3% hes 36; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    291
430
395
427
429
394
301
320
BMP-7 OR 0P1,
             Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     430 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                   HSSP; P18075; 1BMP
                                                                                       SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROPEP
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CHAIN

62

RAT

RESULT (
BMP2\_RAT |
ID BMP2, AC P49(
DT 01-1
DT 01-1
DT 01-2
DT 01-2

388

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Best Loca Matches

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Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
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INTERCHAIN (BY SIMILARITY).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                              -i- SUBUNIT: HOWODIMER, DISULFIDE-LINKED.
-i- TISSUE SPECIFICITY: FEMUR, CALVARIA, TRACHEA, LUNG AND OVARY.
-i- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               63 GLYNTLN---PEASASPCCVPQDLEPLTILYYVGRTPKV--EQLSNMVVKSCKC 111
                                                                                                                                                                                                                            ŝ
                                                                                                                                                                                                                  Feng J.Q., Chen D., Feng M., Harris M.A., Mundy G.R., Harris Submitted (SEP-1993) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: INDUCES CARTILAGE AND BONE FORMATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 393;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BONE MORPHOGENETIC PROTEIN 2.
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01-FEB-1996 (Rel. 33, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
BONE MORPHOGENETIC PROTEIN 2 PRECURSOR (BMP-2) (BMP-2A).
BMP2 OR BMP-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7D20865852E0F213 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28.8%; Score 182.5; DB 1; 37.7%; Pred. No. 2.7e-12; ive 21; Mismatches 31;
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15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL.
                                                                                                 Oryctolagus cuniculus (Rabbit).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        44664 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
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282
295
324
328
359
134
199
337
                                                                                                                                                    NCBI_TaxID=9986;
                                                                                 BMP2 OR BMP-2.
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15-JUL-1998
01-OCT-2000
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019006;
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BMP2_DAMDA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8;
                                                                                                                            SEQUENCE OF 1-351 FROM N.A.
MEDLINE=90228966; PubMed=1970330;
Dickinson M.E., Kobrin M.S., Silan C.M., Kingsley D.M., Justice M.J.,
Miller D.A., Ceci J.D., Lock L.F., Lee A., Buchberg A.M.,
Siracusa L.D., Lyons K.M., Derynck R., Hogan B.L.M., Copeland N.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         288 KRLKSSCKRHPLYVDF-SDVGWNDWIVAPPGYHAFYCHGECPFPLADHLNS--TNHAIVQ 344
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... agreement (See http://
... a34201.
... a075; 1BMP.
MGI:88177; BMP2.
... interPro; IPR00111; ..
InterPro; IPR00111; ..
InterPro; IPR001139; ..
DR Pfam; PF00019; TGF-beta; 1.
DR Pfam; PF00019; TGF-beta; 1.
DR ROSITE; PS00250; TGF_BETA_1; 1.
DR ROSITE; PS00250; TGF_BETA_1; 1.
TRW Signal; Growth factor; Cytckine; Bone; Cartilage; Glycoprotein.
T SIGNAL
... 198 BY SIMILARITY.
... SIGNAL
... 284 BY SIMILARITY.
... SIGNAL
... 391 BY SIMILARITY.
... TLFID 327 393 BY SIMILARITY.
... TLFID 327 393 BY SIMILARITY.
... TLFID 358 358 INTERCHAIN (BY "
... TLFID 358 358 INTERCHAIN (BY "
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               Feng J.Q., Harris M.A., Ghosh-Choudhury N., Feng M., Mundy G.R., Harris S.E., "Structure and sequence of mouse bone morphogenetic protein-2 gene (BMP-2): comparison of the structures and promoter regions of BMP-2
                                                                                                                                                                                                            Jenkins N.A.; "Chromosomal localization of seven members of the murine TGF-beta superfamily suggests close linkage to several morphogenetic mutant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BONE MORPHOGENETIC PROTEIN 2.
BY SIMILARITY.
BY SIMILARITY.
INTERCHAIN (BY SIMILARITY).
INTERCHAIN (BY SIMILARITY).
N-LINKED (GLCNAC. . ) (POTENTIAL).
N-LINKED (GLCNAC. . ) (POTENTIAL).
N-LINKED (GLCNAC. . ) (POTENTIAL).
T -> S (IN REF. 2).
GL -> HE (IN REF. 2).
G -> R (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63 GLYNTLN---PEASASPCCVPQDLEPLTILYYVGRTPKV--EQLSNMVVKSCKC 111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28.8%; Score 182.5; DB 1; Length 394; 37.7%; Pred. No. 2.7e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FD6A0F10587EED54 CRC64;
                                                                                                                                                                                                                                                                             395 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21; Mismatches
                                                                                               iochim. Biophys. Acta 1218:221-224(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
#EDLINE=94289485; PubMed=8018727;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      43; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      394 AA;
                                                                              and BMP-4 genes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BMP2_RABIT
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CONFLICT
SEQUENCE
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BMP2\_RABIT ID BMP2

RESULT

Matches

8 ò 8

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -i- FUNCTION: INDUCES CARTILAGE AND BONE FORMATION (BY SIMILARITY).
-i- SUBUNIT: HOMODIMER, DISULFIDE-LINKED (BY SIMILARITY).
-i- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
INTERCHAIN (BY SIMILARITY).
N-LINKED (GLCNAC. ...) (POTENTIAL).
N-LINKED (GLCNAC. ...) (POTENTIAL).
N-LINKED (GLCNAC. ...) (POTENTIAL).
N-LINKED (GLCNAC. ...) (POTENTIAL).
                                                                                                                                         Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AF041421; AAB96785.1; -.
InterPro; IPR001111; -.
InterPro; IPR001113; -.
InterPro; IPR0024083; -.
Pfam; PF00019; TGF-beta; 1.
PRIMTS; PR00689; TGFD_Propeptide; 1.
PRINTS; PR00689; INHIBINA.
Signal; Growth factor; Cytokine; Bone; Cartilage; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            63 GLYNTLN---PEASASPCCVPQDLEPLTILYYVGRTPKV--EQLSNMVVKSCKC 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wan X.L., Sears J., Chen S., Sears M.; "Cloning and expression of BMP-2/-4 from rabbit ocular ciliary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28.8%; Score 182.5; DB 1; Length 395; 37.7%; Pred. No. 2.7e-12;
                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN-NEW ZEALAND WHITE; TISSUE-Ocular ciliary epithelium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                             epithelium.";
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
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BONE MORPHOGENETIC PROTEIN
                                                                                                                                     Eukaryotā; Metazoa; Chordata; Craniata; Vertebrata; Eut
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31;
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15-JUL-1998 (Rel. 36, Last sequence update)
01-CTT-2000 (Rel. 40, Last annotation update)
BONE MORPHOGENETIC PROTEIN 2 PRECURSOR (BMP-2).
01-OCT-2000 (Rel. 40, Last annotation update)
BONE MORPHOGENETIC PROTEIN 2 PRECURSOR (BMP-2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               396 AA
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Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                       resolution.";
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CARBOHYD
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                                                                                                                                                                                             Blakey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CHAIN
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6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RNLEENCCVRPLYIDFRQDLGWK-WVHEPKGYYANFCSGPCPY----LRSADTTHSTVL 62
Dama dama (Fallow deer) (Cervus dama).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetaricodactyla, Ruminantia, Pecora, Cervoldea,
Cervidae, Cervinae, Cervus.
                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL.

BY SIMILARITY.

BONE MORPHOGENETIC PROTEIN 2.

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

N-LINKED (GLCNAC. ...) (POTENTIAL).

N-LINKED (GLCNAC. ...) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                (GLCNAC. ) (POTENTIAL, (GLCNAC. ) (POTENTIAL). (GLCNAC. .) (POTENTIAL).
                                                                                             Feng J.Q., Chen D., Ghosh-Choudhury N., Esparza J., Mundy G.R.,
Harris S.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00019; TGF-beta; 1.
Pfam; PF00089; TGFb_propeptide; 1.
PROSITE; PS00250; TGFB_BETA_1: 1.
Signal; Growth factor; Cytokine; Bone; Cartilage; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63 GLYNTLN---PEASASPCCVPQDLEPLTILYYVGRTPKV--EQLSNMVVKSCKC 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 396;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-OCT-1989 (Rel. 12, Created)
01-OCT-1989 (Rel. 12, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
BONE MORPHOGENETIC PROTEIN 2 PRECURSOR (BMP-2A).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LINKED (GLCNAC. . .) (P. 5FE23A0AC7F91572 CRC64;
                                                                                                                                                28.8%; Score 182.5; DB 1; 37.7%; Pred. No. 2.8e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 28.8%; Score 182.5; Di
Best Local Similarity 37.7%; Pred. No. 2.8e-
Matches 43; Conservative 21; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   396 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                       TISSUE=Antler;
MEDLINE=97157076; Pubmed=9003457;
                                                                                                                                                                                                                                                                                      EMBL; AJ001817; CAA05033.1; -. HSSP; P18075; 1BMP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        44646 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                            InterPro; IPR001111; -. InterPro; IPR001839; -.
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396
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            338
396 AA;
                                                             SEQUENCE FROM N.A.
                                                                                                                                       distal promoter.";
                                        NCBI_TaxID=30532;
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P12643;
                                                                                                                                                                                                                                                                                                                                                                                                          DISULFID
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8
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-!- FUNCTION: INDUCES CARTILAGE AND BONE FORMATION.
-!- SUBUNIT: HOMODIMER, DISULFIDE-LINKED.
-!- TISSUE SPECIFICITY: PARTICULARLY ABUNDANT IN LUNG, SPLEEN AND COLON AND IN LOW BUT SIGNIFICANT LEVELS IN HEART, BRAIN, PLACENTA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                 Shore E.M., Xu M.-Q., Calvert G., Moriatis J., Kaplan F.S.; "Human bone morphogenetic protein 2 (BMP-2) genomic DNA sequence."; Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                               Wozney J.M., Rosen V., Celeste A.J., Mitsock L.M., Whitters M.J.,
Kriz R.W., Hewick R.M., Wang E.A.;
"Notel regulators of bone formation: molecular clones and
activities.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ø
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LIVER, SKELETAL MUSCLE, KIDNEY, PANCREAS, PROSTATE, OVARY AND SMALL INTESTINE.
Chordata; Craniata; Vertebrata; Euteleostomi;
Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
20653A3987R25E60 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       at 2.7
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Pfam: PF00688; TGF_propeptide; 1.
PROSITE; PS00250; TGF_BETA_1; 1.
Signal; Growth factor; Cytokine; Bone; Cartilage; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19;
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                       Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-99175323; Pubmed=10074410;
Scheufler C., Sebald W., Huelsmeyer M.;
"Crystal structure of human bone morphogenetic protein-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BONE MORPHOGENETIC PROTEIN
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Pred. No. 2.8e-12;
1; Mismatches 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS) OF 292-396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
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                                                                                               SEQUENCE FROM N.A.
MEDLINE-89072730; PubMed-3201241;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28.8%; Scc
37.7%; Pre
tive 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AF040249; AAF21646.1; -. EMBL; AL033568; CAB82007.1; -. PIR; B37278; B37278. PDB; 3BMP; 12-MAR-00. MIM; 112261; --
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                                                                                                                                                                                                                                                      Science 242:1528-1534(1988).
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AA;
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Matches 43; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                             NCBI_TaxID=9606;
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45575 MW; 150AC64A47D2E15F CRC64;

398 AA;

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SEQUENCE
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                  Nishimatsu S., Suzuki A., Shoda A., Murakami K., Ueno N.;
"Genes for bone morphogenetic proteins are differentially transcribed
in early amphibian embryos.";
        62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
INTERCHAIN (BY SIMILARITY).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-Y (IN REF. 2).
N-Y (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; X55031; CAA45018.1; -.

EMBL; X63424; CAA45018.1; -.

PIRS, S16244, S16244.

PIRS, JH6087; JH6087.

HSSP; P18075; 1BMP.

InterPro; IPR001131; -.

InterPro; IPR001839; -.

Pfam; PF00019; TGF-beta; 1.

Pfam; PF00688; TGF-beta; 1.

Pfam; PF00589; TGF-BETA_1; 1.

Pfam; PF00580; TGF-BETA_1; 1.

S1gnal; Growth factor; Cytokine; Bone; Cartilage; Glycoprotein.
       RNLEENCCVRPLYIDFRQDLGWK-WVHEPKGYYANFCSGPCPY----LRSADTTHSTVL
                                                                                                                                        01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
01-JUL-1993 (Rel. 26, Last annotation update)
BONE MORPHOGENETIC PROTATION 2-1 PRECURSOR (BMP-2-I).
Xenopus laevis (African clawed frog).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                           63 GLYNTLN---PEASASPCCVPQDLEPLTILYYVGRTPKV--EQLSNMVVKSCKC 111
                                                                                                                                                                                                                                                                              ~
                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE=91274367; PubMed=2054389;
Plessow S., Koester M., Knoechel W.;
"CDNA sequence of Xenopus laevis bone morphogenetic protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BONE MORPHOGENETIC PROTEIN 2-I.
                                                                                                                                                                                                                                                                                                                                                                       398 AA
                                                                                                                                                                                                                                                                                                Biochim. Biophys. Acta 1089:280-282(1991)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL.
                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                MEDLINE-92378616; PubMed-1510675;
                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             398
363
395
397
397
1137
202
340
16
                                                                                                                                                                                                              Xenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                        NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          285
298
327
331
362
137
340
                                                                                                                     BMPA_XENLA
P25703;
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CONFLICT
CONFLICT
CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE=92378616; PubMed=1510675;
Nishimatsu S., Suzuki A., Shoda A., Murakami K., Ueno N.;
"Genes for bone morphogenetic proteins are differentially transcribed
                                                                                                                                                                                                             : |: :| |||||| |:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|
                                                                                        Gaps
                                                                                                                                                               9 RNLEENCCVRPLYIDFRQDLGWK-WVHEPKGYYANFCSGPCPY----LRSADTTHSTVL 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POTENTIAL.
BONE MORPHOGENETIC PROTEIN 2-II.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
INTERCHAIN (BY SIMILARITY).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
BONE MORPHOGENETIC PROTEIN 2-II PRECURSOR (BMP-2-II).
Xenopus laevis (African clawed frog).
Bukaryota, Metazoa, Chordata, Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPRU01005, ...
Pfam; PR00019; TGF-beta; 1.
Pfam; PR00688; TGFb_ropeptide; 1.
PROSITE; PS00250; TGF_BETA_1; 1.
Signal; Growth factor; Cytokine; Bone; Cartilage; Glycoprotein.
                                                                                                                                                                                                                                                                                                                               63 GLYNTLN---PEASASPCCVPQDLEPLTILYYVGRTPKV--EQLSNMVVKSCKC 111
                                                                                    19;
                                                                                                                                                                                                                                                                                                                                                                         Length 398;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 182.5; DB 1; Length 398; Pred. No. 2.8e-12;
                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                60E41FA2C8E603DC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Score 182.5; DB 1;
; Pred. No. 2.8e-12;
21; Mismatches 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    398 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                45616 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   in early amphibian embryos.";
    28.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; X63425; CAA45019.1; -. PIR; JH0688; JH0688.
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                                                                                    43; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HSSP; P18075; 1BMP.
Interpro; IPR001111; -.
Interpro; IPR001839; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                284
398
395
397
397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Xenopodinae; Xenopus
NCBI_TaxID=8355;
    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           398 AA;
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Best Local Similarity
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298
327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BMPB_XENLA P30884;
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Page

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Gaps

. 9

Indels

39;

23; Mismatches

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Conservative
                                                                                                                                                                                                                                                                                                                                                      TISSUE=Placenta;
                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MIM; 201250; -.
                                                                                                                                                                                                                                                            GDF5 OR CDMP1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MIM; 200700;
 40;
                                                                                                                                                                   GDF5_HUMAN
P43026;
                                                                                                                                                       GDF5_HUMAN
  Matches
                                                  음
                                                                             δ
                                                                                                     q
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 ъ,
                                                                                                                                                                                                                                                                                                                                                                          292 KRLKSSCRRHPLYVDF-SDVGWNDWIVAPPGYHAFYCHGECPFPLADHLNS--TNHAIVQ 348
  Gaps
                         RNLEENCCVRPLYIDFRQDLGWK-WVHEPKGYYANFCSGPCPY----LRSADTTHSTVL 62
                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN=CD-1; TISSUE=Embryo;
MEDLINE=94195427; PubMed=8145850;
Storm E.E., Huynh T.V., Copeland N.G., Jenkins N.A., Kingsley D.M.,
                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INTERCHAIN (BY SIMILARITY).
N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                          GLYNTLN---PEASASPCCVPQDLEPLTILYYVGRTPKV--EQLSNMVVKSCKC 111
                                                                                         349 TLVNSVNTNIPKA----CCVPTELSAISML-YLDENEKVVLKNYQDMVVEGGGG 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL.
POTENTIAL.
GROWTH/DIFFERENTIATION FACTOR 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00019; TGF-beta; 1.
Pfam; PF00688; TGFD_propeptide; 1.
PRINTS; PR00438; GFCYSKNOT.
PROSITE; PS00250; TGF_BETA_1; 1.
Signal; Growth factor; Cytokine; Glycoprotein; Polymorphism.
SIGNAL
 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CD0D5DE48185D2E3 CRC64;
                                                                                                                                                                                                     01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
GROWTH/DIFFERENTIATION FACTOR 5 PRECURSOR (GDF-5).
 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                   495 AA
 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   or send an email to license@isb-sib.ch).
                                                                                                                                                                    PRT;
21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 S
                                                                                                                                                                                           01-NOV-1995 (Rel. 32, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             54885 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; U08337; AAA18778.1; -. HSSP; P18075; 1BMP.
Conservative
                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MGD; MGI:95688; Gdf5.
InterPro; IPR001111; -
InterPro; IPR001839; -.
InterPro; IPR002400; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      375
495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               460
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459
183
                                                                                                                                                                                                                                                           Mus musculus (Mouse)
                                                                                                                                                                                                                                              GDF5 OR GDF-5 OR BP
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                                                                                                                                                                                                                                                                                                NCBI_TaxID=10090;
43;
                                                                                                                                                                   GDF5_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DISULFID
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CHAIN
                                                                                                                                                       GDF5_MOUSE
                        6
                                                                          63
Matches
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Score 182; DB 1; Length 495; Pred. No. 3.9e-12;

28.7%; 37.0%;

Query Match Best Local Similarity

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              388 KNLKARCSRKALHVNFK-DMGWDDWIIAPLEYEAFHCEGLCEFPLRSHLEPTNHAVIQTL 446
                                                                                                                                                         01-07-1995 (Rel. 32, Created)
01-FE-1996 (Rel. 40, Last sequence update)
01-OT-2000 (Rel. 40, Last annotation update)
GROWTH/DIFFERENTIATION FACTOR 5 PRECURSOR (GDF-5) (CARTILAGE-DERIVED MORPHOGENETIC PROTEIN 1) (CDMP-1).
9 RNLEENCCVRPLYIDFRQDLGW-KWVHEPKGYYANFCSGPCPY-LRS--ADTTHSTVLGL 64
                                                                                                                                                                                                                                                                                                                            Hoetten G., Neidhardt H., Jacobowsky B., Pohl J.;
Cloning and expression of recombinant human growth/differentiation
factor 5.";
                                                                                                                                                                                                                                                  Craniata; Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Homo.
                                               65 YNTLNPEASASPCCVPQDLEPLTILYYVGRTPKV-EQLSNMVVKSCKC 111
                                                              Biochem. Biophys. Res. Commun. 204:646-652(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PHALANGES ARE ALMOST SQUARE.
SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
                                                                                                                                     501 AA.
                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; X80915; CAA56874.1; -. EMBL; U13660; AAA57007.1; -. HSSP; P18075; 1BMP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00019; TGF-beta; 1.
                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR001111; ...
InterPro; IPR001839; ...
InterPro; IPR002400; -...
                                                                                                                                                                                                                                    Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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DISULFID
                                                                                                                                     CARBOHYD
SEQUENCE
                                              DISULFID
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                                                                                                                     CARBOHYD
       PROPEP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Euechinoidea; Echinacea; Echinoida; Strongylocentrotidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                         RNLEENCCVRPLYIDFRQDLGW-KWVHEPKGYYANFCSGPCPY-LRS--ADTTHSTVLGL 64
                                                                                                          GROWTH/DIFFERENTIATION FACTOR 5.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
INTERCHAIN (BY SIMILARITY).
N-LINKED (GLCNAC. . .) (POTENTIAL).
S -> T (IN REF. 1).
VPRSR -> APGGG (IN REF. 1).
A -> S (IN REF. 1).
T -> A (IN REF. 1).
S -> L (IN REF. 1).
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                                                                                                                                                                                                                                                                                                                                                                                                                      39; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ponce M.R., Micol J.L., Davidson E.H.;
Submitted (FEB-1995) to the EMBL/GenBank/DDBJ databases.
-1- SUBUNIT: HOMODIMER, DISULFIDE-LINKED (PROBABLE).
-1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
                                                                                                                                                                                                                                                                                                                          EF631EA03417A348 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Strongylocentrotus purpuratus (Purple sea urchin)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00019; TGF-beta; 1.
Pfam; PF00688; TGFb_propeptide; 1.
PRINTS; PR00438; GFCYSKNOT.
PROSITE; PS00250; TGF_BETA_1; 1.
Growth factor; Cytokine; Glycoprotein; Signal.
SIGNAL.
                                    PROSITE; PS00250; TGF_BETA_1; 1.
Signal; Growth factor; Cytokine; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                     ; Pred. No. 4e-12; 23; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    461 AA
                                                                                                                                                                                                                                                                                                                                                                            28.7%; Score 182;
37.0%; Pred. No. 40
                                                                                            POTENTIAL.
                                                                             POTENTIAL.
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Pfam; PF00688; TGFb_propeptide; 1.
PRINTS; PR00438; GFCYSKNOT.
PROSITE; PS00250; TGF_BETA_1; 1.
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                                                                                                                                                                                                                                                                                                                          55640 MW;
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Matches 40; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
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                                                                                              381
501
466
498
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500
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189
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382
400
429
433
465
1189
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254
276
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P48969;
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                                                                                                                                                                                                                                                                                                                        SEQUENCE
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                                                                                            PROPEP
CHAIN
                                                                           SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBUNIT: DIMERIC, LINKED BY ONE OR MORE DISULFIDE BONDS.
SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Biochem. Biophys. Res. Commun. 206:608-613(1995).

-1- FUNCTION: INHIBINS ARE GONADAL GLYCOPEPTIDES THAT INHIBIT THE SECRETION OF FOLLITROPIN BY THE PITUITARY GLAND. ON THE OTHER HAND ACTIVINS ACTIVATE THE SECRETION OF FOLLITROPIN. ACTIVINS REGULATE GROWTH AND DIFFERRITIATION OF BENBRYONAL CARCINOMA CELLS, INDUCE ERYTHROPOIESIS, STIMULATE INSULIN SECRETION, AND PROMOTE NEURAL CELL SURVIVAL. ACTIVINS ARE ALSO IMPORTANT IN EMBRYONIC AXIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   355 NSDWQCKRKNLFVNF-EDLDWQEWIIAPLGYVAFYCQGECAFPLNGHANATNHAIVQTLV 413
                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                              NLEENCCVRPLYIDFRQDLGW-KWVHEPKGYYANFCSGPCPYLRSAD---TTHSTVLGLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                             N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
2573D54B6625F7EF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hoetten G., Neidhardt H., Schneider C., Pohl J., "Cloning of a new member of the TGF-beta family: a putative new activin beta C chain.";
                                                                                                                                                                                                                                                                                                                                                           ;
9
                                                                                                                                                                                                                                                                                                28.5%; Score 181; DB 1; Length 461; 34.6%; Pred. No. 4.7e-12; ive 22; Mismatches 42; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       414 HHMSPSHVPQPCCAPTKLSPITVLYYDDSRNVVLKKYKNMVVRACGC 460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        66 NTLNPEASASPCCVPQDLEPLTILYY-VGRTPKVEQLSNMVVKSCKC 111
                                                                                                                                   INTERCHAIN (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-OCT-1996 (Rel. 34, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
INHIBIN BETA C CHAIN PRECURSOR (ACTIVIN BETA-C CHAIN).
                         PROTEIN HOMOLOG.
                                                  BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
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  POTENTIAL
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PRINTS; PR00438; GFCYSKNOT.
PRINTS; PR00672; IMHIBINBC.
PROSITE; PS00250; TGF_BETA_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (Rel. 34, Created)
(Rel. 34, Last sequ
(Rel. 35, Last anno
                                                                                                                                                                                                                  51881 MW;
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                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 34...
Lac 37; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
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Interpro; IPR001839; -.
Interpro; IPR002400; -.
338
461
426
458
460
425
149
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31
339
380
393
425
402
461 AA;
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01-OCT-1996 (
01-NOV-1997 (
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P55103:
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DECA_DROPS
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MEDLINE=97224404; PubMed=9070865;
MEDLINE=97224404; PubMed=9070865;
Fang J., Wang S.Q., Smiley E., Bonadio J.;
"Genes coding for mouse activin beta C and beta E are closely linked and exhibit a liver-specific expression pattern in adult tissues.";
Biochem Biophys. Res. Commun. 231:655-661(1997).
-: FUNCTION: IMHIBINS ARE GONADAL GIYCOPEPTIDES THAT INHIBIT THE SECRETION OF FOLLITROPIN BY THE PITUITARY GLAND. ON THE OTHER HAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACTIVINS ACTIVATE THE SECRETION OF FOLLITROPIN. ACTIVINS REGULATE GROWTH AND DIFFERENTIATION OF EMBRYONAL CARCINOMA CELLS, INDUCE ERYTHROPOTESIS, STIMULATE INSULIN SECRETION, AND PROMOTE NEURAL CELL SURVIVAL. ACTIVINS ARE ALSO IMPORTANT IN EMBRYONIC AXIAL
                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                 15 CCVRPLYIDFRQDLGW-KWVHEPKGYYANFCSGPCPYLRS-----ADTTHSTVLGLY--N 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Structure, chromosomal localization, and expression analysis of the mouse inhibin/activin beta C (Inhbc) gene.";
 Contraceptive; Hormone; Glycoprotein; Signal.
                              INHIBIN BETA C CHAIN.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
INTERCHAIN (BY SIMILARITY).
N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
M-LINKED (GLCNAC. ..) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Schmitt J., Hoetten G., Jenkins N.A., Gilbert D.J., Copeland N.G., Pohl J., Schrewe H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                             10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BONDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LIVER.
                                                                                                                                                                       Length 352;
                                                                                                                                                                                             38; Indels
                                                                                                                                                                                                                                                                            Lau A.L., Nishimori K., Matzuk M.M.; "Structural analysis of the mouse activin beta C gene."; Biochim. Biophys. Acta 1307:145-148(1996).
                                                                                                                                                                                                                                                              67 TLNPEASASPCCVPQDLEPLTILYYVGRTPKVE-QLSNMVVKSCKCS 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBUNIT: DIMERIC, LINKED BY ONE OR MORE DISULFIDE TISSUE SPECIFICITY: MAINLY EXPRESSED IN THE ADULT SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
                                                                                                                                                                                                                                                                                                                               IHBC_MOUSE

ID IHBC_MOUSE

AC P5:104; 061452;

DT 01-007-1996 (Rel. 34, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 30-MAY-2000 (Rel. 39, Last annotation update)

DE NHIBIN BETA C CHAIN PRECURSOR (ACTIVIN BETA-C CHAIN)
                                                                                                                                                                      Score 180; DB 1;
Pred. No. 4.5e-12;
                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=129; TISSUE=Liver;
MEDLINE=96435913; PubMed=8838799;
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                                                                                                                                                                       28.4%; Scc
37.4%; Pre
tive 19;
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Mammalia; Eutheria; Rodentia;
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                                                                                                                                      38238
                                                                                                                                                                                             Conservative
                      236
352
248
317
349
351
110
1110
inhibitor;
                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse).
                                                                                                             143
161
352 AA;
                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=10090;
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Follitropin
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                                            DISULFID
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                                                                 DISULFID
                                                                             DISULFID
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                                                                                                     CARBOHYD
                                                                                                               CARBOHYD
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                                                                                                                                     SEQUENCE
           SIGNAL
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pteryota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7237;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15 CCVRPLYIDFRQDLGWK-WVHEPKGYYANFCSGPCPYLRSAD-----TTHSTVLGLYNT 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hormone; Glycoprotein; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INTERCHAIN (BY SIMILARITY).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          68 LNPEASA----SPCCVPQDLEPLTILYYVGRTPKVE-QLSNMVVKSCKCS 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 352;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28.4%; Score 180; DB 1; Length 35; 37.8%; Pred. No. 4.5e-12; Live 20; Mismatches 31; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             220812FD73717185 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DECAPENTAPLEGIC PROTEIN PRECURSOR (DPP-C PROTEIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL.
INHIBIN BETA C C
BX SIMILARITY.
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15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -> G (IN REF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                621 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam: PF00019; TGF-beta; 1.
PRINTS; PR00438; GFCYSKNOT.
PROSITE; PS00250; INHIBINBC.
PROSITE; PS00250; TGF_BETA_1; 1.
FOLLITROPIN INhibitor; Contraceptive; HOD SIGNAL
1 18 POTENTIAL.
CHAIN 237 POTENTIAL.
DISULEID 240 248 BY SIMILARI;
DISULEID 247 317 BY SIMILARI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL.
                                                                                                                                                                                                                                EMBL; X90842; CAA62347.1; JOINED.
EMBL; X908419, CAA62333.1; -
EMBL; U40773; AAC52723.1; -
EMBL; U40772; AAC52723.1; JOINED.
EMBL; U95962, AAC53164.1; -
HSSP; P18075; IBNP.
MGD; MGI:105932; Inhbc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
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                                                                                                                                                                                                        EMBL; X90841; CAA62347.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best_Local Similarity 37.8%; Matches 42; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             39401
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                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR001318; -. InterPro; IPR001839; -. InterPro; IPR002400; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           352 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15 CCVRPLYIDFRQDLGW-KWVHEPKGYYANFCSGPCPY-LRS--ADTTHSTVLGLYNTLNP 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24 CSRRPLHVNFK-ELGWDDWIIAPLEYEAYHCEGVCDFPLRSHLEPTNHAIIQTLMNSMDP 82
                                                                                                          STRAIN=BALB/C; TISSUE-Liver;
MEDILNE=94195427; PubMed=8145850;
Storm E.E., Huynh T.V., Copeland N.G., Jenkins N.A., Kingsley D.M.,
Lee S.-J.;
              Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse).
Sukaryota: Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                       "Limb alterations in brachypodism mice due to mutations in a new member of the TGF beta-superfamily."; Nature 368:639-643(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 179; DB 1; Length 125; Pred. No. 2e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GROWTH/DIFFERENTIATION FACTOR
                                                                                                                                                                                                                     -!- SUBUNIT: HOMODIMER, DISULFIDE-LINKED (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INTERCHAIN (BY SIMILARITY 10FA2A5B7748DA32 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  71 EASASPCCVPQDLEPLTILYY-VGRTPKVEQLSNMVVKSCKC 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    :: |||| | |::||| | ::||| 83 GSTPPSCCVPTKLTPISILYIDAGNNVVYKQYEDMVVESCGC 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=C3H/KW;
MEDLINE=95046894; PubMed=7958439;
King J.A., Marker P.C., Seung K.J., Kingsley D.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-FEB-1996 (Rel. 33, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
BONE MORPHOGENETIC PROTEIN 5 PRECURSOR (BMP-5)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY.
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BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Growth factor; Cytokine; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00019; TGF-beta; 1.
PROSITE; PS00250; TGF_BETA_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last seq
01-FEB-1996 (Rel. 33, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28.2%;
38.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                      MGD; MGI:95689; Gdf6.
InterPro; IPR001839;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           125 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
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                                                                                              SEQUENCE FROM N.A
                                                               NCBI_TaxID-10090;
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P49003;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2
       514 KNHEETCRRHSLYVDF-ADVGWDDWIVAPPGYDAYYCHGKCPF-PLADHFNSTNHAVVQT 571
                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00019; TGF-beta; 1.
Pfam; PF00688; TGF_propeptide; 1.
PROSITE; PS00250; TGF_BETA_1; 1.
Growth factor; Developmental protein; Differentiation; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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evolution at the decapentaplegic locus in Drosophila.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   . .) (POTENTIAL). . .) (POTENTIAL). . . . (POTENTIAL).
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01-NVV-1995 (Rel. 32, Last sequence update)
01-NVV-1997 (Rel. 35, Last annotation update)
GROWTH/DIFFERENTIATION FACTOR 6 PRECURSOR (GDF-6) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 621;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     64 LYNTLNPEASASPCCVPQDLEPLTILYYVGR-TPKVEQLSNMVVKSCKC 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            46; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INTERCHAIN (BY SIMILARITY).
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3FD7141FB5509651 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL.
BY SIMILARITY.
DECAPENTAPLEGIC PROTEIN
                                                                                                                                                                                                 AND MIDGUT MESODERM (BY SIMILARITY).
SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 180; DB 1;
Pred. No. 8.2e-12;
3; Mismatches 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (GLCNAC.
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POLY-GLN.
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                                                                                                                                                                                                                                                                                                                                                                       EMBL; U63856; AAC47553.1; -
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365
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621 AA;
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01-NOV-1995
01-NOV-1997
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GDF6_MOUSE
ID GDF6_MOUSE
AC 01-NOV-1995
DT 01-NOV-1995
DT 01-NOV-1995
DT GROWTH/DIFFFE
'Molecular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            42;
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CARBOHYD
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CARBOHYD
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Best Local S
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                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    348 KQACKKHELYVSFR-DLGWQDWIIAPEGYAAFYCDGECSFPLNAHMNATNHAIVQTLVHL 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12 EENCCVRPLYIDFRQDLGWK-WVHEPKGYYANFCSGPCPYLRSAD---TTHSTVLGLYNT 67
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BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

INTERCHAIN (BY SIMILARITY).

N-LINKED (GLCNAC. . .) (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).
'BMP5 and the molecular, skeletal, and soft-tissue alterations in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE-Bone;
MEDLINE-91088608; PubMed=2263636;
Cleste A.J., Iannazzl J.A., Taylor R.C., Hewick R.M., Rosen V.,
Wang E.A., Wozney J.M.;
"Identification of transforming growth factor beta family members
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .,
                                                                                                                                                                                                                                                                                                      Pfam: PF00119; TGF-beta; 1.
Pfam: PF00618; TGF-beta; 1.
PRIMTS: PR00488; TGFD_propeptide; 1.
PRIMTS: PR00428; GFCYSKNOT.
PROSTITE; P800250; TGF_BETA_1; 1.
Signal; Growth factor; Cytokine; Bone; Cartilage; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28.2%; Score 179; DB 1; Length 452; 35.2%; Pred. No. 7.5e-12; ive 22; Mismatches 40; Indels
         short ear mice.";
Dev. Biol. 166:112-122(1994).
-!- FUNCTION: INDUCES CARTILAGE AND BONE FORMATION.
-!- SUBUNIT: HOMODIMER, DISULETDE-LINKED (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL.
BONE MORPHOGENETIC PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 68 LNPEASASPCCVPQDLEPLTILYYVGRTPKV-EQLSNMVVKSCKC 111
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BMP5_HUMAN

ID BMP5_HUMAN

STANDARD; PRT; 454 AA.

AC P22003; O9NTM5;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DT 01-OCT-2000 (BMP-5).
GN BMP5.
CC Bukaryota; Metazoa; Chordata; Craniata; Vertebrata;
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
CC Bummalla; Eutheria; Primates; Catarrhini; Hominidae

OX NCBI_TAXID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC SEQUENCE FROM N.A.
RC SEQUENCE FROM N.A.
RA Celaste A.J., Iannazzi J.A., Taylor R.C., Hewick R.
RA Gelsete A.J., Jannazzi J.A., Taylor R.C., Hewick R.
RA Wang E.A., Wozney J.M., Taylor R.C., Hewick R.
RA Wang E.A., Wozney J.M., Taylor R.C., Hewick R.
RT "Identification of transforming growth factor beta
                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ₹
                                                                                                                                                                                                                   EMBL; L41145; AAA64612.1; -. HSSP; P18075; 1BMP.
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Matches 37; Conservative
                                                                                                                                                                                                                                                             InterPro; IPR001111; -.
InterPro; IPR001839; -.
InterPro; IPR002400; -.
                                                                                                                                                                                                                                                                                                                                                                                                   320
452
417
                                                                                                                                                                                                                                                                                                                                                                                                                                             449
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393
452 AA;
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351
380
384
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CARBOHYD
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                      SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        350 KQACKKHELYVSFR-DLGWQDWIIAPEGYAAFYCDGECSFPLNAHMNATNHAIVQTLVHL 408
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
INTERCHAIN (BY SIMILARITY).
N-LINKED (GLCNAC. . .) (POTENTIAL).
MAG 631277413CCC22EE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00019; TGF-beta; 1.
Pfam; PF00688; TGFD_propeptide; 1.
PRINTS; PR00438; GFCYSRNOT.
PROSTIE; PS00250; TGF_BETA_1; 1.
Signal; Growth factor; Cytokine; Bone; Cartilage; Glycoprotein.
SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
present in bone-inductive protein purified from bovine bone.";
Proc. Natl. Acad. Sci. U.S.A. 87:9843-9847(1990).
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01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
GROWTH/DIFFERENTIATION FACTOR 7 PRECURSOR (GDF-7) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 454;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BONE MORPHOGENETIC PROTEIN 5.
                                                                                                                                                                  -1- FUNCTION: INDUCES CARTILAGE AND BONE FORMATION.
-1- SUBUNIT: HOMODIMER, DISULETDE-LINKED (BY SIMILARITY).
-1- TISSUE SPECTRICITY: EXPRESSED IN THE LUNGS AND LIVER.
-1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       40; Indels
                                                                                                                 Tracey A.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            68 LNPEASASPCCVPQDLEPLTILYYVGRTPKV-EQLSNMVVKSCKC 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28.2%; Score 179; DB 1; 35.2%; Pred. No. 7.5e-12; iive 22; Mismatches 40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            151 AA
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51736 MW;
                                                                                    SEQUENCE OF 279-454 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; M60314; AAA36736.1; -. EMBL; AL133386; CAB81657.1;
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InterPro; IPR001839; -.
InterPro; IPR002400; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIR; A39263; A39263.
HSSP; P18075; 1BMP.
MIM; 112265; -.
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327
345
395
454 AA;
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353
382
386
418
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P43029:
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transforming growth factor-beta superfamily predominantly expressed
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37.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                47873
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Best Local Similarity 37.3%
Matches 38; Conservative
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                                                                                                                                                                                                                                                                                                                    436
433
433
400
27
89
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InterPro; IPR001839
                                                                                                                                                                                                                                                                                                                                                                                                                436 AA;
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095393;
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PROPEP
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01-0CT-1996 (Rel. 34, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
GROWTH/DIFFERENTIATION FACTOR 6 PRECURSOR (GDF-6) (CARTILAGE-DERIVED
MORPHOGENETIC PROTEIN 2) (CDMP-2) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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SEQUENCE FROM N.A.
STRAIN=BALB/C; TISSUE-Liver;
MEDLINE=94195427; PubMed=8145850;
Storm E.E., Huynh T.V., Copeland N.G., Jenkins N.A., Kingsley D.M., Lee S.-J.;
"Limb alterations in brachypodism mice due to mutations in a new member of the TGF beta-superfamily.";
Nature 368:639-643(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .;
9
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MEDLINE-95050604; PubMed-7961761;
Chang S., Hoang B., Thomas J.T., Vukicevic S., Luyten F.P.,
Ryba N.J.P., Kozak C.A., Reddi A.H., Moos M.;
"Cartilage-derived morphogenetic proteins. New members of the
                                                                                                                                                                                                                                                                                                                                                                               GROWTH/DIFFERENTIATION FACTOR 7. BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1; Length 151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            I- SUBUNIT: HOMODIMER, DISULFIDE-LINKED (BY SIMILARITY).
I- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          65 YNTLNPEASASPCCVPQDLEPLTILYYVGRTPKV-EQLSNMVVKSCKC 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               42; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                      INTERCHAIN (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0E496AACB5827759 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27.8%; Score 176; DB 1;
illarity 37.0%; Pred. No. 5e-12;
Conservative 20; Mismatches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         436 AA
                                                                                                                                                                                                                                                                                                           Pfam; PF00019; TGF-beta; 1.
PROSITE; PS00250; TGF_BETA_1; 1.
Growth factor; Cytokine; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL
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POLY-GLY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15697 MW;
                                                                                                                                                                                                                                                           EMBL; U08339; AAA18780.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                       HSSP; P18075; 1BMP.
MGD; MGI:95690; Gdf7.
InterPro; IPR001839;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bos taurus (Bovine).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             151 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 40; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9913;
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P55106;
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PROPEP
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Bukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBL_raxID-9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INTERCHAIN (BY SIMILARITY).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
BO68BELZEF8ABEID CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
9
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BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 175; DB 1; Length 436;
Pred. No. 1.9e-11;
in long bones during human embryonic development.";
Liol. Chem. 268:28227-28234 (1994).
-!- SUBUNIT: HOWODIMER, DISULEIDE-LINKED (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       39; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                :: |||| | | ::||| | ::||| 394 GSTPPSCCVPTKLTPISILYIDAGNNVVYNEYEEMVVESCGG 435
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BONE MORPHOGENETIC PROTEIN 10 PRECURSOR (BMP-10).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    424 AA
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(Rel. 40, Last sequence update)
(Rel. 40, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Pred. No. 1.9e
19; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BY SIMILARITY
BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00019; TCF-beta; 1.
Pfam; PF00688; TGFD_propeptide; 1.
PROSITE; PS00250; TGF_BETA_1; 1.
Growth factor; Cytokine; Glycoprotein.
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Lee S. -J.;
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                                                                                                                                                                                                                                                                                             Signal.
SIGNAL
                                                                                                                                                                                                                                                                                                                                             PROPEP
                                                                                                                                                                                                                                                                                                                                                                 CHAIN
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entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RNLEENCCVR-PLYIDFRQDLGW-KWVHEPKGYYANFCSGPCPYLRS---ADTTHSTVLG 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBRYONIC DORSAL HYPODERM, FOR VIABILITY OF LARVAE AND FOR CELL VIABILITY OF THE EPITHELIAL CELLS IN THE IMAGINAL DISKS. ACTS
                                                                                                                                                                                                                                                                                                                                                                               BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
INTERCHAIN (BY SIMILARITY).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
WW. 3FDB3B7221BB2254 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TWO CELLULAR RESPONSE THRESHOLDS WITHIN THE DORSAL HALF OF THE DROSOPHILA EMBRYO. REQUIRED FOR THE PROPER DEVELOPMENT OF THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1; Length 424;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Arthropoda; Trachéata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Coleoptera; Polyphaga;
Cucujiformia; Tenebrionidae; Tribolium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (BY
                                                                                                                                                                                                                                                                                                                                                              BONE MORPHOGENETIC PROTEIN 10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64 LYNTLNPEASASPCCVPQDLEPLTILYY-VGRTPKVEQLSNMVVKSCKC 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 27.5%; Score 174.5; DB 1; Length Best Local Similarity 37.6%; Pred. No. 2.1e-11; Matches 41; Conservative 15; Mismatches 46; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOGETHER WITH SCW (BY SIMILARITY).
SUBUNIT: HOMODIMER OR HETERODIMER, DISULFIDE-LINKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY).
SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
                                                                                                                                                                                    Pfam; PF00019; TGF-beta; 1.
Pfam; PF00688; TGFb_propeptide; 1.
PRINTS; PR00669; INHIBINA.
Signal; Growth factor; Cytokine; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              372 AA
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                                                                                                                                                                                                                                                                                                                   POTENTIAL.
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01-OCT-2000 (Rel. 40, Last annotati
DECAPENTAPLEGIC PROTEIN PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               48047 MW;
                                                                      EMBL; AF101441; AAC77462.1;
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                                                                                                                Interpro; IPR001111; -.
Interpro; IPR001839; -.
Interpro; IPR002405; -.
                                                                                                                                                                                                                                                                                                                                                            424
389
421
423
388
67
131
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323
352
356
388
67
131
424 AA;
                                                                                                 HSSP; P18075; 1BMP
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Q26974;
                                                                                                                                                                                                                                                                                                                                                                                    DISULFID
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CHAIN
                                                                                                                                                                                                                                                                                                                   SIGNAL
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DECA_TRICA
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modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          265 KNLKDPCRRRQMYVDF-GSVGWNDWIVAPLGYDAYYCGGECEYPIPDHMNTTNHAIVQSL 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nervous system:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9 RNLEENCCVRPLYIDFRQDLGWK-WVHEPKGYYANFCSGPCPYL---RSADTTHSTVLGL 64
                                                                                                                                                                                                                                                                                                Growth factor; Developmental protein; Differentiation; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                               BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
INTERCHAIN (BY SIMILARITY).
N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-AUG-1992 (Rel. 23, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
EMBRYONIC GROWTH/DIFFERENTIATION FACTOR 1 PRECURSOR (GDF-1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 372;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       65 YNTLNPEASASPCCVPQDLEPLTILYYVGRTPKV--EQLSNMVVKSCKC 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         324 VNSMKPKEVPGPCCVPTQLGQMSML-YLGSDGSVILKNYKEMVVVGCGC 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -i- SUBUNIT: HOMODIMER, DISULFIDE-LINKED (BY SIMILARITY).
-i- SUBCELLULAR LOCATION: SECRETED.
-i- TISSUE SPECIFICITY: EXPRESSED IN THE BRAIN.
-i- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            45; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C9991AB75D2E3173 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'Expression of growth/differentiation factor 1 in the
                                                                                                                                                                                                                                                                                                                                                                                                            DECAPENTAPLEGIC PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              conservation of a bicistronic structure.";
Proc. Natl. Acad. Sci. U.S.A. 88:4250-4254(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ch 27.4%; Score 174; DB 1; 1 Similarity 35.8%; Pred. No. 2.1e-11; 39; Conservative 17; Mismatches 45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           372
                                                                                                                                                                                                                                                                                                                                                          POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL
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                                                                                                                                                           InterPro; IPR001111; -.
InterPro; IPR001839; -.
Pfam, PF00019; TGF-beta; 1.
Pfam, PF00688; TGFb_propeptide; 1.
PROSITE; PS00250; TGF_BETA_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-91239545; PubMed-2034669;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GDF1_HUMAN STANDARD; P P27539; 044344; 01-AUG-1992 (Rel. 23, Created) 01-AUG-1992 (Rel. 23, Last sequol-ocr-2000 (Rel. 40, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       42435 MW;
                                                                                                         EMBL; U63132; AAB38392.1;
                                                                                                                                                                                                                                                                                                                                                                                                                               337
369
371
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  372 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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300
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336
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1134
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                                                                                                                                    HSSP; P18075;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL.
EMBRYONIC GROWTH/DIFFERENTIATION FACTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CCVRPLYIDFRQDLGW-KWVHEPKGYYANFCSGPC--PYLRSAD-----TTHSTVLGLYN 66
                                                                                                                                                                                                                                                                                                                                               1.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
N'ENECHALN (BY SIMILARITY).
N'EINKED (GLCNAC. . .) (POTENTIAL).
POLY-ALA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. MEDLINE-87090408; Pubmed-3467201; Padgett R.W., St Johnston R.D., Gelbart W.M.; At anscript from a Drosophila pattern gene predicts a protein homologous to the transforming growth factor-beta family."; Nature 325:81-84(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27.4%; Score 174; DB 1; Length 372; 35.8%; Pred. No. 2.1e-11; Live 17; Mismatches 41; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              67 TLNPEASASPCCVPQDLEPLTILYYVGRTPKV-EQLSNMVVKSCKC 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 326 AAAPGAADLPCCVPARLSPISVLFFDNSDNVVLRQYEDMVVDECGC 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                   -> A (IN REF. 2).
10A484A406304232 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DECA_DROME STANDARD; PRT; 588 AA., P07713; P91651; P01713; P91651; P01 AAR-1988 (Rel. 07, Created) P1-APR-1988 (Rel. 07, Last sequence update) P15-DEC-1998 (Rel. 37, Last annotation update) PECAPENTAPLEGIC PROTEIN PRECURSOR (DPP-C PROTEIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Richter B., Long M., Lewontin R.C., Nitasaka E.;
                                                                                                                                                                                                                                                  PRINTS; PR00438, GFCYSKNOT.
PROSITE; PS00250; TGF_BETA_1; 1.
Signal; Growth factor; Cytokine; Glycoprotein.
                                                                                                                                                                                                                                                                                                   POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drosophila melanogaster (Fruit fly).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-DP CN BW;
MEDLINE-97225213; PubMed-9071586;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ψ¥;
                                                                                                                                             EMBL; AC003972; AAB94786.1;
PIR; C39364; C39364.
HSSP; P18075; 1BMP.
MIM; 602880; -.
                                                                                                                                                                                                                         InterPro; IPR002400; -. Pfam; PF00019; TGF-beta; 1
                                                                                                                                   EMBL; M62302; AAA58501.1;
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                                                                                                                                                                                                         nterPro; IPR001839; -.
                                                                                                                                                                                                                                                                                                                253
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296
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336
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152
118
372 AA;
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les 38; Conserv
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the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                          Panganiban G.E.F., Rashka K.E., Neitzel M.D., Hoffmann F.M.; "Biochemical Characterization of the Drosophila dpp protein, a member of the transforming growth factor beta family of growth factors."; Mol. Cell. Biol. 10:2669-2677(1990).
                                                                                                                                                                                                                                                             HOWODIMERS ELICIT A BASAL RESPONSE AND SCW/SCW HOWODIMERS ALONE ARE INFFECTIVE IN SPECIFYING A DORSAL PATTERN.
TISSUE SPECIFICITY: EXPRESSED IN THE IMAGINAL DISCS ASSOCIATED WITH ESTABLISHMENT OF THE PROXIMAL DISTAL AXIS OF THE APPENDAGES,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   481 KNHDDTCRRHSLYVDF-SDVGWDDWIVAPLGYDAYYCHGKCPF-PLADHFNSTNHAVVQT 538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                     TWO CELLULAR RESPONSE THRESHOLDS WITHIN THE DORSAL HALF OF THE DROSOPHILA EMBRYO. REQUIRED FOR THE PROPER DEVELOPMENT OF THE EMBRYONIC DORSAL HYPODERM, FOR VIABILITY OF LARVAE AND FOR CELL VIABILITY OF THE EPITHELIAL CELLS IN THE IMAGINAL DISKS. ACTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Growth factor; Developmental protein; Differentiation; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BY SIMILARITY.
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INTERCHAIN (BY SIMILARITY).
N-LINKED (GLCNAC. .) (POTENITAL).
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"Nucleotide variation and conservation at the dpp locus, a gene controlling early development in Drosophila."; Genetics 145:311-323(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ..
8
                                                                                                                                                                                                                                    TOGETHER WITH SCW.
SUBUNIT: HETERODIMERS OF SCW/DPP ARE THE ACTIVE SUBUNIT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 588;
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-> M (IN STRAIN DP CN BW).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DECAPENTAPLEGIC PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 172; DB 1;
Pred. No. 5.5e-11;
                                                                                                                                                                                                                                                                                                                                               SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16; Mismatches
                                                              AND SEQUENCE OF 457-476
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00019; TGF-beta; 1.
Pfam; PF00688; TGFb_propeptide; 1.
PROSITE; PS00250; TGF_BETA_1; 1.
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                                                                              MEDLINE=90258853; PubMed=1692958
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35.8%;
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PIR; A26158; A26158.
HSSP; P18075; 1BMP.
FlyBase; FBgn0000490; dpp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      39; Conservative
                                                                                                                                                                                                                                                                                                                                AND MIDGUT MESODERM.
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CHARACTERIZATION,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Molecular evolution at the decapentaplegic locus in Drosophila.";
Genetics 145:297-309(1997).

-!- FUNCTION: ACTS AS AN EXTRACELLULAR MORPHOGEN TO ESTABLISH AT LEAST
TWO CELLULAR RESPONSE THRESHOLDS WITHIN THE DORSAL HALF OF THE
DROSOPHILA EMBRYO. REQUIRED FOR THE PROPER DEVELOPMENT OF THE
EMBRYONIC DORSAL HYPODERM, FOR VIABILITY OF LARVAE AND FOR CELL
VIABILITY OF THE EPITHELIAL CELLS IN THE IMAGINAL DISKS. ACTS
TOGETHER WITH SCW (BY SIMILARITY).

-!- SUBUNIT: HETERODIMERS OF SCW/DPP ARE THE ACTIVE SUBUNIT, DPP/DPP
                                                                                                                                                                                                                                                               Drosophila simulans (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HOMODIMERS ELICIT A BASAL RESPONSE AND SCW/SCW HOMODIMERS ALONE ARE INEFFECTIVE IN SPECIFYING A DORSAL PATTERN (BY SIMILARITY). TISSUE SPECIFICITY: EXPRESSED IN THE IMAGINAL DISCS ASSOCIATED WITH ESTABLISHMENT OF THE PROXIMAL-DISTAL AXIS OF THE APPENDAGES, AND MIDGUT MESODERN (BY SIMILARITY). SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Newfeld S.J., Padgett R.W., Findley S.D., Richter B.G., Sanicola M., de Cuevas M., Gelbart W.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Growth factor; Developmental protein; Differentiation; Glycoprotein;
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BY SIMILARITY.
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N-LINKED (GLCNAC. .) (POTENTIAL).
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N-LINKED (GLCNAC. .) (POTENTIAL).
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DECAPENTAPLEGIC PROTEIN.
                                                                                                                                                                                                        DECAPENTAPLEGIC PROTEIN PRECURSOR (DPP-C PROTEIN).
                                                                                                                                               (Rel. 37, Last sequence update) (Rel. 37, Last annotation update)
                                                               593 AA.
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Pfam; PF00688; TGFD_propeptide; 1.
PROSITE; PS00250; TGF_BETA_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-97225212; PubMed-9071585;
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FlyBase; FBgn0015673; Dsim\dpp.
                                                                                                                   15-DEC-1998 (Rel. 37, Created)
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                                                               STANDARD;
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593 AA;
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SEQUENCE FROM N.A.
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P91706;
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Archosauría; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      252 SCKRHPLYVDF-NDVGWNDWIVAPPGYSAFYCHGECPFPLADHLNS--TNHAIVQTLVNS 308
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38.5%; Pred. No. 3.7e-11;
ive 18; Mismatches 30; Indels 19; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                    Francis P.H., Richardson M.K., Brickell P.M., Tickle C.;
"Bonoe morphogenetic proteins and a signalling pathway that controls
patterning in the developing chick limb.";
Development 120:209-218(1994).
-!- FUNCTION: INDICES CARTILAGE AND BONE FORMATION (BY SIMILARITY).
-!- SUBGUNT: HOWODIMER, DISULFIDE-LINKED (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BONE MORPHOGENETIC PROTEIN 2.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
INTERCHAIN (BY SIMILARITY).
N-LINKED (GLCNAC. .) (POTENTIAL).
                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                  544 LVNNMNPGKVPKACCVPTQLDSVAMLYLNDQSTVVLKNYQEMTVVGCGC 592
                                                64 LYNTLNPEASASPCCVPQDLEPLTILYYVGR-TPKVEQLSNMVVKSCKC 111
                                                                                                                                                                               01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
BONE MORPHOGENETIC PROTEIN 2 PRECURSOR (BMP-2) (FRAGMENT).
BMP2 OR BMP-2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00019; TGF-beta; 1.
Pfam; PF00889; TGFP_propeptide; 1.
PROSTIE; PS00250; TGF_BETA_1; 1.
Growth factor; Cytokine; Bone; Cartilage; Glycoprotein.
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                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                       Gallus gallus (Chicken).
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353 AA;
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                                                                                                                                                          BMP2_CHICK
Q90751;
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PROPEP
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                                                                                                                              RESULT 85
BMP2_CHICK
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LN---PEASASPCCVPQDLEPLTILYYVGRTPKV--EQLSNMVVKSCKC 111

89

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5;

8;

46; Indels

16; Mismatches

Conservative

Query Match Best Local Similarity Matches 39; Conserv

27.1%; Score 172; DB 1; Length 593; 35.8%; Pred. No. 5.6e-11;

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9
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A ZHAO-ICR; TISSUE-Placenta;

MEDLINE-97000308; PubMed-8843393;

MEDLINE-97000308; PubMed-8843393;

MEDLINE-97000308; PubMed-8843393;

Than of C., Hogan B.L.;

Evidence that mouse Bmp8a (Op2) and Bmp8b are duplicated genes that play a role in spermatogenesis and placental development.";

Mech. Dev. 57:159-168[1986].

C -1- FUNCTION: INDUCES CARTILAGE AND BONE FORMATION MAY BE THE OSTEOINNUCTIVE FACTOR RESPONSIBLE FOR THE PHENOMENON OF EPITHELIAL OSTEOENESIS. PLAYS A ROLE IN CALCIUM REGULATION AND BONE HOMBOSTAGIS (BY SIMILARITY).

C -1- SUBDUTT: HOMODIMER, DISCLETIDE-LINKED.

C -1- SUBCELLULAR LOCATION: SECRETED (BY SIMILARITY).

C -1- SUBCELLULAR LOCATION: STREET TOF-BETA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R HSSP; P18075; IBMP.
R HSSP; P18075; IBMP.
R MGD: MGI:107335; Bmp8b.
R InterPro; IPR001111; ---
DR InterPro; IPR001111; ---
DR Pfam; PF00019; TGF-beta; 1.
DR Pfam; PF00048; TGF-beta; 1.
DR PROSITE; PS00250; TGF-BETA_1; 1.
DR PROSITE; PS00250; TGF-BETA_1; 1.
ENGRITE; PS00250; TGF-BETA_1; 1.
DR PROSITE; PS00250; TGF-B
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                                                                                                                                                                                                                                                                                        Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus.
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LLINKED (GLCNAC. .) (POTENTIAL).

N-ILINKED (GLCNAC. ..) (POTENTIAL).

ERADB7B8C7EC4839 CRC64;
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309 VNSKIPRA----CCVPTELSAISML-YLDENEKVVLKNYQDMVVEGGGG 352
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40.0%; Pred. No. 4.7e-11;
:ive 16; Mismatches 39; Indels
                                                                                                                                                              01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
BONE MORPHOGENETIC PROTEIN 8B PRECURSOR (BMP-8B).
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BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
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Mammalia; Eutheria; Rodentia;
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                                                                                                                          STANDARD;
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364
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155
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                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10090;
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2298
327
331
363
155
                                                                            RESULT 86
BM8B_MOUSE
ID BM8B_MOUSE
AC P55105;
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DISULFID
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                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          299 RKNKKNCRRHALYVDF-SDVGWNDWIVAPPGYQAFYCHGDCPFFLADHLNS--TNHAIVQ 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN-WHITE LEGHORN;
MEDLINE-94163974; PubMed-8119128;
MEDLINE-94163974; PubMed-8119128;
Francis P.H., Richardson.R., Brickell P.M., Tickle C.;
"Bone morphogenetic proteins and a signalling pathway that controls patterning in the developing chick limb.";
Development 120:209-218(1994).
-!- FUNCTION: INDUCES CARTILAGE AND BONE FORMATION.
-!- SUBUNIT: HOWODIMER, DISULFIDE-LINKED (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19;
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|: |||| :::||| | ::||| | 355 KPDIIPRVCCVPTELSAISLLYY-DRNNNVLRRRENMWVQACGC 398
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                                                                                                                                              01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
BONE MORPHOGENETIC PROTEIN 4 PRECURSOR (BMP-4).
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                                                                                                                           405
                                                                                                                           PRT;
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                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                    Gallus gallus (Chicken)
                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9031;
                                                                                                                         BMP4_CHICK
Q90752;
                                                                                                                                                                                                                                                                                                                                   Gallus
                                                                                   87
                                                                                                    BMP4_CHICK
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69 NPEASASPCCVPQDLEPLTILYYVGRTPKV--EQLSNMVVKSCKC 111

ENCCVRPLYIDFRQDLGW-KWVHEPKGYYANFCSGPCPY-LRSA--DTTHSTVLGLYNTL 68

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                                                                                                                                                                                                                                                                                                        'Deer antler tissue contains two types of bone morphogenetic protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19; Gaps
                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoidea;
Cervidae; Cervinae; Cervus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL,
BOY SIMILARITY.
BONE MORPHOGENETIC PROTEIN 4.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCNAC...) (POTENTIAL).
N-LINKED (GLCNAC...) (POTENTIAL).
N-LINKED (GLCNAC...) (POTENTIAL).
N-LINKED (GLCNAC...) (POTENTIAL).
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Pfam; PF00019; TGF-beta; 1.
PROMITE; PS00250; TGF-BETA_1; 1.
Signal; Growth factor; Cytokine; Bone; Cartilage; Glycoprotein.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             359 TLVNSVNSSIPKA----CCVPTELSAISML-YLDEYDKVVLKNYQEMVVEGCGC 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            63 GLYNTLN---PEASASPCCVPQDLEPLTILYYVGRTPKV--EQLSNMVVKSCKC 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 408;
                                                                                                                                                                                                                                                                                                                                    Biochim. Biophys. Acta 1263:163-168(1995).
- FUNCTION: INDUCES CARTILAGE AND BONE FORMATION.
-!- SUBUNT: HOWDDIMER, DISULFIDE-LINKED (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
                                                                                                                                                                                                                                                          MEDLINE=95367593; PubMed=7640308;
Feng J.Q., Chen D., Esparza J., Harris M.A., Mundy G.R.,
Harris S.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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                                                       01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
BONE MORPHOGENETIC PROTEIN 4 PRECURSOR (BMP-4).
                               408 AA.
                                                                                                                                    dama (Fallow deer) (Cervus dama).
                                 PRT;
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                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR001111; -. InterPro; IPR001839; -.
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408
373
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407
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208
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408 AA;
                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                              NCBI_TaxID=30532;
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308
337
341
372
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                            BMP4_DAMDA
Q29607;
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               BMP4_DAMDA
                                                                                                                                       Dama
RESULT
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408 AA.

PRT;

STANDARD;

BMP4\_HUMAN

RESULT 89
BMP4\_HUMAN

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MESODERM INDUCTION, TOOTH DEVELOPMENT, LIMB FORMATION AND FRACTURE
                                                                                                                                                                                                                                                                                                                                                                                                     Deardorff M.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Olda S., Ilmura T., Marucka Y., Takeda K., Sasaki S.;
"Cloning and sequence of bone morphogenetic protein 4 (BMP-4) from a human placental CDNA library.";
DNA Seq. 5:273-275(1995).
-i- FUNCTION: INDUCES CARTILAGE AND BONE FORMATION. ALSO ACT IN
                                                                                                                                                                                                                                                                                                                                                            AEQUENCE FROM N.A.
MEDLINE=98368971; PubMed=9701626;
Shore E.M., Xu M., Shah P.B., Janoff H.B., Hahn G.V., Deardorff M.A.
Sovinsky L., Spinner N.B., Zasloff M.A., Wozney J.M., Kaplan F.S.;
"The human bone morphogenetic protein 4 (BMP-4) gene: molecular
structure and transcriptional regulation.";
Calcif. Tissue Int. 63:221-228(1998).
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R Pfam; PF00019; TGP-beta; 1.

R Pfam; PF00019; TGP-beta; 1.

R PROSTE; PS00250; TGF_BETA_1; 1.

SIGNAL 19

T CHAIN 293 408 BONE MORPHOGENETIC PROTEIN 4.

DISULFID 308 373 BY SIMILARITY.

T DISULFID 341 407 BY SIMILARITY.

T DISULFID 372 372 INTERCHAIN (BY SIMILARITY).

T CARBOHYD 143 143 N-LINKED (GLCNAC...) (POTENTIAL).

T CARBOHYD 208 208 N-LINKED (GLCNAC...) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -i- SUBGNIT: HOMODIMER, DISULFIDE-LINKED (BY SIMILARITY).
-i- SUBCELLULAR LOCATION: SECRETED INTO THE EXTRACELLULAR MATRIX.
-i- TISSUE SPECIFICITY: EXPRESSED IN THE LUNGS AND LOWER LEVELS SE
IN THE KIDNEY. PRESENT ALSO IN NORMAL AND NEOPLASTIC PROSTATE
TISSUES, AND PROSTATE CANCER CELL LINES.
-i- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                            Wozney J.M., Rosen V., Celeste A.J., Mitsock L.M., Whitters M.J., Kriz R.W., Hewick R.M., Wang E.A.; "Novel regulators of bone formation: molecular clones and activities.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BY SIMILAKITY.
INTERCHAIN (BY SIMILARITY).
N-LINKED (GLÜNAC. .) (POTENTIAL).
N-LINKED (GLÜNAC. .) (POTENTIAL).
P12644; Q9UM80;
01-CT-1989 (Rel. 12, Created)
01-CT-1989 (Rel. 12, Last sequence update)
01-CT-2000 (Rel. 40, Last annotation update)
BONE MORPHOGENETIC PROTEIN 4 PRECURSOR (BMP-4) (BMP-2B).
                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE-89072730; PubMed-3201241;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE-Placenta;
MEDLINE-96063017; PubMed-7579580;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; M22490; AAA51835.1; -.
EMBL; U43842; AAC72278.1; -.
EMBL; D30751; BAA06410.1; -.
PIR; C37278; C37278
HSSP; P18075; 1BMP.
                                                                                                                                                                                                                                                                                                                            Science 242:1528-1534(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 7-408 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR001111; -. InterPro; IPR001839; -.
                                                                                                                    (Human)
                                                                                                                  Homo sapiens
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MEDLINE-90228966; PubMed=1970330;
Dickinson M.E., Kobrin M.S., Silan C.M., Kingsley D.M., Justice M.J.,
Miller D.A., Ceci J.D., Lock L.F., Lee A., Buchberg A.M.,
Siracus L.D., Lyons K.M., Derynck R., Hogan B.L.M., Copeland N.G.,
                                                                                                                                                                                                                                                                                                                                          | :|| ||:|| ||:|| 302 RKKNKNCRRHSLYUDF-SDVGWNDWIVAPPGYQAFYCHGDCPFPLADHLNS--TNHAIVQ 358
                                                                                                                                                                                                                                                                                                    9 RNLEENCCVRPLYIDFRQDLGWK-WVHEPKGYYANFCSGPCPY----LRSADTTHSTVL 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Takaoka K., Yoshikawa H., Hasimoto J., Masuhara K., Miyamoto S.,
Suzuki S., Ono K., Matsui M., Oikawa S., Tsuruoka N.,
"Gene cloning and expression of a bone morphogenetic protein derived
                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=129/SV; TISSUE-Liver;
MEDLINE-96081880; PubMed=7499338;
MEDLINE-96081880; PubMed=7499338;
Feng J.Q., Chen D., Cooney A.L., Tsai M., Harris M.A., Tsai S.Y.,
Feng M., Mundy G.R., Harris S.E.;
"The mouse bone morphogenetic protein-4 gene. Analysis of promoter utilization in fetal rat calvarial osteoblasts and regulation by GOUP-FFI orphan receptor.";
J. Biol. Chem. 270:28364-28373(1995).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kurihara T., Kitamura K., Takaoka K., Nakazato H.;
"Murine bone morphogenetic protein-4 gene: existence of multiple
promoters and exons for the 5'-untranslated region.";
Blochem. Blophys. Res. Commun. 192:1049-1056(1993).
   N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
V -> A (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                            63 GLYNTLN---PEASASPCCVPQDLEPLTILYYVGRTPKV--EQLSNMVVKSCKC 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                               19;
                                                                                                                                                                                         Length 408;
                                                                                                                                                                                                                                                     35; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Dickinson M.E., van der Meer-De Jong R., Hogan B.L.M.;
Submitted (XXX-1992) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAY-1991 (Rel. 18, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
BONE MORPHOGENETIC PROTEIN 4 PRECURSOR (BMP-4) (BMP-2B)
BMP4 OR BMP-4 OR DVR-4.
                                                              -> A (IN REF. 2).
79B01179DBB98204 CRC64;
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                                                                                                                                                                                   26.9%; Score 170.5; DB 1; 37.7%; Pred. No. 5.5e-11; ive 17; Mismatches 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Clin. Orthop. Relat. Res. 294:344-352(1993).
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Mammalia; Eutheria; Rodentia;
                                                                                           46555 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     from a murine osteosarcoma.
                                                                                                                                                                                                                                               43; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genomics 6:505-520(1990)
   350
365
152
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365
152
408 AA;
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P21275;
                            CARBOHYD
CONFLICT
   CARBOHYD
                                                                                           SEQUENCE
                                                                                                                                                                                      Query Match
                                                                                                                                                                                                               Best Local
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BMP4_MOUSE
BMP4_MOUSE
AC P21275M
AC P21275M
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DT
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its was by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Chen D., Feng J.Q., Feng M., Harris M.A., Mundy G.R., Harris S.E.;
"Cloning and sequence of bone morphogenetic protein 4 cDNA from fetal
rat calvarial cell.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              302 RKKNKNCRRHSLYVDF-SDVGWNDWIVAPPGYQAFYCHGDCPFPLADHLNS--TNHAIVQ 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RNLEENCCVRPLYIDFRQDLGWK-WVHEPKGYYANFCSGPCPY----LRSADTTHSTVL 62
                                                                                                                                                                                                                                                                                                                                                                                                                                     BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
INTERCHAIN (BY SIMILARITY).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
-!- SUBUNIT: HOMODIMER, DISULFIDE-LINKED (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: SECRETED INTO THE EXTRACELLULAR MATRIX.
-!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  . .) (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                 BETA_1; 1.
Cytokine; Bone; Cartilage; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26.9%; Score 170.5; DB 1; Length 408; 37.7%; Pred. No. 5.5e-11; ive 17; Mismatches 35; Indels 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
01-TB-1996 (Rel. 33, Last annotation update)
BONE MORPHOGENETIC PROTEIN 4 PRECURSOR (BMP-4) (BMP-2B).
                                                                                                                                                                                                                                                                                                                                                                                                                            BONE MORPHOGENETIC PROTEIN
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C -> S (IN REF. 2).
35053D844624EF9D CRC64;
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35;
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                                                                                                                                                                           EMBL; X56848; CAA40179.1; -.
EMBL; S65032; AAB28021.1; -.
EMBL; L47480; AAC37698.1; ALT_INIT.
EMBL; D1481; BAA03555.1; -.
PIR; B34201; B34201.
PIR; S29523; S29523.
HSSP; P18075; 1BMP.
                                                                                                                                                                                                                                                                                                                             Pfam; PF00019; TGF-beta; 1.
Pfam; PF00688; TGFD_propeptide; 1.
PROSITE; PS00250; TGF_BETA_1; 1.
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373
405
407
372
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365
407
408 AA;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      DISULFID
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CONFLICT
SEQUENCE
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Q06826;
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BY SIMILARITY.
BY SIMILARITY.
INTERCHAIN (BY SIMILARITY).
N-LINKED (GLCNAC. .) (POTENTIAL).
(H) (GLCNAC. .) (FOTENTIAL).
(M) 61E92B4BBD5624F3 CRC64;
                 -!- FUNCTION: INDUCES CARTILAGE AND BONE FORMATION.
-!- SUBUNIT: HOMODIMER, DISULFIDE-LINKED (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: SECRETED INTO THE EXTRACELLULAR MATRIX.
-!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
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                                                                                                                                                                                                                                                                                                              PIR; S33173; S33173.
PIR; S38443; S38343.
PIR; S38843; S38343.
InterPro; IPR001111; -.
InterPro; IPR0011839; -.
InterPro; IPR0019; TGF-Deta; 1.
Pfan; PF00689; TGF-Dropeptide; 1.
Pfan; PF00689; TGF-Dropeptide; 1.
PROSITE; PS00250; TGF-BETA_1; 1.
Signal; Growth factor; Cytokine; Bone; Cartilage; Glycoprotein.
Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63 GLYNTLN---PEASASPCCVPQDLEPLTILYYVGRTPKV--EQLSNMVVKSCKC 111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 408;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN-NEW ZEALAND WHITE; TISSUE-ocular ciliary epithelium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- SUBUNIT: HOMODIMER, DISULFIDE-LINKED (BY SIMILARITY).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eut
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26.9%; Score 170.5; DB 1 37.7%; Pred. No. 5.5e-11; ive 17; Mismatches 35
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15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
BONE MORPHOGENETIC PROTEIN 4 PRECURSOR (BMP-4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    409 AA
Biochim. Biophys. Acta 1174:289-292(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  46540 MW;
                                                                                                                                                                                                                                                                                               EMBL; Z22607; CAA80329.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          43; Conservative
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408
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365
408 AA;
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Best Local Similarity
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046576;
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CHAIN
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BMP4_RABIT
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REPARENCE OF THE PROPERTY OF T
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Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Euechinoidea; Echinacea; Echinoida; Strongylocentrotidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   303 RKKNKNCRRHALYVDF-SDVGWNDWIVAPPGYQAFYCHGDCPF-PLADHFNSTNHAIVQT 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. MEDINE-9504489; Angerer R.C., Vale W.W.; Stenzel P., Angerer L.M., Smith B.J., Angerer R.C., Vale W.W.; "The univin gene encodes a member of the transforming growth factor-beta superfamily with restricted expression in the sea urchin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9 RNLEENCCVRPLYIDFRQDLGWK-WVHEPKGYYANFCSGPCPYLRSAD----TTHSTVLG 63
                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL.

BY SIMILARITY.

BY SIMILARITY.

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BY SIMILARITY.

BY SIMILARITY.

N-LINKED (GLCNAC. . ) (POTENTIAL).

N-LINKED (GLCNAC. . ) (POTENTIAL).
SUBCELLULAR LOCATION: SECRETED INTO THE EXTRACELLULAR MATRIX. SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
                                                                                                                                                                                                                                                                                                           Pfam; PF00019; TGF-beta; 1.
Pfam; PF00689; TGF-beta; 1.
PROSITE; PS00250; TGF_BETA_1; 1.
Signal; Growth factor; Cytokine; Bone; Cartilage; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64 LYNTLN---PEASASPCCVPQDLEPLTILYYVGRTPKV--EQLSNMVVKSCKC 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26.7%; Score 169.5; DB 1; Length 409; 38.1%; Pred. No. 7e-11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           35557561447AD625 CRC64;
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01-FEB-1996 (Rel. 33, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           383 AA
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                                                                                                                                                                                                                                                           EMBL; AF042497; AAB97467.1; -.
InterPro; IPR001111; -.
InterPro; IPR001839; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      43; Conservative
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                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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  DETECTED ONLY IN THESE CELL TYPES.
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BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
INTERCHAIN (BY SIMILARITY).
ININKED (GLCNAC. . .) (POTENTIAL).
N'LINKED (GLCNAC. . .) (POTENTIAL).
...TINKED (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           330 IIQTLVNSIDNRAVPKVCCAPIKESGISMLYFDNNENVVLRQYEDMVVEACGC 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    60 TVLGLYNTLNPEASASPCCVPQDLEPLTILYYVGRTPKV-EQLSNMVVKSCKC 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26.7%; Score 169; DB 1; Length 383; 33.6%; Pred. No. 7.4e-11; Live 20; Mismatches 41; Indels
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01-OCT-2000 (Rel. 40, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
BONE MORPHOGENETIC PROTEIN 10 PRECURSOR (BMP-10).
                                                                                                                                                                                                                                                                                                                   Pfam: PF00019; TGF-beta; 1.
Pfam: PF00689; TGF-propeptide; 1.
PRINTS; PR00438; GFCYSKNOT.
GROSTTE, P800250; TGF_BETA.1; 1.
Growth factor; Cytokine; Glycoprotein; Signal.
BAND. BY PLUTEUS STAGE, IT IS DETECTED ONLY SIMILARITY: BELONGS TO THE TGF-BETA FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               42636 MW;
                                                                                                                                                                                                                      EMBL; U10533; AAA57553.1; -.
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Matches 38; Conservative
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Interpro; IPR001839; -.
Interpro; IPR002400; -.
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PubMed=10072785;
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                                                                                                                                                                                                                                           P18075;
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TO 09R229;
DT 01-0CT-2000
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DE BMP10.
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Natran F.D., Drier E.A., Oppermann H.;
"Osteogenic protein-2. A new member of the transforming growth
factor-beta superfamily expressed early in embryogenesis.";
J. Biol. Chem. 267:25220-2527(1992).

I. Biol. Chem. 267:25220-2527(1992).

I. FUNCTION: INDUCES CAFFILAGE AND BONE FORMATION. MAY BE THE
CSTEDINDUCTIVE FACTOR RESPONSIBLE FOR THE PHENOMENON OF
EPITHELIAL OSTEOGENESIS. PLAYS A ROLE IN CALCIUM REGULATION
AND BONE HOMEOGYASIS. BY SIMILARITY).

C. ISUBUNIT: HOMODIMER, DISULEIDE-LINKED.
C. ISUBUNIT: HOMODIMER, DISULEIDE-LINKED.
C. ISUBURITH STAGE: EXTENSIVE EXPRESSION FOUND IN 8-DAY EMBRYOS,
EELL DRASTICALLY IN 10-DAY EMBRYOS AND VIRTUALLY ABSENT IN 17-
DAY EMBRYOS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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01-OCT-2000 (Rel. 40, Last annotation update)
BONE MORPHOGENETIC PROTEIN 8A PRECURSOR (BMP-8A) (OSTEOGENIC PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9 RNLEENCCVR-PLYIDFRQDLGW-KWVHEPKGYYANFCSGPCPYLRS---ADTTHSTVLG 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Interchain (By Similarity).
N-Linked (GLONAC. . .) (POTENTIAL).
N-Linked (GLONAC. . .) (POTENTIAL).
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POTENTIAL.
BONE MORPHOGENETIC PROTEIN 10.
BY SIMILARITY.
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BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                     InterPro; IPR002405; -.
PRINTS; PR00669; INHIBINA.
PROSTE; PS00250; IGE_BETA; I.
Signal; Growth factor; Cytokine; Glycoprotein.
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MEDLINE=93094231; PubMed=1460021;
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01-FEB-1994 (Rel. 28, Last seq
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                                                                                                                                                                                                                                                                              MGD; MGI:1338820; Bmp10.
                                                                                                                                                                                                                                                                                                        InterPro; IPR001839; -.
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tgfb3p.rsp

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InterPro; IPR001111; -. InterPro; IPR001839; -.
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MIM; 602284; -.
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P30885;
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                                                                                        the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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P34820; Q9NUF0;
01-FEB-1994 (Rel. 28, Last sequence update)
01-FEB-1994 (Rel. 28, Last sequence update)
01-CCT-2000 (Rel. 40, Last annotation update)
BONE MORPHOGENETIC PROTEIN 8 PRECURSOR (BMP-8) (OSTEOGENIC PROTEIN 2)
(OP-2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BY SIMLARILI.
INTERCHAIN (BY SIMILARITY).
N-LINKED (GLCNAC. .) (POTENTIAL).
"-**INVED (GLCNAC. .) (POTENTIAL).
                                                                                                                                                                                                                                                                                     MGD; MGI:104515; Bmp8a.
InterPro; IPR001111; -
InterPro; IPR001113; -
InterPro; IPR001403; -
Pfam; PF00019; TGF-beta; 1.
Pfam; PF00688; TGFb_propeptide; 1.
PRINTS; PR00438; GFCZSKNOT
PROSITE; PS00250; TGF_BETA_1; 1.
Signal; Growth, factor; Cytokine; Bone; Cartilage; Glycoprotein.
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MEDLINE=93094231; PubMed=1460021;
Oezkaynak E., Schnegelsberg P.N.J., Jin D.F., Clifford G.M.,
Warren F.D., Drier E.A., Oppermann H.;
"Osteogenic protein-2. A new member of the transforming growth
factor-beta superfamily expressed early in embryogenesis.";
J. Biol. Chem. 267:25220-25227(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ouery Match 26.5%; Score 168; DB 1; Length 399; Best Local Similarity 37.5%; Pred. No. 9.9e-11; Matches 39; Conservative 14; Mismatches 45; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL.
BONE MORPHOGENETIC PROTEIN 8A.
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Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
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SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
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BY SIMILARITY.
BY SIMILARITY.
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340
399 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15 CCVRPLYIDFRQDLGW-KWVHEPKGYYANFCSGPCPY-LRSA--DTTHSTVLGLYNTLNP 70
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BY SIMILARITY.
BY SIMILARITY.
INTERCHAIN (BY SIMILARITY).
INTERCHAIN (BY SIMILARITY).
N-LINKED (GLCNAC. . .) (POTENTIAL).
KPN -> MPD (IN REF. 2).
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Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
FUNCTION: INDUCES CARTILAGE AND BONE FORMATION. MAY BE THE OSTEDINDUCTIVE FACTOR RESPONSIBLE FOR THE PHENOMENON OF EPITHELIAL OSTEOGRNESIS. PLAYS A ROLE IN CALCIUM REGULATION AND BONE HOMEOSTASIS (BY SIMILARITY). SUBJUNT: HOMODIMER, DISGULFIDE-LINKED. SUBJULIAR LOCATION: SECRETED. SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPRU01400, 1976-beta; 1.
Pfam, PR00019; TGF-beta; 1.
Pfam, PR0068; TGF-bropetide; 1.
PRINTS; PR00438; GFCXSKNOT.
PROSITE; PS00250; TGF_BETA_1; 1.
Signal; Growth factor; Cytokine; Bone; Cartilage; Glycoprotein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      44; Indels
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AE2338D9F11B1DD9 CRC64;
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01-JUL-1993 (Rel. 26, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
BONE MORPHOGENETIC PROTEIN 4 PRECURSOR (BMP-4)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Pred. No. 1e-10; 13; Mismatches
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EMBL; AL033527; CAB75681.1; -
PIR; A45056; A45056.
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Matches 39; Conservative
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GDF3_MOUSE
ID GDF3_MOUSE
AC Q07104;
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"Genes for bone morphogenetic proteins are differentially transcribed in early amphibian embryos."; Blochem. Biophys. Res. Commun. 186:1487-1495(1992).
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                                                                                                                                                                                                                                                                                                                                                    POTENTIAL.

BY SIMILARITY.

INTERCHAIN (BY SIMILARITY).

N-LINKED (GLCNAC. . .) (POTENTIAL).

N-LINKED (GLCNAC. . . .) (POTENTIAL).
                                               Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00019; TGF-beta; 1.
Pfam; PF00688; TGF_propeptide; 1.
PROSITE; PS00250; TGF_BETA_1; 1.
Signal; Growth factor; Cytokine; Bone; Cartilage; Glycoprotein.
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01-FEB-1991 (Rel. 17, Last sequence update)
01-0CT-2000 (Rel. 40, Last annotation update)
EMBRYONIC GROWTH/DIFFERENTIATION FACTOR 1 PRECURSOR (GDF-1).
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HSSP; P18075; 1BMP.
InterPro; IPR001111; -.
InterPro; IPR001839; -.
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401 AA;
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P20863;
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DISULFID
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DISULFID
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SEQUENCE
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ID GDF1_M

AC P20863

AC 01-FEB

DT 01-FEB

DT 01-CCT

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                                                                                                                                                                                                                                                                                                                                                       conservation of a bicistronic structure.";
Proc. Natl. Acad. Sci. U.S.A. 88:4250-4254(1991).
-!- FUNCTION: MAY MEDIATE CELL DIFFERENTIATION EVENTS DURING EMBRYONIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         251 CRTRRLHVSFR-EVGWHRWVIAPRGFLANFCQGTCALPETLRGPGGPPALNHAVLRALMH 309
                                                                                                                                                                                                                                                                                                                               "Expression of growth/differentiation factor 1 in the nervous system:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBRYONIC GROWTH/DIFFERENTIATION FACTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15 CCVRPLYIDFRODLGW-KWVHEPKGYYANFCSGPCPY---LRSAD----TTHSTVLGLYN 66
                                                                                                                                                 Identification of a novel member (GDF-1) of the transforming growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                           -:- SUBUNIT: HOMODIMER, DISULFIDE-LINKED (BY SIMILARITY).
-:- SUBCELLULAR LOCATION: SECRETED.
-:- TISSUE SPECIFICITY: EXPRESSED ALMOST EXCLUSIVELY IN THE NERVOUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
INTERCHAN (BY SIMILARITY).
N-LINKED (GLCNAC. .) (POTENTIAL).
C -> S (IN REF. 2).
C -> S (IN REF. 2).
T-> MW; DE341F046226C1EE CRC64;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Score 164.5; DB 1; Length 357;
; Pred. No. 2.1e-10;
17; Mismatches 41; Indels 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      67 TLNPEASA-SPCCVPQDLEPLTILYYVGRTPKV-EQLSNMVVKSCKC 111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; ...
InterPro; ...
InterPro; ...
InterPro; IPR002400; -..
Pran; PF0019; TGF-beta; 1.
PRINTS; PR00438; GFCYSKNOT.
PROSITE; PS00250; TGF_BETA_1; 1.
PROSITE; PS00250; TGF_BETA_1; 1.
PROSITE; PS00410; Gytokine; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AA.
                                                                                                                                                                           factor-beta superfamily.";
Mol. Endocrinol. 4:1034-1040(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                             [2]
SEQUENCE FROM N.A.
MEDLINE=91239545; PubMed=2034669;
                                                                       SEQUENCE FROM N.A.
MEDLINE=91133438; PubMed=1704486;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; M62301; AA37676.1; --
PIR; A35683; A35683.
HSSP; P18075; IBMP.
MGD; MGI:95683; Gdf1.
InterPro; IPR001839; --
InterPro; IPR002400; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; M57639; AAA37674.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 25.9%;
Best Local Similarity 35.5%;
Matches 38; Conservative 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           38676
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237
357
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191
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280
284
321
191
145
357 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SYSTEM
                                                                                                                                                                                                                                                                                                       S. -J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7;
                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

JOHNS C.M., Simon-Chazottes D., Guenet J.-L., Hogan B.L.;

Jones C.M., Simon-Chazottes D., Guenet J.-L., Hogan B.L.;

Jeolation of Vgr-2, a novel member of the transforming growth
factor-beta-related gene family,";

Mol. Endocrinol. 6:1961-1968(1992).

I- SUBONIT: HOMODIMER OR HETERODIMER (POTENTIAL). BUT, IN CONTRAST
TO OTHER MEMBERS OF THIS FAMILY, CAN NOT BE DISULFIDE-LINKED.

I- SUBCELLULAR LOCATION: SECRETED (PROBABLE).

I- TISSUE SPECIFICITY: PRIMARILY IN ADULT BONE MARROW, SPLEEN, THYMUS
AND ADIPOSE TISSUE.

I- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                             McPherron A.C., Lee S.-J.;
GDF-3 and GDF-9: two new members of the transforming growth
factor-beta superfamily containing a novel pattern of cysteines.";
J. Biol. Chem. 268:3444-3449(1993).
                                                                                           Mus musculus (Mouse).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
01-OCT-1994 (Rel. 30, Created)
01-OCT-1994 (Rel. 30, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
GROWIH/DIFFERENTIATION FACTOR 3 PRECURSOR (GDF-3) (VG-1-RELATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GROWTH/DIFFERENTIATION FACTOR 3.
BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCNAC. .) (POTENTIAL)
N-LINKED (GLCNAC. .) (POTENTIAL)
G -> R (IN REF. 2).
LL -> FV (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 35.1%; Pred. No. 3.5e-10;
Matches 40; Conservative 21; Mismatches 34; Indels 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 366;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -> R (IN REF. 2).
EB2D7CBB4FA63E71 CRC64;
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35.1%; Pred. No. 3.5e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Interior, armovator, pfam, problem 1.
Pfam, Pro0019; TGF-beta; 1.
Pfam, Pro0688; TGFD_propeptide; 1.
PRUTS; PR00438; GFCYSKNOT.
PROSITE; PS00250; TGF_BETA_1; 1.
Signal, Growth factor; Cytokine; Glycoprotein.
Signal,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL.
                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE-93155193; PubMed-8429021;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MW.
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InterPro; IPR001111; -.
InterPro; IPR001839; -.
InterPro; IPR002400; -.
                                                                PROTEIN 2).
GDF3 OR GDF-3 OR VGR-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     252
366
331
331
363
365
308
168
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313
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HSSP; P18075; 1BMP.
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366 AA;
                                                                                                                                              NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
59 STVLGLYNTLNPEASASPCCVPQDLEPLTILYY-VGRTPKVEQLSNMVVKSCKC 111
                                                          313 AFMQALMHMADPKVPKA-VCVPTKLSPISMLYQDSDKNVILRHYEDMVVDECGC 365
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N-LINKED (GLCNAC. . .) (POTENTIAL)
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BY SIMILARITY.
BY SIMILARITY.
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                                                                                                                                                                                                                                                                       01-0CT-2000 (Rel. 40, Created)
1-0CT-2000 (Rel. 40, Last sequence update)
01-0CT-2000 (Rel. 40, Last annotation update)
GROWTH/DIFFERENTIATION FACTOR 3 PRECURSOR (GDF-3).
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; Pred. No. 6.5e-10;
22; Mismatches 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS; PRO0669; INHIBINA.
PROSITE; PS00250; TGF_BETA; 1.
Signal; Growth factor; Cytokine; Glycoprotein.
SIGNAL 1 24 POTENTIAL.
                                                                                                                                                                                                                   364 AA
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InterPro; IPR001839; -.
InterPro; IPR002405; -.
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34.3%;
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                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human)
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9606;
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CARBOHYD
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264 NFCHRH------QLFINF-QDLGWHKWVIAPRGFMANYCHGECPFSMTTYLNSSN-Y 312

NYCFRNLEENCCVRPLYIDFRQDLGW-KWVHEPKGYYANFCSGPCP----YLRSADTTH 58

2

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vus elap vo scophthalmu Ralmo sal

Q28240 c Q9dep5 Q9ddi8

Ogygvi xenopus lae Qgygvi xenopus lae Qg90723 gallus gall Qg1csy2 sus scrofa Qg0m97 equus cabal Qg604 branchiosto Qgu418 branchiosto Qgu418 branchiosto 3 gallus gall 0 gallus gall sus scrofa equus cabal

Opw65 carassius a Q91696 xenopus lae Q9m218 ovis aries Q9860 cynops pyrr P91720 drosophila 002424 caenorhabdi 076514 caenorhabdi

ou:

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Q28240
Q9DEP5
Q9DDI8
Q9YGV1
Q90723
Q98950
Q9ESY2
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Copyright (c) 1993 - 2000 Compugen Ltd
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Q9R2B8
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sp_vertebrate:*
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TISSUE-TAMOXIFEN-TREATED PROSTATIC ADENOCARCINOMA;
MEDLINE-88166349; PubMed-3162414;
Madisen L., Webb N.R., Rose T.M., Marquardt H., Ikeda T., Twardzik D.,
Seyedin S., Purchio A.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE-TAMOXIFEN TREATED PROSTATIC ADENOCARCINOMA; MEDLINE-89090808; Pubmed-2850146; MEDLINE-80908080B; Pubmed-2850146; Medlsen L., Rose T.M., Purchio A.F.; Structural and sequence analysis of TGF-beta 2 cDNA clones predicts two different precursor proteins produced by alternative mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 ALDTNYCFRNLEENCCVRPLYIDFRQDLGWKWVHEPKGYYANFCSGPCPYLRSADTTHST 60
                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 splicing.";
DNA 7:493-497(1988).
-!- SIMILARITY: TO TRANSFORMING GROWTH FACTOR (TGF) BETA FAMILY.
EMBL; M19154; AAA50404.1; -.
             Q921v8 n
Q9det1 c
O73818 x
Q91703 x
Q99yhw9 c
Q90388 c
P79707 c
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   013107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ouery Match

84.4%; Score 535; DB 4; Length 442;
Best Local Similarity 79.5%; Pred. No. 1.8e-52;
Matches 89; Conservative 14; Mismatches 9; Indels
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5D7A3C2ED51753D5 CRC64;
                                                                                                                                                                                            01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
TRANSFORMING GROWTH FACTOR-BETA-2 PRECURSOR.
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                                 073818
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                         Q9DET1
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Pfam; PF00688; TGFb_propeptide; 1.
PRINTS; PR00438; GFCYSKNOT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Probom; PD000357; ; 1. PROSITE; PS00250; TGF_BETA; 1. SMART; SM00204; TGFB; 1. Glycoprotein; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            50573 MW;
   PRELIMINARY;
 400
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InterPro; IPR001839; -.
InterPro; IPR002400; -.
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442 AA;
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DNA 7:1-8(1988).
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Plisov S.Y. Ivanov S.V., Plisova T.M., Lerman M., Perantoni A.O.;
"Rat transforming growth factor-beta2, complete coding sequence.";
"Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
"Le SIMILARITY: TO TRANSFORMING GROWTH FACTOR (TGF) BETA FAMILY.
"REMBL, AR135989, AAD244484.1; -...
"InterPorty: IPRO013111; -...
"Reference in PRO01111; -...
"Reference in PRO01111; -...
"Reference in PRO01119; -...
"Reference in
                                                                                                                                                                                                                                                                                                                                                            SERAIN-WISTAR; TISSUE-MUSCLE;
STRAIN-WISTAR; TISSUE-MUSCLE;
Koishi K., Dalzell K.G.B., McLennan I.S.;
Structure and expression of TGF-beta 2 messages in the rat muscle.";
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
-i- STMILARITY: TO TRANSFORMING GROWTH FACTOR (TGF) BETA FAMILY.
EMBL; AFI53013; AAD34160.1; -.
                                                                                                                                                                                                                                      Rattus norvegicus (Rat).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rattus norvegicus (Rat).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 ALDINYCFRNLEENCCVRPLYIDFRQDLGWKWVHEPKGYYANFCSGPCPYLRSADTTHST 60
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                                                                                                                                     Last sequence update)
Last annotation update)
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
TRANSFORMING GROWTH FACTOR BETA 2 PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Score 530; DB 11;
; Pred. No. 6.3e-52;
14; Mismatches 10;
                                                          414 AA
                                                                                                             Created)
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InterPro; IPR001839; -...
Pfam; PF00019; TGF-beta; 1.
Pfam; PF00688; TGFb_propeptide; 1.
PROSITE; PS00250; TGF_BETA; 1.
                                                                                                                                                                                   TGF-BETA 2 SHORT FORM PRECURSOR. TGF-BETA2.
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78.6%;
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Best Local Similarity 78.69
Matches 88; Conservative
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01-MAR-2001 (
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SEQUENCE 41
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Kroishi K., Dalzell K.G.B., WcLennan I.S.;
Kroishi K., Dalzell K.G.B., WcLennan I.S.;
Structure and expression of TGF-beta 2 messages in the rat muscle.";
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: TO TRANSFORMING GROWTH FACTOR (TGF) BETA FAMILY.
EMBL; AFI52012; AAD34159.1; -.
                                                                                 Gaps
                                                                                                                                                                                                                                                              Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                      1 ALDINYCFRNLEENCCVRPLYIDFRQDLGWKWVHEPKGYYANFCSGPCPYLRSADTTHST 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 ALDINYCFRNLEENCCVRPLYIDFRQDLGWKWVHEPKGYYANFCSGPCPYLRSADTTHST 60
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0
                                                                                                               61 VLGLYNTLNPEASASPCCVPQDLEPLTILYYVGRTPKVEQLSNMVVKSCKCS 112
                                                                                                                            61 VLGLYNTLNPEASASPCCVPQDLEPLTILYYVGRTPKVEQLSNMVVKSCKCS 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        83.6%; Score 530; DB 11; Length 414; 78.6%; Pred. No. 6.3e-52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 83.6%; Score 530; DB 11; Length 442; Best Local Similarity 78.6%; Pred. No. 6.7e-52; Matches 88; Conservative 14; Mismatches 10; Indels
                                                   Indels
 485DE768E720B2D1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            69C81A19CE06C253 CRC64;
                                                                                                                                                                                                                      01-NOV-1999 (TrEMBLrel. 12, Last sequence update) 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
                                                   10;
                                                  14; Mismatches
                                                                                                                                                                                                            (TrEMBLrel. 12, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00019; TGF-beta; 1.
Pfam; PF00688; TGFD_propeptide; 1.
PROSITE; PS00250; TGF_BETA; 1.
                                                                                                                                                                                                                                           TGF-BETA 2 LONG FORM PRECURSOR
 47711 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              50533 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-MAR-2001 (TrEMBLrel. 16,
                                                   Conservative
                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        SMART; SM00204; TGFB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR001111; -. InterPro; IPR001839; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              442 AA;
 414 AA;
                                       Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAR-2001 (TrEMBI
TGF-BETA2 PROTEIN.
TGF-BETA2.
                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                               NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Glycoprotein.
SEQUENCE 44
                                                                                                                                                                                                            01-NOV-1999
                                                  88;
SEQUENCE
                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09R2B8;
                                                                                                                                                                                       Q9WUQ8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9R2B8
                                                  Matches
                                                                                                                                                                   RESULT
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LOUGHER TO THE TOTAL TYPES. MANY CELLS SYNTHESIZE TGF-BETA 1 AND ESSENTIALLY ALL OF THEM HAVE SPECIFIC RECEPTORS FOR THIS REPTIDE TGF-BETA 1 NEGLIATES THE ACTIONS OF MANY OTHER PEPTIDE TGF-BETA AND DETERMINES A POSITIVE OR NEGATIVE DIRECTION OF THEIR EFFECTS.

-1 SUBUNIT: HOMODIMER, DISULFIDE-LINKED (BY SIMILARITY).

-1 SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.

REMBL; AROUDINGS TO THE TGF-BETA FAMILY.

REMBL; AROUSINGS TO THE TGF-BETA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
                                          ij
Konrad L., Albrecht M., Aumueller G.; "The rat TGF-beta2 gene: Sequence analysis and expression pattern
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 ALDINYCFRNLEENCCVRPLYIDFRQDLGWKWVHEPKGYYANFCSGPCPYLRSADTTHST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryotá; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                         the rat testis.";
Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
-1- SIMILARITY: TO TRANSFORMING GROWTH FACTOR (TGF) BETA FAMILY.
EMBL; AJ132718; CAB42003.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             83.3%; Score 528; DB 11; Length 414; 78.6%; Pred. No. 1.1e-51; ive 13; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            002730; 09750; 17 CTEMBLrel. 04, Created) 01-JUL-1997 (TEMBLrel. 04, Last sequence update) 01-OCT-2000 (TEMBLrel. 15, Last annotation update) TRANSFORMING GROWTH FACTOR BETA 1 (TGF-BETA 1) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 VLGLYNTLNPEASASPCCVPQDLEPLTILYYVGRTPKVEQLSNMVVKSCKCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. Taylor T.K., James E.R., McGonigle S., Yoho E.R.; Submitted (APR-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3AEF0912F5B550D5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              112 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00019; TGF-beta; 1.
PRINTS; PR00438; GFCYSKNOT.
S7800250; TGF_BETA; 1.
Growth factor; Mitogen; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                           Pfam; PF00019; TGF-beta; 1.
Pfam; PF00688; TGFD_propeptide; 1.
PROSITE; PS00250; TGF_BETA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oryctolagus cuniculus (Rabbit).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         414 AA; 47689 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 2-99 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                           HSSP; PO8112; 2TGI.
InterPro; IPR001111; -.
InterPro; IPR001839; -.
                                                                                                                                                                                                                                                                                                                                                                                                                         SMART; SM00204; TGFB;
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SOLUTION

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Euteleostei; Ostariophysi;
                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi; Cypriniformes; Cyprinidae; Cyprininae; Cyprinis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 ALDTNYCFRNLEENCCVRPLYIDFRQDLGWKWVHEPKGYYANFCSGPCPYLRSADTTHST
                                                                                                                                                                                                                                                                                                                     Gene 191:103-107(1997).
-!- FUNCTION: TGF-BETA 2 HAS SUPPRESSIVE EFFECTS ON INTERLEUKIN-2 DEPENDENT T-CELL GROWTH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BY SIMILARITY.

BY SIMILARITY.

INTERCHAIN (BY SIMILARITY).

N-LINKED (GLCNAC. ) (POTENTIAL).

N-LINKED (GLCNAC. ) (POTENTIAL).

N-LINKED (GLCNAC. ) (POTENTIAL).
                                                                                                                                                                                                                                                            Sumathy K., Desai K.V., Kondaiah P.;
"Isolation of transforming growth factor-beta2 cDNA from a fish, Cyprinus carpio by RT-PCR.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TRANSFORMING GROWTH FACTOR BETA 2.
                  01-FEB-1997 (TrEWBLrel. 02, Created)
01-FEB-1997 (TrEWBLrel. 02, Last sequence update)
01-MAR-2001 (TrEWBLrel. 16, Last annotation update)
TRANSFORMING GROWTH FACTOR BETA 2 (TGF-BETA 2) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
TRANSFORMING GROWTH FACTOR BETA 1 (TGF-BETA 1) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                           -!- SUBUNIT: HOMODIMER, DISULFIDE-LINKED (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94D930FA970A3FD3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 VLGLYNTLNPEASASPCCVPQDLEPLTILYYVGRTPKVEQLSNM 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    318 ILGLYNTINPEASASPCCVSQDLEPLTILYYIGKTPKIEQLSNM 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      77.1%; Score 489; DB 13;
77.9%; Pred. No. 2.4e-47;
Live 14; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            130 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mesocricetus auratus (Golden hamster).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SMART; SM00204; TGFB; 1.
Growth factor; Mitogen; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last seq
01-MAR-2001 (TrEMBLrel. 16, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                   MEDLINE-97354301; PubMed-9210595;
                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR01111; --
InterPro; IPR001111; --
InterPro; IPR001839; --
Pfam; PF00019; TGF-beta; 1.
Pfam; PF00688; TGF-propeptide;
PROSITE; PS00250; TGF-BETA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MW.
                                                                                                             Cyprinus carpio (Common carp)
                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; U66874; AAB62983.1; -. HSSP; P08112; 2TGI.
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361
251
235
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336
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41931 k
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 361 ;
361 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                  NCBI_TaxID=7962;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          008714; 070331;
                                                                                                                                                                                                                                     TISSUE-HEART
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DISULFID
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                                                                                                                                                                                                                                                            1 ALDINYCFRNLEENCCVRPLYIDFRQDLGWKWVHEPKGYYANFCSGPCPYLRSADTTHST 60
                                                                                                                                                                                                                                                                                1 ALDINYCFSSTERNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 ALDINYCFRNLEENCCVRPLYIDFRQDLGWKWVHEPKGYYANFCSGPCPYLRSADTTHST 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (AUG-1999) to the EMBL/Genbank/DDBJ databases.
-!- SIMILARITY: TO TRANSFORMING GROWTH FACTOR (TGF) BETA FAMILY.
EMBL: AF175709; AAD49431.1; -.
INTERPO: 11737; 1KLA.
INTERPO: IPR001111; -.
InterPro: IPR001839; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nixon A.J., Brower-Toland B.T., Sandell L.J.; "Molecular cloning of equine transforming growth factor beta 1 ra divergent nucleotide structure that encodes a novel bioactive peptide among mammalian species.";
TRANSFORMING GROWTH FACTOR BETA 1.
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INTERCHAIN (BY SIMILARITY).

D -> FS (IN REF. 2).

PLEDIYYY. -> ATARRYTI. (IN REF. 2).

W; 53C5B7D46355A6F3 CRC64;
                                                                                                                                                                                                                                                                                                                                61 VLGLYNTLNPEASASPCCVPQDLEPLTILYYVGRTPKVEQLSNMVVKSCKCS 112
                                                                                                                                                                                                                                                                                                                                                     61 VLGLYNTLNPEASASPCCVPQDLEPLTILYYVGRTPKVEQLSNMVVKSCKCS 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            139 VLALYNQHNPGASAAPCCVPQVLEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 390
                                                                                                                                                                                         78.9%; Score 500; DB 6; Length 112; 76.8%; Pred. No. 4e-49; ive 11; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                77.4%; Score 491; DB 6; Length 390; 75.9%; Pred. No. 1.5e-47; Live 11; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           390 AA; 43860 MW; 220FE40DFCCA6016 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eŭkaryota, Metazoa, Chordata, Craniata, Vertebrata,
Mammalia, Eutheria, Perissodactyla, Equidae, Equus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                             390 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
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01-MAR-2001 (TrEMBLRE1 16, Last s
TRANSFORMING GROWTH FACTOR BETA 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00019; TGF-beta; 1.
Pfam; PF00688; TGF-propeptide; 1.
PROSITE; PS00250; TGF-BETA; 1.
                                                                                                                                      12795 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 75.9% nes 85; Conservative
                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SMART; SM00204; TGFB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Equus caballus (Horse)
                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 86; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9796;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Glycoprotein
SEQUENCE 3
            DISULFID
DISULFID
                                             DISULFID
DISULFID
DISULFID
CONFLICT
                                                                                                                                    SEQUENCE
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TGFB1

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Indels

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NCBI\_TaxID=10036;

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RESULT Q98854

Matches

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Mesocricetus

Length 361;

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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TGF-B3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 12
Q9MYZ1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9MY21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9N1S3
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                                                            Wong D.T., Donoff R.B., Yang J., Song B.Z., Matossian K., Nagura N., Elovic A., McBride J., Gallagher G., Todd R., "Sequential expression of transforming growth factors alpha and beta by eosinophils during cutaneous wound healing in the hamster."; Am. J. Pathol. 143:130-142(1993).
                                                                                                                                                                                                                 STRAIN-SYRIAN; TISSUE-SPIENN;
MEDLINE=98234044; PubMed=9573100;
MeDby P.C., Tryon V.V., Chandrasekar B., Freeman G.L.;
MeDby P.C., Tryon V.V., Chandrasekar B., Freeman G.L.;
Melby P.C., Tryon V.V., Chandrasekar B., Freeman G.L.;
Melby P.C., Tryon V.V., Chandrasekar B., Freeman G.L.;
Infect. Immun. 66:2135-2142(1998)
PROLIFERATION, DIFFERENTIATION, AND OTHER FUNCTIONS IN MANY CELL TYPES. MANY CELLS SYNTHESIZE TGF-BETA I AND ESSENTIALLY ALL OF THEM HAVE SPECIFIC RECEPTORS FOR THIS PEPTIDE. TGF-BETA I REGULATES THE ACTIONS OF MANY OTHER PEPTIDE GROWTH FACTORS AND DETERMINES A POSITIVE OR NIGATIVE DIRECTION OF THEIR EFFECTS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19 ALDINYCESSTEKNCCVRQLXIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDIQYSK 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TRANSFORMING GROWTH FACTOR BETA 1.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
G.S. SIMILARITY.
G.S. S. (IN REF. 2).
W, 8841DD6CF39CCA77 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -1- SUBUNIT: HOMODIMER, DISULFIDE-LINKED.
-1- SIMILARITY: TO OTHER GROWTH FACTORS OF THE TGF-BETA FAMILY.
EMBL: X60296; CAA42838.1; -.
EMBL: AF046214; AAC40099.1; -.
HSSP: P01137; 1KLA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 VLGLYNTLNPEASASPCCVPQDLEPLTILYYVGRTPKVEQLSNMVVKSCKCS 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 130;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
TRANSFORMING GROWTH FACTOR-BETA 2 (FRAGMENT).
Mesocricetus auratus (Golden hamster).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              77.0%; Score 488; DB 11;
75.9%; Pred. No. 1.1e-47;
iive 10; Mismatches 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 399 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR01839; -.
Pfam; PF00019; TGF-beta; 1.
ProDom; PB00357; -; 1.
PROSITE: PS00250; TGF_BETA; 1.
SWART; SM00204; TGFB; 1.
Growth factor; Mitogen; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
SEQUENCE FROM N.A.
STRAIN-LVG (SYR);
MEDLINE-93304479; PubMed-8317544;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Œ.
                                                                                                                                                                                                 SEQUENCE OF 26-115 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        93
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18
130
34
96
129
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19
25
33
33
66
59
130 AA;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10036;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mesocricetus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         85;
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DISULFID
DISULFID
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PROPEP
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                                                                                                                                                                                                                                                                                                       1 ALDINYCFRNLEENCCVRPLYIDFRQDLGWKWVHEPKGYYANFCSGPCPYLRSADTTHST 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Gaps
Ramesh G., Kondaiah P., Seshagiri P.B.; "Differential expression and selective localization of transforming growth factor-beta isoforms in the hamster uterus during estrous cycle.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Capreolus capreolus (Roe deer).

Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoidea;
Cervidae; Odocolleinae; Capreolus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=TESTIS;
wagener A., Blottner S., Fickel J.;
"Detection of growth factors in the testes of roe deer (Capreolus capreolus).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
-!-SIMILARITY: TO TRANSFORMING GROWTH FACTOR (TGF) BETA FAMILY.
EMBL; AF152592; AAF73231.1; -.
                                                                                                                                                                                                                             Length 399;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 81;
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                                                                                                                                                                                                                                                                  Indels
                       CLUMILITED (AUG-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; AX007214; AAG0247.1; ...

NON_TER 399 399

SEQUENCE 399 **
                                                                                                                                                                                                                                                                                                                                                                             8515C856478E4BCC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
TRANSFORMING GROWTH FACTOR BETA 3 (FRAGMENT).
                                                                                                                                                                                                                                                                  11;
                                                                                                                                                                                                                           76.0%; Score 482; DB 11; 76.9%; Pred. No. 1.6e-46; ive 13; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 463; DB 6;
Pred. No. 4.4e-45;
1; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           91 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 81 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-OCT-2000 (TrEMBLrel. 15, Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00019; TGF-beta; 1.
PROSITE; PS00250; TGF_BETA; 1.
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9250 MW;
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98.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 76.0%
Best Local Similarity 76.9%
Matches 80; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 73.0
Best Local Similarity 98.8
Matches 80; Conservative
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CHAIN
    Growth
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Rao U.R., Klei T.R.;

"CDNA clouing of gerbil transforming growth factor-beta by PCR.";

"CDNA clouing of gerbil transforming growth factor-beta by PCR.";

"CDNA clouing of gerbil transforming growth factor-beta by PCR.";

"CDNA clouing of gerbil transforming growth factor-beta by PCR.";

"CDNA Clouing of gerbil transforming growth factor-beta by PCR.";

"CONDETERATION, DIFFEREWINATION, AND OTHER FUNCTIONS IN MANY CELL TYPES. MANY CELLS SYNTHESIZE TGF-BETA 1 AND ESSENTIALLY ALL OF THEM HAVE SPECIFIC RECEPTORS FOR THIS PEPTIDE GROWTH FACTORS AND DETERMINES A POSITIVE OR NEGATIVE DIRECTION OF THEIR EFFECTS.

"I- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.

"EMBL, AF161218, AAD45726.1; -..

R HSSP; PO1137; 1KLA.

"R HSSP; PO1137; 1KLA.

"R PFAM: PG00199; TGF-BETA; 1.

"R PROSITE: PG00250; TGF-BETA; 1.
                                                                                                                                                                                                                                                                                                                                            0; Gaps
                                                                                                                                                                                                                                                                                                                                                                9 RNLEENCCVRPLYIDFRQDLGWKWVHEPKGYYANFCSGPCPYLRSADTTHSTVLGLYNTL 68
                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Caprinae; Capra.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Meriones unguiculatus (Mongolian jird).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Gerbillinae;
                                                                                                                                            Wang B., Zhang Y.;
"Goat ovarian TGF beta 2 cDNA sequence.";
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
-! - SIMILARIY: TO TRANSFORMING GROWTH FACTOR (TGF) BETA FAMILY.
EMBL; AF276986; AAF87742.1;
                                                                                                                                                                                                                                                                                                                     Length 91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9R184;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
TRANSFORMING GROWTH FACTOR BETA 1 (TGF-BETA 1) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                  68.6%; Score 435; DB 6; Length 91 79.1%; Pred. No. 7.2e-42; ive 11; Mismatches 8; Indels
                                                                                                                                                                                                                                                                  9]
10412 MW; 59694FF30EAA1FAA CRC64;
01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
TGF BETA 2 (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                 69 NPEASASPCCVPQDLEPLTILYYVGRTPKVE 99
                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                Pfam; PF00019; TGF-beta; 1.
PROSITE; PS00250; TGF_BETA; 1.
                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 79.1:
Matches 72; Conservative
                                                                                                                   SEQUENCE FROM N.A.
TISSUE-OVARIAN FOLLICLE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                       InterPro; IPR001839; -.
                                                Capra hircus (Goat).
                                                                                                                                                                                                                                                                                91 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FISSUE=LYMPH NODE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=10047;
                                                                                              NCBI_TaxID=9925;
                                                                                                                                                                                                                                                        91
                                                                                                                                                                                                                                           Glycoprotein.
NON_TER 9
SEQUENCE 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Meriones
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Gaps
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                                                                                                                                                                                                                                                                                                                                   12 EENCCVRPLYIDFRQDLGWKWVHEPKGYYANFCSGPCPYLRSADTTHSTVLGLYNTLNPE 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoidea;
Cervidae; Cervinae; Cervus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Francis S.M., Suttie J.M.;
"Detection of growth factors and proto-oncogene mRNA in the growing tip of red deer (Cervus elaphus) antler using reverse-transcriptase polymerase chain reaction (RT-PCR).";
J. Exp. Zool. 281:36-42(1998).
-!-FUNCTION: TGF-BETA 2 HAS SUPPRESSIVE EFFECTS ON INTERLEUKIN-2 DEPENDENT T-CELL GROWTH.
-!- SUBUNIT: HOMODIMER, DISGUEDE-LINKED (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
                                                                                                                                                                                                                                                                 ö
                                             TRANSFORMING GROWTH FACTOR BETA 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TRANSFORMING GROWTH FACTOR BETA
                                                                                                                                                                                                                      Length 101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
TRANSFORMING GROWTH FACTOR BETA 2 (TGF-BETA 2) (FRAGMENT)
TGFB2 OR TGF BETA-2.
Cervus elaphus (Red deer).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       65.0%; Score 412; DB 6; Length 86; 79.1%; Pred. No. 2.7e-39; ive 11; Mismatches 7; Indels
                                                                                                                                                                                                                                                               18; Indels
                                                               BY SIMILARITY.
BY SIMILARITY.
INTERCHAIN (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INTERCHAIN (BY SIMILARITY).
                                                                                                                                                     11724 MW; ABF1CFDA264AEFED CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A5AE8B62D78E80E5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                67 TLNPEASASPCCVPQDLEPLTILYYVGRTPKVEQLSNMVVK 107
                                                                                                                                                                                                                                                                                                                                                                                                                    Score 422; DB 11;
Pred. No. 2.4e-40;
9; Mismatches 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          86 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SMART; SM00204; TGFB; 1.
Growth factor; Mitogen; Glycoprotein.
Mitogen; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-98233260; PubMed-9571767;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00019; TGF-beta; 1.
PROSITE; PS00250; TGF_BETA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; U62111; AAB05257.1; -. HSSP; P08112; 2TGI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         67
66
86
9848 MW;
                                                                                                                                                                                                                    Query Match 66.6%;
Best Local Similarity 73.3%;
Matches 74; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR001839; -.
                                                             10
72
71
101
                                                                                                        71
101
101 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
Matches 68; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DISULFID
NON_TER
SEQUENCE
                                                             DISULFID
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SEQUENCE
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ö Treaction (RT-qcPCR) assay to measure Torbeta mRNA of teleost fish.";

Fish Shellfish Immunol. 10:61-85(2000).

Fish Shellfish Immunol. 10:61-85(2000).

Fish Shellfish Immunol. 10:61-85(2000).

FISH SHELL RELY TO BE AN IMPORTANT CYTOKINE REGULATING IMMUNE RESPONSE. MAY ALSO HAVE A ROLE IN OTHER PHYSIOLOGICAL SYSTEMS.

FISHER SPECIATY. HIGHER LEVELS FOUND IN MONDUCLEAR CELLS FROM PERIPHERAL BLOOD THAN IN SPECIA FOUND IN MONDUCLEAR CELLS FROM PERIPHERAL BLOOD THAN IN SPECIA PANILY.

FIRST POLITY: BELONGS TO THE TGF-BETA FAMILY.

RMBL: ARIAO563; AAA46997.1; -..

InterPro; IPRO01111; -..

RICHEPRO; IPRO01111; -..

REPEAR FOUND: PRO010939; TGF-beta; 1.

REPEAR FOUND: TGF-beta; 1.

REPEAR FOUND: TGF-BETA; 1. Tompkins W.A.F.; "Cloning and sequencing hybrid striped bass (Morone saxatilis x M. chrysops) transforming growth factor-beta (TGF-beta), and development of a reverse transcription quantitative competitive polymerase chain 283 ESCCVRKLYIDFRKDLGWKWIHEPTGYFANYCIGPCTYIWNTENKYSQVLALYKHNPGA 342 Gaps ENCCVRPLYIDFRQDLGWKWVHEPKGYYANFCSGPCPYLRSADTTHSTVLGLYNTLNPEA 72 Morone chrysops x Morone saxatilis (white bass x striped bass). Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Percoidei; BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
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BY SIMILARITY.
INTERCHAIN (BY SIMILARITY).
N-LINKED (GLCNAC...) (POTENTIAL).
N-LINKED (GLCNAC...) (POTENTIAL).
N-LINKED (GLCNAC...) (POTENTIAL).
N-LINKED (GLCNAC...) (POTENTIAL).
N-LINKED (GLCNAC...) (POTENTIAL). ; 0 (POTENTIAL). TRANSFORMING GROWTH FACTOR BETA. Length 382; DB 13; Length 382; Harms C.A., Kennedy-Stoskopf S., Horne W.A., Fuller F.J., Indels 3124D8C34EA74D72 CRC64; 01-MAY-2000 (TrEMBLrel. 13, Created) 01-MAY-2000 (TrEMBLrel. 13, Last sequence update) 01-MAR-2001 (TrEMBLrel. 16, Last annotation update) TRANSFORMING GROWTH FACTOR BETA PRECURSOR. SITE 63.7%; Score 404; DB 13; I 69.0%; Pred. No. 1e-37; ive 12; Mismatches 19; 73 SASPCCVPQDLEPLTILYYVGRTPKVEQLSNMVVKSCKCS 112 Glycoprotein; Signal. CELL ATTACHMENT 382 AA. SEQUENCE FROM N.A., AND TISSUE SPECIFICITY. Score 396; POTENTIAL. PRT; MEDLINE=20394636; PubMed=10938723; X. 62.5%; 43846 Conservative PRELIMINARY; SMART; SM00204; TGFB; 1. Growth factor; Mitogen; 382 286 348 379 381 347 73 108 113 124 259 113 124 259 235 382 AA; Similarity Moronidae; Morone. NCBI\_TaxID=45352; TISSUE-KIDNEY :69 TGF-BETA. DISULFID DISULFID DISULFID DISULFID DISULFID CARBOHYD CARBOHYD CARBOHYD CARBOHYD CARBOHYD SEQUENCE Query Match PRT;

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PRELIMINARY;
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Best Local Similarity
Matches 58; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  76 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE-MACROPHAGE
                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10118;
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                                                                                             01-MAY-2000
                                                                                                                           01-MAY-2000
                                                                                                                                                   01-MAR-2001
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                                                                                                                                                                                                                  Rattus sp.
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                                       HD DATE OF THE PRINCE OF THE P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Cyprininae; Cyprinus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TRANSFORMING GROWTH FACTOR BETA.
BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63 GLYNTLNPEASASPCCVPQDLEPLTILYYVGRTPKVEQLSNMVVKSCKC 111
Pred, No. 8.3e-37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
TRANSFORMING GROWTH FACTOR BETA PRECURSOR.
                                                                                                                                                                                                                                       SASPCCVPQDLEPLTILYYVGRTPKVEQLSNMVVKSCKCS 112
                                                                                                                                                                                                                                                               Probom; PD000357; -; 1. PROSITE; PS00250; TGF_BETA; 1. SMART; SM00204; TGFB; 1. Growth factor; Mitogen; Glycoprotein; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                             376 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
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Pfam; PF00688; TGFb_propeptide; 1.
                                                         10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cyprinus carpio (Common carp).
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                              69.08;
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                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
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280
373
375
                        Best Local Similarity
Matches 69; Conserv
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376 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 65; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=7962;
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76
125
167
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09PTQ2
AC 09PTQ2
AC 09PTQ2
DT 01-MAY
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Matches
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RESULT Q9QW26

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               36 PKGYYANFCSGPCPYLRSADTTHSTVLGLYNTLNPEASASPCCVPQDLEPLTILYYVGRT 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Actinopterygii; Neopterygii; Teleostei; Buteleostei; Ostariophysi; Cypriniformes; Cyprinidae; Cyprininae; Carassius.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                          TRANSFORMING GROWTH FACTOR BETA ISOFORM 2 (FRAGMENT).
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                                                                                                                                                                                                                                                                                                                                                       Smith T.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   F4ACF0803CF270EC CRC64;
                          Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
TRANSFORMING GROWTH FACTOR BETA (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 339; DB 11;
Pred. No. 4.3e-31;
9; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BY SIMILARITY.
INTERCHAIN (BY
                                                                                                                                                                                                                                                                                                                                                    R.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    factor; Mitogen; Glycoprotein.
                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE-9323033; Pubmed-8486763;
Nishida M., Springhorn J.P., Kelly R.
J. Clin. Invest. 91:1934-1941(1993).
HSSP; PO8112; 2TGI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Created)
Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR001839; ...
Pfam; PF00019; TGF-beta; 1.
PROSITE; PS00250; TGF_BETA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             >87 TI
87 B
55 II
87
10007 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Carassius auratus (Goldfish).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          53.5%;
ilarity 76.3%;
Conservative
                                                     (TrEMBLrel. 16,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8346 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (TrEMBLrel. 05,
                          (TrEMBLrel. 13,
                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR001839; -. Pfam; PF00019; TGF-beta; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          96 PKVEQLSNMVVKSCKC 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SMART; SM00204; TGFB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SMART; SM00204; TGFB; 1.
Growth factor; Mitogen:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ProDom; PD000357; -; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
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Low C.A., Taylor I., Birkbeck H., Tatner M., Secombes C.J.; "Partial mRNA sequence for Transforming Growth Factor beta in turbot (Scophthalmus maximus L.).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23 DFRQDLGWKWVHEPKGYYANFCSGPCPYLRSADTTHSTVLGLYNTLNPEASASPCCVPQD 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Scophthalmus maximus.
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Actinopteryqii, Neopterygii, Teleostei, Euteleostei, Neoteleostei, Actinopteryqii, Neoteleostei, Percomorpha, Acanthopterygii, Percomorpha; Pleuronectidei, Scophthalmidae, Scophthalmus.
NCBI_TaxID=52904;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MYOSTATIN PRECURSOR.
Salmo salar (Atlantic salmon).
Eukaryota; Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "The myostatin gene is expressed in multiple organs of Atlantic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases EMBL; AJ276709; CAC10178.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Andersen O.;
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (DEC-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.
                                                                                                                                                          01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
TRANSFORMING GROWTH FACTOR-BETA 1 PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62 AA; 7138 MW; 936D0EC6C9D1E294 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           35.2%; Score 223; DB 13;
58.1%; Pred. No. 4.6e-18;
iive 10; Mismatches 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL.
                                                                                                                                     Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAR-2001 (TrEMBLrel. 16, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   41878 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AJ297267; CAC19541.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21
373
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265
373 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. TISSUE=HEAD KIDNEY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 36; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=8030;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ostbye T.K.;
                                                                                                                                  01-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        83 LE 84
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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E_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           salmon.
                                                                                  Q9DEP5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09DDI8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Siqnal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT
                                RESULT
                                                          Q9DEP5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                09DDI8
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                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBDITITE (MAY-1999) to the EMBL/GenBank/DDBJ databases.

-!-FUNCTION: TGF-BETA 1 IS A MULTIFUNCTIONAL PEPTIDE THAT CONTROLS
PROLIFERATION, DIFFERENTIATION, AND OTHER FUNCTIONS IN MANY CELL
TYPES. MANY CELLS SYNTHESIZE TGF-BETA 1 AND ESSENTIALLY ALL OF
THEM HAVE SPECIFIC RECEPTORS FOR THIS PEPTIDE. TGF-BETA 1
REGULATES THE ACTIONS OF MANY OTHER REPPTIDE GROWTH FACTORS AND
DETERMINES A POSITIVE ON NEGATIVE DIRECTION OF THEIR EFFECTS.
-!- SUBDIT: HOMODIMER, DISULFIDE-LINKED (BY SIMILARITY).
                                                                                                                                  Gaps
                                                                                                     23 DFRODLGWKWVHEPKGYYANFCSGPCPYLRSADTTHSTVLGLYNTLNPEASASPCCVPQD 82
                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
11-OCT-2000 (TREMBLREL. 15, Last annotation update)
12-CT-2000 (TREMBLREL. 15, Last annotation update)
13-CT-2000 (TRANSFORMING)
14-CT-2000 (TGF-BETA 1) (TRANSFORMING GROWTH
15-CT-2000 (TGF-BETA-1) OR TGF-BI.
15-CT-2000 (TGF-BI.)
15-C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Francis S.M., Suttie J.M.; "Detection of growth factors and proto-oncogene mRNA in the growing tip of red deer (Cervus elaphus) antler using reverse-transcriptase polymerase chain reaction (RT-PCR)."; J. Exp. 2001. 281:36-42(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoidea;
Cervidae; Cervinae; Cervus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wagener A., Blottner S., Fickel J.; "Detection of growth factors in the testes of roe deer (Capreolus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TRANSFORMING GROWTH FACTOR BETA 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
0
     Length 87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 6; Length 50;
                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EENCCVRPLYIDFRQDLGWKWVHEPKGYYANFCSGPCPYLRSADTTH 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ODDDAE48C640759F CRC64;
51.9%; Score 329; DB 13;
64.4%; Pred. No. 6.7e-30;
ive 13; Mismatches 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 230; DB 6;
Pred. No. 6e-19;
6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                        50 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00019; TGF-beta; 1.
PROSITE; PS00250; TGF_BETA; 1.
Growth factor; Mitogen; Glycoprotein.
                                                                                                                                                                                                          83 LEPLTILYYVGRTPKVEQLSNMVVKSC 109
                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=98233260; PubMed=9571767;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AF152591; AAF73230.1; -. HSSP; P01137; 1KLA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      50
6012 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 36.3%;
Best Local Similarity 76.6%;
Matches 36; Conservative
                                                  56; Conservative
                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              >50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR001839; -
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. TISSUE=ANTLER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              50 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9860;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=TESTIS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        capreolus).
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SEQUENCE
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                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12
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Gaps

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16;

373 AA.

Length 62;

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Length 373;
MYOSTATIN.
C355D71D83E66C4D CRC64;
                                           DB 13;
                                           Score 213.5;
                                            33.78;
                                             Query Match
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Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15 CCVRPLYIDFRQDLGWK-WVHEPKGYYANFCSGPCPYLRSAD---TTHSTVLGLYNTLNP 70
                                                                                                                                                        Shah S.B., Hume C.R., Dodd J.;
Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
-i- SHILLARITY: TO TRANSFORMING GROWTH FACTOR (TGF) BETA FAMILY.
EMBL; U55871; AAB01194.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 373;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         36; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9FADC8212145602E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         373 AA; 41405 MW; E2ACFCCCD3A4C8B5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          71 EASASPCCVPQDLEPLTILYYVGRTPKV-EQLSNMVVKSCKC 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | : ||||| | | : ||||| | | 331 EGTPQPCCVPVRLSPISILYYDNSDNVVLRHYEDMVVDECGC 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 207; DB 13;
Pred. No. 1.9e-15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18; Mismatches
                                                                                                                                                                                                                                                            InterPro; IPR001111; -.
InterPro; IPR001111; -.
InterPro; IPR001839; -.
InterPro; IPR002400; -.
Pfam; PF00019; TGF-beta; 1.
Pfam; PF00688; TGFb, propeptide; 1.
PRODOM; PD00038; GFCYSKNOT.
PROSITE; PS00250; TGE_BETA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR00111; ...
InterPro; IPR00111; ...
InterPro; IPR001839; ...
InterPro; IPR002809; ...
InterPro; IPR002809; ...
InterPro; IPR002809; ...
Pfam; Pr00688; TGFb_propeptide; IPR058my; PR006488; TGFb_propeptide; IPR05my; PR000357; ...; IPR05m; PR0017E; PR002509; TGF_BETA; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     373 AA; 41503 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        32.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-FEB-1997 (TrEMBLrel. 02, 01-FEB-1997 (TrEMBLrel. 02, 01-MAR-2001 (TrEMBLrel. 16,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       42; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          SMART; SM00204; TGFB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gallus gallus (Chicken).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SMART; SM00204; TGFB;
                                                                                                                SEQUENCE FROM N.A. STRAIN=WHITE LEGHORN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
                                                                   NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9031;
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SEQUENCE 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Glycoprotein
SEQUENCE 37
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=99169090; PubMed=10068640;
Sun B.I., Bush S.M., Collins-Racie L.A., Lavallie E.R.,
DiBlasio-Smith E.A., Wolfman N.M., McCoy J.M., Sive H.L.;
"derriere: a TGF-beta family member required for posterior development
in Xenopus.";
                                                                                                           253 CKKRRLXIDFK-DVGWQNWVIAPRGYMANYCHGECPYPLTEMLRG--TNHAVLQTLVHSV 309
                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                 12 EENCCVRPLYIDFRQDLGWKWVHEPKGYYANFCSGPCPYLRSADTTHSTVLGLYNTLNPE 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15 CCVRPLYIDFRQDLGWK-WVHEPKGYYANFCSGPCPY----LRSADTTHSTVLGLYNTL 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mphibla; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus.
NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
GROWTH FACTOR CVG1.
CVG1.
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Development 126:1467-1482(1999).
-!- SIMILARITY: TO TRANSFORMING GROWTH FACTOR (TGF) BETA FAMILY.
EMBE: AF1065135, AAD19837.1; -.
HSSP: P18075; 1BMP.
                                            17;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         32.8%; Score 208; DB 13; Length 354; 42.3%; Pred. No. 1.4e-15; Live 15; Mismatches 35; Indels 10
Pred. No. 3.6e-16;
                                                                                                                                                                          72 ASASPCCVPQDLEPLTILYY-----VGRTPKVEQLSNMVVKSCKCS 112
                                                                                                                                                                                                      332 GTAGPCCTPTKMSPINMLYFNRKEQIIYGKIPSI-----VVDRCGCS 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          879CAE9A23F2E42F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          69 NPEASASPCCVPQDLEPLTILYYVGRTPKV-EQLSNMVVKSCKC 111
                                                                                                                                                                                                                                                                                                                                                                                                      01-WAY-1999 (TrEMBLrel. 10, Last sequence update)
01-WAR-2001 (TrEMBLrel. 16, Last annotation update)
                                                                                                                                                                                                                                                                                                                                            354 AA
           38.0%; Pred. NC. +ive 13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Xenopus laevis (African clawed frog)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR001111; --
InterPro; IPR001111; --
InterPro; IPR001111; --
InterPro; IPR00183; --
Fam; PF00019; TGF-beta; 1.
PFam; PF00688; TGFb_propeptide; 1.
PR0Dom; PD000357; --; 1.
PROSITE; PS00250; TGF_BETA; 1.
SWART; SW00204; TGFB; 1.
GlyCoprotein.
SEQUENCE 354 AA; 40316 MW; 879CA
                                                                                                                                                                                                                                                                                                                                                                                      Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        44; Conservative
                                          Conservative
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                  Best Local Similarity
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                                                                                                                                                                                                                                                                                      RESULT 23
09976V1
COPYGV1
DT 01-MAY
DE DERRIES
COC Xenopu

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39; DB 6;

Length 375;

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12 EENCCVRPLYIDFRQDLGWKWVHEPKGYYANFCSGPCP--YLRSADTTHSTVLGLYNTLN 69
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Branchiostoma floridae (Florida lancelet) (Amphioxus).
Eukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae;
                                                          Hosoyama T., Yamanouchi K., Tojo H., Tachi C.;
"Molecular cloning of equine myostatin cDNA and serum level
myostatin in horse.";
Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, AB033341; BAB16046.1; -.
SEQUENCE 375 AA; 42736 MW; 6F424ECBEE4D9936 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63 GLYNTLNPEASASPCCVPQDLEPLTILYYVGRTPKV-EQLSNMVVKSCKC 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  09FF5FE6C9785DD1 CRC64;
                                                                                                                                                                                                                                                                                                                          70 PEASASPCCVPQDLEPLTILYYVGRTPKV-EQLSNMVVKSCKCS 112
                                                                                                                                                                                                                                                                                                                                            332 PRGSAGPCCTPTKMSPINMLYFNGKEQIIYGKIPAMVVDRCGCS 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-WAY-1999 (TrEMBLrel. 10, Created)
01-WAY-1999 (TrEMBLrel. 10, Last sequence update)
01-WAR-2001 (TrEMBLrel. 16, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             32.2%; Score 204; DB 5; Le 40.9%; Pred. No. 4.1e-15; Live 15; Mismatches 40;
                                                                                                                                                                                         32.3%; Score 204.5; DB 6
39.4%; Pred. No. 3.7e-15;
tive 15; Mismatches 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR00111; -.
InterPro; IPR00111; -.
InterPro; IPR001839; -.
InterPro; IPR001839; -.
InterPro; IPR002405; -.
Ffam; PP00019; TGF beta; 1.
Pfam; PF00688; TGFb_propeptide; 1.
Prolom; PD000357; -:
PROSITE; PS00250; TGF_BETA; 1.
SMART; SMO0204; TGFB; 1.
SEQUENCE 361 AA; 41517 MW; 09F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=98401944; PubMed=9733108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BONE MORPHOGENETIC PROTEIN 2/4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 40.99
Matches 45; Conservative
                                                                                                                                                                                                                            41; Conservative
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                               SEQUENCE FROM N.A. STRAIN-THROUOGHBRED;
                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=7739;
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                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12 EENCCVRPLYIDFRQDLGWKWVHEPKGYYANFCSGPCP--YLRSADTTHSTVLGLYNTLN 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Equus caballus (Horse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-20078370; PubMed-10612246;
Stratil A., Kopecny M.;
"Genomic organization, sequence and polymorphism of the porcine myostatin (GDF8 MSTN) gene.";
Anim. Genet. 30.468 470(1999.",
-!- SIMILARITY: TO TRANSFORMING GROWTH FACTOR (TGF) BETA FAMILY. EMBL. AJ237920; CAB40844.1; -.
HSSP: P18075; 1BMP.
InterPro; IPR001839; -.
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             Length 373;
                                              Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EASASPCCVPQDLEPLTILYYVGRTPKV-EQLSNMVVKSCKC 111
                                                                                                                                                         (TrEMBLrel. 13, Created)
(TrEMBLrel. 13, Last sequence update)
(TrEMBLrel. 16, Last annotation update)
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Last annotation update)
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                                              36;
           Query Match 32.6%; Score 207; DB 13; Best Local Similarity 41.2%; Pred. No. 1.9e-15; Matches 42; Conservative 18; Mismatches 36;
                                                                                                                                                                                                                                                            AA.
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                                                                                                                                                                                                                                                            162
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     162 AA; 18290 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (TrEMBLrel. 16, TrEMBLrel. 16, (TrEMBLrel. 16,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00019; TGF-beta; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS; PRO0438; GFCYSKNOT
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                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SMART; SM00204; TGFB; 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                       Sus scrofa (Pig).
                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9823;
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01-MAY-2000 (
01-MAR-2001 (
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01-MAR-2001
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MSTN.
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Q9GM97
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Gaps

Indels 10;

Length 361;

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Local Similarity
nes 41; Conserv
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Query Match
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Q9PW65
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nomo saptamento (mamun).
Eukaryota; Matazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gu J.R., Wan D.F., Zhao X.T., Zhou X.M., Jiang H.Q., Zhang P.P.,
Qin W.X., Huang Y., Qiu X.K., Qian L.F., He L.P., Li H.N., Yu Y.,
Yu J., Han L.H.;
"Novel Human cDNA clones with function of inhibiting cancer cell
                                                                                                                        Eukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae;
Branchiostoma.
                                                                                                                                                                                Yasui K., Saiga H., Uemura M., Semba I.;
"Early body formation and expression pattern of genes encoding secreted proteins, BbBMP2/4, BbWnt7, and BbWnt8 in lancelets.";
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
-! SIMILARITY: TO TRANSPORMING GROWTH FACTOR (TGF) BETA FAMILY.
EMBL; AF206325; AAF19841.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                  40; Indels 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63 GLYNTLNPEASASPCCVPQDLEPLTILYYVGRTPKV-EQLSNMVVKSCKC 111
                                                                                                                                                                                                                                                                                                                                                                                                            Length 411;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        growth.";
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
EMBL: AF218018; AAG17260.1; -.
Hypothetical protein.
SEQUENCE 426 AA; 47454 MW; 339276317BD5B408 CRC64;
                                                                                                                                                                                                                                                                                                                                                                     411 AA; 46929 MW; F579898060F18355 CRC64;
                                                             01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
BONE MORPHOGENETIC PROTEIN 2/4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
HYPOTHETICAL 47.5 KDA PROTEIN.
HOMO sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                        ; Score 204; DB 5;
; Pred. No. 4.7e-15;
15; Mismatches 40;
                              411 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     426 AA
                                                   (TrEMBLrel. 13, Created)
                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                          InterPro; IPR001111; --
InterPro; IPR001111; --
InterPro; IPR001839; --
InterPro; IPR002405; --
Pfam; PF00019; TGF-beta; 1.
Pfam; PF00688; TGFb_propeptide; 1.
                                                                                                                                                                                                                                                                                                                       PRINTS; PR00669; INHIBINA.
PROSITE; PS00250; TGF_BETA; 1.
SMART; SM00204; TGFB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                        32.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                               45; Conservative
                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                            Branchiostoma belcheri
                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
                                                                                                                                                                                                                                                     HSSP; P18075; 1BMP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                               NCBI_TaxID=7741;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
                                                 01-MAY-2000 (
01-MAY-2000 (
01-MAR-2001 (
                                                                                                                                                                                                                                                                                                                                                         Glycoprotein
                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                      Q9U418;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9HBP0;
                          090418
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    29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 30
Q9HBP0
                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
   RESULT
Q9U418
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                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15 CCVRPLYIDFRODLGWK-WVHEPKGYYANFCSGPCP-----YLRSADTTHSTVLGLYNTL 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUB-BRAIN, PITUITARY;

TISSUB-BRAIN, PITUITARY;

TISSUB-BRAIN, PITUITARY;

TOOMING and characterization of activin beta A subunit.";

MOI. Cell. Endocrinol. 0:0-0(1999).

L. SIMILARIY: TO TRANSFORMING GROWTH FACTOR (TGF) BETA FAMILY.

EMBL; AF165032; AAD50448.1; -.

RISSP; P18075; 1BMD.

InterPro; IPR001191; -.

InterPro; IPR0011939; -.

R InterPro; IPR001839; -.

R Pfam; PF00668; TGFD_bropeptide; 1.

PRINTS; PR00669; INHIBINAA.

R PRINTS; PR006607; INHIBINAA.

R PROSITE; PS00250; TGF_BETA; 1.

R SMARR; SM00204; TGFB_BTA; 1.

R Glycoprotein; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15 CCVRPLYIDFRQDLGWK-WVHEPKGYYANFCSGPCP----YLRSADTTHSTVLGLYNT- 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Cyprininae; Carassius.
                                                   10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 404;
      Length 426;
                                                   36; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GYSPFNNIKSCCVPTRLRAMSMLYY-NEEQKIIKKDIQNMIVEECGCS 404
                                                                                                                                                                                                          380 GHSPFANLKSCCVPTKLRPMSMLYYDDGQNIIKKDIQNMIVECGCS 426
                                                                                                                                                                                69 -- NPEASASPCCVPQDLEPLTILYY - VGRTPKVEQLSNMVVKSCKCS 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACTIVIN BETA A.
3AFB41BE62A8C0DC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                68 -LNPEASASPCCVPQDLEPLTILYYVGRTPKV--EQLSNMVVKSCKCS
                                                                                                                                                                                                                                                                                                                                                                                                           01-MAY-2000 (TrEMBLrel. 13, Last sequence update) 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
Last sequence update)
Last annotation update)
31.5%; Score 200; DB 4;
37.4%; Pred. No. 1.4e-14;
iive 21; Mismatches 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31.2%; Score 198; DB 13;
38.0%; Pred. No. 2.2e-14;
Live 19; Mismatches 36
                                                                                                                                                                                                                                                                                                                                               404 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              367 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                    01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                404 AA; 44799 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Carassius auratus (Goldfish).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1996 (TrEMBLEE). 01,
01-NOV-1996 (TrEMBLEE). 01,
01-MAR-2001 (TrEMBLEE). 16,
ACTIVIN D PRECURSOR.
                                              40; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACTIVIN BETA A PRECURSOR.
                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                         Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q91696
ID Q91696
AC Q91696;
DT 01-NOV-DT 01-NOV-DT ARR-COTON DT ARR-COTON DE ACTIVIN
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Query Match
Best Local Similarity
Matches 38; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=8330;
                                                                                                                                                                                                                                                                                                                                                                     01-FEB-1997 (
01-FEB-1997 (
01-MAR-2001 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               41;
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Matches
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P91720
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10 NLEEN----CCVRPLYIDFRQDLGWK-WVHEPKGYYANFCSGPCPYLRS-----ADTTHST 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ovis aries (Sheep).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
Bovidae, Caprinae, Ovis.
Xenopus laevis (African clawed frog).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
                                                                                                                                                                                 Oda S., Nishimatsu S., Murakami K., Ueno N.; Molecular cloning and functional analysis of a new activin beta subunit: a dorsal mesoderm-inducing activity in Xenopus."; Biochem. Biophys. Res. Commun. 210:581-588(1995).

EMBL; D49543; BAAO8494.1; --
HSSP; P18075; IBMP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lian Z., Jin H., Li N.;
"Cloning of intron 2 of the myostatin gene in sheep.";
Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
-- SIMILARITY: TO TRANSFORMING GROWTH FACTOR (TGF) BETA FAMILY.
EMBL; AF266758; AAP78069.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 VLGLYNTLNPEASASPCCVPQDLEPLTILYYVGRTPKV--EQLSNMVVKSCKCS 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         || | | :::|::| || | | :::|::| || 315 VLNLIKANNIQTAVNSCCVPTKRRPLSMLYF-DRNNNVLKTDIADMIVEACGCS 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 367;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                35; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1
185 185
185 AA; 20923 MW; BA9634203A552850 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'ACTIVIN D'.
C7E6334BD606FA04 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31.2%; Score 197.5; DB 1:
36.0%; Pred. No. 2.3e-14;
ive 25; Mismatches 35,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               185 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                         InterPro; IPR001111; -.
InterPro; IPR001839; -.
InterPro; IPR002400; -.
Pfam; PF00019; TGF-beta; 1.
Pfam; PF006688; TGFb_propetide; 1.
PRINTS; PR00438; GFCYSKNOT.
                                                                                                                                                            MEDLINE=95275314; PubMed=7755637;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Probom; PD000357; -: 1.
PROSITES, PS00250; TGF_BETA; 1.
SMART; SM00204; TGFB; 1.
Glycoprotein; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        254 367
367 AA; 41729 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00019; TGF-beta; 1.
PROSITE; PS00250; TGF_BETA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (TrEMBLrel. 15, CTrEMBLrel. 15, ICTEMBLrel. 16, ICTEMBLREL. 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                          Xenopodinae; Xenopus.
NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MYOSTATIN (FRAGMENT).
MSTN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9940;
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NON_TER
NON_TER
SEQUENCE 185
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01-0CT-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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Q9MZ18
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308 CCKKQFYVSFK-DIGWSDWVIAPPGYTANYCEGDCPMYITGTSGSGFSFHAAVINQYRMR 366
                                                 Gaps
                                                                                          12 EENCCVRPLYIDFRQDLGWKWVHEPKGYYANFCSGPCPYLRSADTTHSTVLGLYNTLNPE 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15 CCVRPLYIDFRQDLGWK-WVHEPKGYYANFCSGPCP-YLR----SADTTHSTVLGLYNT- 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cynops pyrrhogaster (Japanese common newt).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Caudata; Salamandroidea; Salamandridae; Cynops.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Yamamoto T., Nakayama Y., Abe S.; "Expression of activin beta subunit genes in Sertoli cells of newt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Biochem. Biophys. Res. Commun. 224:451-456(1996).
-1- SIMILARITY: TO TRANSFORMING GROWTH FACTOR (TGF) BETA FAMILY.
EMBL; D84516; BAA12693.1; -.
HSSP; P18075; 1BMP.
                                               5,
    Length 185;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 413;
                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        367 GYSPFTSVKSCCVPTKLRAMSMLYYDDGQNIIKKDIQNMVVEECGCS 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                68 -LNPEASASPCCVPQDLEPLTILYY-VGRTPKVEQLSNMVVKSCKCS 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   413 AA; 46303 MW; 46F66D112AA1B010 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                  (TrEMBLrel. 02, Last sequence update) (TrEMBLrel. 16, Last annotation update)
    9
                                                                                                                                                                                  72 ASASPCCVPQDLEPLTILYYVGRTPKV-EQLSNMVVKSC 109
                                                                                                                                                                                                            DB 13;
Score 196.5; DB 6
Pred. No. 1.4e-14;
6; Mismatches 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30.4%; Score 193; DB 13; 38.3%; Pred. No. 8.2e-14; iive 17; Mismatches 39
                                                                                                                                                                                                                                                                                                                                                    413 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             614 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00019; TGF-beta; 1.
Pfam; PF00689; TGF-beta; 1.
PRINTS; PR00439; GFCYSKNOT.
PRINTS; PR00670: INHIBINBA.
PRODOM; PD000357; -; 1.
PROSITE; PS00250; TGF_BETA; 1.
SWART; SW00204; TGFB; 1.
Glycoprotein.
SEQUENCE 413 AA; 46303 MW; 46F661
                                                                                                                                                                                                                                                                                                                                                                                                 02, Created)
                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE-TESTIS;
MEDLINE-96295508; PubMed-8702409;
                                          16;
  31.0%;
38.4%;
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                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR000491; -. InterPro; IPR001111; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR001839; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACTIVIN BETA-A SUBUNIT
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076514
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                                                                       Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               :| |:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|
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                                                                                                                                                               SEQUENCE FROM N.A.
MEDILNE-97225212; PubMed-9071585;
Newfeld S.J., Padgett R.W., Findley S.D., Richter B.G., Sanicola M.,
de Cuevas M., Gelbart W.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                               de Cuevas M., Gelbart W.M.;

"Molecular evolution at the decapentaplegic locus in Drosophila.";
Genetics 145:297-309(1997).

"Holecular evolution at the decapentaplegic locus in Drosophila.";
Genetics 145:297-309(1997).

"- SIMILARITY: TO TRANSFORMING GROWTH FACTOR (TGF) BETA FAMILY.

EMBL; U63855; AAC47555.1; -.

HSSP; P18075; 1BMP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Yandell M.D., Ross R.M., Suzuki Y., Wood W.B., "Characteristics of dbl-1, a C. elegans decapentaplegic homologue, support a conserved role for BMP-family signaling in bilaterian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             development.";
Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
1- SINILARITY: TO TRANSFORMING GROWTH FACTOR (TGF) BETA FAMILY.
EMBL: AF004395; AAC27729.1; -.
HSSP; P18075; 1BMP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10;
                                              Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63 GLYNTLNPEASASPCCVPQDLEPLTILYYVG-RTPKVEQLSNMVVKSCKC 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              564 TLVNNLNPGKVPKACCVPTQLEGISMLYLNDQRTVVLKNYQDMTVVGCGC 613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 614;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               42; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOF20A4093403DCF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUL-1997 (TrEMBLrel. 04, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DECAPENTAPLEGIC PROTEIN HOMOLOG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30.3%; Score 192; DB 5;
40.0%; Pred. No. 1.6e-13;
tive 14; Mismatches 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            365 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00019; TGF-beta; 1.
Pfam; PF00688; TGF-beta; 1.
PRINTS; PR00438; GFCFSKNOT.
PRODOM; P0000357; -; 1.
PROSITE; PS00250; TGF_BETA; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                   Interpro; IPR001111; -.
Interpro; IPR001839; -.
Pfam; PF00019; TGF-beta; 1.
Pfam; PF00688; TGFb_propeptide;
                      Drosophila virilis (Fruit fly).
                                                                                                                                                                                                                                                                                                                                                                                  FlyBase; FBgn0013109; Dvir\dpp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ProDom; PD000357; -; 1.
PROSITE; PS00250; TGF_BETA; 1.
SMART; SM00204; TGFB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       614 AA; 69055 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       44; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Interpro; IPR001111; -.
Interpro; IPR001839; -.
Interpro; IPR002400; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                             Ephydroidea; Dro
NCBI_TaxID=7244;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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                                                                                                                                                                                                          Gaps
                                                                                                                                                                                 12 BENCCVR-PLYIDFRQDLGWK-WVHEPKGYYANFCSGPCPYLRSAD---TTHSTVLGLYN 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12 EENCCVR-PLYIDFRQDLGWK-WVHEPKGYYANFCSGPCPYLRSAD---TTHSTVLGLYN 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-N2;
Morita K., Chow K.L., Ueno N.;
Morita K., Chow K.L., Ueno N.;
Morita K., Chow M.L., Ueno N.;
Morita K., Chow M.L., Ueno N.;
Morita K., Chow Mander Tail Ray Pattern Formation of C. elegans are
Regulated by a Member of TGFD Family.";
Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
ENBL: ARO14998; ARC26791.1;
HSSP; P18075; 1BMP.
                                                                                                                                             1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7;
                                                                                                 30.2%; Score 191.5; DB 5; Length 365; 39.6%; Pred. No. 1.1e-13; live 16; Mismatches 41; Indels 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 365;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    41; Indels
                                                                                                                                                                                                                                                                67 TLNPEASASPCCVPQDLEPLTILYY-VGRTPKVEQLSNMVVKSCKC 111
                                                                                                                                                                                                                                                                                       319 SLRPDEVPPCCVPTETSPLSILYMDVDKVIVIREYADMRVESCGC 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIRPDEVPPPCCVPTETSPLSILYMDVDKVIVIREYADMRVESCGC 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    67 TLNPEASASPCCVPQDLEPLTILYY-VGRTPKVEQLSNMVVKSCKC 111
                                       365 AA; 41768 MW; 937BFF3459F02C7E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              365 AA; 41781 MW; 4DECEE5C528BA3FF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
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Pred. No. 1.1e-13;
                                                                                                                                                                                                                                                                                                                                                                                                           365 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00019; TGF-beta; 1.
Pfam; PF00688; TGF-beta; 1.
PRINTS; PR00438; GFCYSKNOT.
Probom; PD000357; -; 1.
PROSITE; PS00250; TGF-BETA; UNKNOWN_1.
SMART; SM00204; TGFB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
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39.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1998 (TrEMBLrel. 08, 01-NOV-1998 (TrEMBLrel. 08, 01-MAR-2001 (TrEMBLrel. 16,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (TrEMBLrel. 01, (TrEMBLrel. 01,
                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                42; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
SMART; SM00204; TGFB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
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                                                                                                                      Best Local Similarity
Matches 42; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=6239;
                    Glycoprotein.
SEQUENCE 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q91403
Q91403;
Q1-NOV-1996 (
Q1-NOV-1996 (
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SEOUENCE 36
                                                                                                      Query Match
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091403
ID 091403
AC 091403;
DT 01-NOV-
DT 01-NOV-
                                                                                                                                                                                                                                                                                                                                                                                                         076514
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Glycoprotein.
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SEQUENCE
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SEQUENCE
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012938
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TISSUB-5-DAY ESTROGEN-WITHDRAWN OVIDUCT;
MEDLINE-2007867; PubMed=10848589;
MONICOE D.G., Jin D.F., Sanders M.M.;
"Estrogen Opposes the Apottotic Effects of Bone Morphogenetic Protein
                     Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                       MEDLINE-95200473; PubMed-7893347; MEDLINE-95200473; PubMed-7893347; Houston B., Thorp B.H., Burt D.W.; Houston B., Thorp B.H., Burt D.W.; "Molecular cloning and expression of bone morphogenetic protein-7 in the chick epiphyseal growth plate."; J. Mol. Endocrinol. 13:289-301(1994).
1- SIMILARITY: TO TRANSFORMING GROWTH FACTOR (TGF) BETA FAMILY. HSSP; P18075; IBMP.
                                                                                                                                                                                                                                                                                                                                                                                                                              14; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                 10 NLEEN-----CCVRPLYIDFRQDLGWK-WVHEPKGYYANFCSGPCPYLRSA---DTT 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          58 HSTVLGLYNTLNPEASASPCCVPQDLEPLTILYYVGRTPKV-EQLSNMVVKSCKC 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7 on Tissue Remodeling.";
Mol. Cell. Biol. 20:4626-4634(2000).
-!- SIMILARITY: TO TRANSFORMING GROWTH FACTOR (TGF) BETA FAMILY
EMBL; AF205877; AAF34179.1;
                                                                                                                                                                                                                                                                                                                                                                      Length 313;
                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                    COA3739197DBAC8F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (TrEMBLrel. 15, Created)
(TrEMBLrel. 15, Last sequence update)
(TrEMBLrel. 16, Last annotation update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update) BONE MORPHOGENETIC PROTEIN-7 (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                    30.0%; Score 190; DB 13; 34.8%; Pred. No. 1.3e-13; iive 22; Mismatches 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            398 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAR-2001 (TrEMBLrel. 16, Last annotat.
BONE MORPHOGENETIC PROTEIN 7 (FRAGMENT).
                                                                                                                                                                                         InterPro; IPR001111; -.
InterPro; IPR001839; -.
InterPro; IPR002400; -.
Pfam; PF00619; TGF-beta; 1.
Pfam; PF0048; TGF-bropeptide; 1.
PRINTS; PR00448; GFCYSKNOT.
PRINTS; PR00450; INHIBINA.
PROSITE; PS00250; TGF_BETA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                   SEQUENCE 313 AA; 35816 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR002405; -. Pfam; PF00019; TGF-beta; 1.
                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 34.8'
Matches 40; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                   SMART; SM00204; TGFB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR001111; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR001839; -
                                                                     NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                              Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-OCT-2000
01-OCT-2000
                                                                                                                                                                                                                                                                                                                        NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q918T6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0918T6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gallus
  δλ
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                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                    57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12 EENCCVRPLYIDFRQDLGW-KWVHEPKGYYANFCSGPCPY-LRS--ADTTHSTVLGLYNT 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Dynamo, a new zebrafish DVR member of the TGF-beta superfamily is expressed in the posterior neural tube and is up-regulated by Sonic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Brachydanio rerio (Zebrafish) (Zebra danio).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Rasborinae; Danio.
                                                                                                                                                                                                                      NLEEN-----CCVRPLYIDFRQDLGWK-WVHEPKGYYANFCSGPCPYLRSA---DTT
                                                                                                                                                                                                                                                                                              58 HSTVLGLYNTLNPEASASPCCVPQDLEPLTILYYVGRTPKV-EQLSNMVVKSCKC 111
                                                                                                                                                                                                                                                                                                               14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 190; DB 13; Length 412; Pred. No. 1.8e-13;
                                                                                                                                               Length 398;
                                                                                                                                                                                   39; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                68 LNPEASASPCCVPQDLEPLTILYY-VGRTPKVEQLSNMVVKSCKC 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DYNAMO PROTEIN.
4076E262C4481121 CRC64;
                                                                                        9C3F625299DD0C37 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUL-1997 (TrEMBLrel. 04, Last sequence update) 01-MAR-2001 (TrEMBLrel. 16, Last annotation update) DYNAMO PROTEIN PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    41;
                                                                                                                                               Score 190; DB 13;
Pred. No. 1.7e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                          412 AA
                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00019; TGF-beta; 1.
Pfam; PF00688; TGFb_propeptide; 1.
PRINTS; PR00488; GFCYSKNOT.
PF0DOM: PD000357; -; 1.
SMART; SM00204; TGFB; 1.
Pfam; PF00688; TGFb_propeptide; 1. PRINTS; PR00669; INHIBINA. PROSITE; PS00250; TGF_BETA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HSSP; P18075; IBMP.
ZFIN; ZDB-GENE-980526-442; dynamo.
InterPro; IPR001111; ...
InterPro; IPR001839; ...
InterPro; IPR002400; ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=97231294; PubMed=9076689; Bruneau S., Rosa F.;
                                                                                                                                                                               22;
                                                                                      45459 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            47071 MW;
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40.0%;
                                                                                                                                               30.0%;
34.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            (TrEMBLrel. 04,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    42; Conservative
                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE-WHOLE EMBRYO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Glycoprotein; Signal SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                     Query Match
Best Local Similarity
Matches 40; Conserv
                                                                                        398 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            412 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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68 -LNPEASASPCCVPQDLEPLTILYYVGRTPKV--EQLSNMVVKSCKC 111
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                                                                                                                                                      09н512
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                                                                                                                RESULT 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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Q9GT26
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9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
Tada T., Hirono I., Aoki T., Takashima F.;
"Cloning and sequencing of carp and medaka activin subunit genes.";
Fisheries Sci. 64:680-685(2000).
EMBL; AB009403; BAB17596.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Liliada T., Hiron N.A.
Tada T., Hirono I., Aoki T., Takashima F.;
"Cloning and sequencing of carp and medaka activin subunit genes.";
Fisheries Sci. 64:680-685(2000).
EMBL; AB009407; BAB17600.1; -.
                                                                                                                                                                                                                                Cyprinus carpio (Common carp).

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Cypriniae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha; Beloniformes; Adrianichthyidae; Oryziinae; Oryzias.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15 CCVRPLYIDFRQDLGWK-WVHEPKGYYANFCSGPCP----YLRSADTTHSTVLGLYNT-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15 CCVRPLYIDFRQDLGWK-WVHEPKGYYANFCSGPCP----YLRSADTTHSTVLGLYNT-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INHIBIN/ACTIVIN (FRAGMENT).
Oryzias latipes (Medaka fish).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29.8%; Score 189; DB 13; Length 115; llarity 36.4%; Pred. No. 6.2e-14; Conservative 20; Mismatches 36; Indels 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  36; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   68 -LNPEASASPCCVPQDLEPLTILYYVGRTPKV--EQLSNMVVKSCKC 111
367 MNPSNMPPSCCVPSKLSPISILYIDAGNNVVYKQYEDMVVESCGC 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13139 MW; 8C8C7C7A784E51D2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               90628E7BC85BA432 CRC64;
                                                                                                                                                                     01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
INHIBIN/ACTIVIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 189; DB 13;
Pred. No. 6.2e-14;
                                                                                                         115 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         . 29.8%; Score 189; 36.4%; Pred. No. 6
                                                                                                                                                  Created)
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                                                                                                         PRT;
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13127 MW;
                                                                                                                                                (TrEMBLrel. 16,
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                                                                                                         PRELIMINARY;
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ses 39; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             115 AA;
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les 39; Conserv
                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=7962;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=8090;
                                                                                                                                                01-MAR-2001
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SEQUENCE
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SEQUENCE
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09DGE8
AC 09DGE8
AC 09DGE8
DT 01-MAR:
DT 01-MAR:
DT 01-MAR:
DC 01-M
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                                                            RESULT 41
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Matches
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Matches
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TISSUE-WHOLE ANIMAL;
Crampton A.L., Luckhart S.;
Crampton A.L., Luckhart S.;
"Isolation and characterization of As60A, a transforming growth factor B gene, from the malaria vector Anopheles stephensi.";
Cytokine 0:0-0(2000).
EMBL; AF284816; AAG13400.1; -.
SEQUENCE 438 AA; 49824 MW; 124BA66DAA832E84 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Anopheles stephensi (Indo-Pakistan malaria mosquito).
Eukaryota: Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoldea;
Anopheles.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13 ENCCVRPLYIDFRQDLGW-KWVHEPKGYYANFCSGPCPYLRSAD---TTHSTVLGLYNTL 68
                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10 NLEEN------CCVRPLYIDFRQDLGWK-WVHEPKGYYANFCSGPCPYLRSA---DTT
                                                                                                                                                                                                                   01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
10-WAR-2001 (TrEWBLrel. 16, Last annotation update)
BA560A15.1 (BONE MORPHOGENETIC PROTEIN 7 (OSTEOGENIC PROTEIN 1))
(FRACMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   58 HSTVLGLYNTLNPEASASPCCVPQDLEPLTILYYVGRTPKV-EQLSNMVVKSCKC 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .
9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29.8%; Score 189; DB 4; Length 177; 34.8%; Pred. No. 9.7e-14; ive 22; Mismatches 39; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29.8%; Score 189; DB 5; Length 438; 36:5%; Pred. No. 2.5e-13; Live 23; Mismatches 37; Indels
Heath P.;
Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AL157414; CAC08434.1; -.
NON_TER 1 1
SEQUENCE 177 AA; 19985 MW; 3DD2ABDD09D6323D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
GBB-00A-LIKE PROTEIN AS60A.
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                                                                                                                                               177
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                                                                                                                                                                                                   Created)
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                                                                                                                                               PRT;
                                                                                                                                                                                            (TrEMBLrel. 16, TrEMBLrel. 16, TrEMBLrel. 16,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    40; Conservative
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                                                                                                                                               PRELIMINARY;
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Matches 38; Conserv
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12 EENCCVRPLYIDFRODLGWKWVHEPKGYYANFCSGPCP--YLRSADTTHSTVLGLYNTLN 69
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Chang C., Hemmati Brivanlou A.;
"Xenopus GDF6, a new antegonist of noggin and a partner of BMPs.";
Development 0:0-0[1999].
-!- SIMILARITY: TO TRANSFORMING GROWTH FACTOR (TGF) BETA FAMILY.
BMBL; AF155125; AAD38402.1; -.
HSSP; P18075; 1BMP.
InterPro; IPR001111; -.
InterPro; IPR001839; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus.
NCBI_TaxID=8355;
-i- SIMILARITY: TO TRANSFORMING GROWTH FACTOR (TGF) BETA FAMILY.
EMBL; AF151692; AAD42221.1; -.
HSSP; P18075; 1BMP.
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                                                                                                                                                                                                                                                                                                                                                                       Length 96;
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                                                                                                                                                                                                                                                                                      383BC564EBD6EF18 CRC64;
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                 29.7%; Score 188; DB 13;
41.2%; Pred. No. 6.6e-14;
ive 12; Mismatches 30;
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01-NOV-1999 (TrEMBLrel. 12, Last seq
01-NAR-2001 (TrEMBLrel. 16, Last ann
GROWTH AND DIFFERENTIATION FACTOR 6.
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Pfam; PF00019; TGF-beta; 1.
Pfam; PF00688; TGFD_propeptide; 1.
PRINTE; PR00669; INHIBINA.
PROSITE; PS00220; TGF_BETA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   70 PEASASPCCVPQDLEPLILYYVGR 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | | | | | | | | : | : : | | : | : | | : | | : | | : | | : | | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : 
                                                                        Interpro; IPR001839; -. Pfam; PF00019; TGF-beta; 1. PROSITE; PS00200; TGF_BETA; 1. SMART; SMO0204; TGFB; 1. Glycoprotein.
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96 AA; 11040 MW;
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35; Conserv
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Matches 40; Conserv
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SEQUENCE 3
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SEQUENCE
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                                                                                                                                                                                                                                             01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
ACTIVIN BETA B SUBUNIT.
Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Archosauria; Aves; Neognathae, Anseriformes; Anatidae; Cairina.
NCBI_TaxID=8855;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Dohrmann C.E., Hemmati-Brivanlou A., Thomsen G.H., Fields A., Woolf T.M., Melton D.A.;
"Expression of activin mRNA during early development in Xenopus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Dev. Biol. 157:474-483(1993).
-!- SINILARITY: TO TRANSFORMING GROWTH FACTOR (TGF) BETA FAMILY EMBL; SG1773; AAB26863.1; -. HSSP; P18075; IBMP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29.7%; Score 188.5; DB 13; Length 370; 38.3%; Pred. No. 2.4e-13; ive 19; Mismatches 36; Indels 11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               370 AA; 41678 MW; AD21502AC45F1DE9 CRC64;
                                  69 NPEASASPCCVPQDLEPLTILYYVGR-TPKVEQLSNMVVKSCKC 111
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
                                                                                                                                                                                            370 AA.
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Pfam: PF00688; TGFb_propeptide;
PRINTS; PR00438; GFCFSKNOT.
PRODOM; PD000357; 7; 1.
PROSITE; PS00250; TGF_BETA; 1.
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Best Local Similarity 38.3%
Matches 41; Conservative
                                                                                                                                                                                               PRELIMINARY;
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InterPro; IPR001839; ...
InterPro; IPR002400; ...
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Xenopus laevis (African clawed frog)
        Development 0:0-0(2000).
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Talbot W.S., Bouwmeester T., Hammerschmidt M.;
"Essential role of Bmp7 (snailhouse) and its prodomain in dorsoventral
patterning of the zebrafish embryo.";
                                                                                                                                                                                                                                                                                                                                                                                                              otx and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9 RNLEENCCVRPLYIDFRQDLGWK-WVHEPKGYYANFCSGPCPY----LRSADTTHSTVL 62
                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.

OKAI N., Taguchi S., Tagawa K., Satoh N.;

Developmental expression of hemichordate orthologs of BMP-4, otx an allow allowed the state of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Buteleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Rasborinae; Danio.
                                                                                                                                                                                 Ptychodera flava.
Eukaryota; Metazoa; Hemichordata; Enteropneusta; Ptychoderidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63 GLYNTLNPEASASPCCVPQDLEPLTILYYVGRTPKV--EQLSNMVVKSCKC 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | ::: | | |||| :| | :::| | : || | 355 TLVHSVKASAVPQACCVPTELSPISML-YLDEYDKVILKNYQEMVVEGCGC 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 405;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29.7%; Score 188; DB 5; Length 405
38.7%; Pred. No. 3e-13;
ive 17; Mismatches 39; Indels
                                                                                                                                                                                                                                                                                                                          Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    405 AA; 45936 MW; D2EB2D2C7560ED13 CRC64;
                                                                                                 Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-WAY-2000 (TrEMBLrel. 13, Created)
01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-WAR-2001 (TrEMBLrel. 16, Last annotation update)
BONE MORPHOGENETIC PROTEIN 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Brachydanio rerio (Zebrafish) (Zebra danio).
                                         405 AA
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                                                                                   Created)
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                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro, IPR002405; -. Pfam; PF00019; TGF-beta; 1. Pfam; PF00688; TGFb_propeptide; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PR00669; INHIBINA.
PROSITE; PS00250; TGF_BETA; 1.
SMART; SM00204; TGFB; 1.
                                                                           01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-MAR-2001 (TrEMBLrel. 16,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best_Local Similarity 38.74
Matches 43; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR001111; -. InterPro; IPR001839; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HSSP; P18075; 1BMP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                           NCBI_TaxID=63121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=7955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Glycoprotein
                                                                                                                                         PF-BMP2/4.
PF-BMP2/4.
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                                     Q9U5E8
                RESULT
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Eleutherodactylus cystignathoides.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Leptodactylidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12 EENCCVRPLYIDFRQDLGWK-WVHEPKGYYANFCSGPC----PYLRSADTTHSTVLGLY 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15 CCVRPLYIDFRQDLGWK-WVHEPKGYYANFCSGPCPY----LRSADTTHSTVLGLYNTL 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
Dai X.Z., Wells D.;
"Vgl gene in the Direct Developing Frog, Syrrhophus cystignathoides
"Vgl gene in the Direct Developing Frog, Syrrhophus cystignathoides
-1- SIMILARITY: TO TRANSFORMING GROWTH FACTOR (TGF) BETA FAMILY.
EMBL; AF201379; AAF17558.1; -
                                                                                                                                                                                                                                                                                                                                                                                                           10;
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                                                                                                                                                                                                                                                                                                                                                      Length 432;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 345;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               37; Indels
                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   66 NTLNPEASASPCCVPQDLEPLTILYYVGRTPKV-EQLSNMVVKSCKC 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ::||| ||| || || :::||: : : : ||||::| |
385 HFINPETVPKPCCAPTQLHGISVLYFDDSSNVILKKYRNMVVRACGC 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases. EMBL; AF248497; AAG09784.1; -. SEQUENCE 345 AA; 40102 MW; DE29048D20DD85AA CRC64;
                                                                                                                                                                                                                                                                         C982AF80E1652156 CRC64;
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U-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
GROWTH/DIFFERENTIATION FACTOR 16 PRECURSOR PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                 29.7%; Score 188; DB 13;
35.5%; Pred. No. 3.2e-13;
tive 22; Mismatches 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29.5%; Score 187; DB 13; 39.4%; Pred. No. 3.3e-13; tive 16; Mismatches 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               345 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                     HOSE, LOUIS, LEAST, LINEAR LANGUAGE, L. LINEAR PROUDLY, TGF-beta; I. Pfam; PF00688; TGF-propeptide; PROSITE; PS00250; TGF-BETA; I.
                                                                                                                                                                                                                                                                         432 AA; 48923 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 41; Conservative
                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 35.5
nes 38; Conservative
                                                                                                                                                                                                                    SMART; SM00204; TGFB; 1. Glycoprotein.
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                                                       HSSP; P18075; 1BMP
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                                                                                                            vokes S.A., Krieg P.A.;
"Gdf16, a novel member of the growth/differentiation factor subgroup of the TGF-beta superfamily, is expressed in the hindbrain and epibranchial placodes.";
Mech. Dev. 95:279-282(2000).
EMBL; AF239676; AAF99597.1;
                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                 15 CCVRPLYIDFRQDLGW-KWVHEPKGYYANFCSGPCPY-LRS--ADTTHSTVLGLYNTLNP 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Papilionoidea; Nymphalidae; Nymphalinae; Junonia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Carroll S.B., Gates J., Keys D.N., Paddock S.W., Panganiban G.E., Selegue J.E., Williams J.A.;
"Pattern formation and eyespot determination in butterfly wings."; Science 265:109-114(1994).
-1- SIMILARITY: TO TRANSFORMING GROWTH FACTOR (TGF) BETA FAMILY. HSSP; P18075; 1BMP.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                   9:
                                                                                                                                                                                                                                                                                                  Length 413;
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                                                                                                                                                                                                                                               5F1B0D7D97E591F6 CRC64;
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01-NAR-2001 (TEMBLE). 16, Last annotation update)
02-MAR-2001 (TEMBLE). 16, Last annotation update)
03-MAR-2001 (FEMBLE). 16, Last annotation update)
04-MAR-2001 (Peacock butterfly) (Precis coenia).
05-MAR-2001 (Peacock butterfly) (Precis coenia).
05-MAR-2001 (Peacock butterfly) (Precis coenia).
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                                                                                                                                                                                                                                                                                                                                                                                                                                   71 EASASPCCVPQDLEPLTILYY-VGRTPKVEQLSNMVVKSCKC 111
                                                                                                                                                                                                                                                                                                                                 37;
                                                                                                                                                                                                                                                                                               29.5%; Score 187; DB 13; 39.2%; Pred. No. 3.9e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29.3%; Score 186; DB 5; 34.8%; Pred. No. 2.1e-13; iive 21; Mismatches 34;
                                                                                                                                                                                                                                                                                             Query Match
29.5%; Score 187; Up. 19.2%; Best Local Similarity 39.2%; Pred. No. 3.9e-1
Matches 40; Conservative 19; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       178 AA
                                                                                                                                                                                                                                  POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
TISSUE-WHOLE ANIMAL;
MEDLINE-94287189; PubMed-7912449;
                                                                                                                                                                                                                                  23 rv
46510 MW;
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PRINTS; PRO0669; INHIBINA.
PROSITE; PSO0250; TGF_BETA; 1.
SMART; SM00204; TGFB; 1.
Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -NOV-1996 (TrEMBLrel. 01,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00019; TGF-beta; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Interpro; IPR001839; -. Interpro; IPR002400; -. Interpro; IPR002405; -.
                                  Xenopodinae; Xenopus.
                                                                                                                                                                                                                                     1
413 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       178 AA;
                                                                                 SEQUENCE FROM N.A.
                                                                                                  PubMed=10906478;
                                                 NCBI_TaxID=8355;
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SEQUENCE
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Q25211
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Davidson A.J., Postlethwait J.H., Yan Y.L., Beier D.R., van Doren C., Foernzler D., Celeste A.J., Crosier K.E., Crosier P.S.; "Isolation of zebrafish gdf7 and comparative genetic mapping of genes belonging to the growth/differentiation factor 5, 6, 7 subgroup of the TGF-beta superfamily."
160 CSRKPLHVNFK-ELGWDDWIIAPLDYEAYHCEGLCDFPLRSHLEPINHAIIQTLMNSMDP 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15 CCVRPLYIDFRQDLGW-KWVHEPKGYYANFCSGPCPY-LRS--ADTTHSTVLGLYNTLNP 70
                                                                                                                                                                                                                                                                        Brachydanio rerio (Zebrafish) (Zebra danio).
Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Rasborinae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
101-MBIR/ACTIVIN (FRAGMENT).
Cyprinus carpio (Common carp).
Eukaryota, Merazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Cyprininae; Cyprinus.
                                                65 YNTLNPEASASPCCVPQDLEPLTILYYVGRTPKVEQLSNMVVKS-----CKC 111
                                                                    130 VNSVNPAAVPKACCVPTQLSSISMLY-----MDEVNNVVKKNYQDMMVVGCGC 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genome Res. 9:121-129(1999).
-!- SIMILARITY: TO TRANSFORMING GROWTH FACTOR (TGF) BETA FAMILY.
EMBL; AF113023; AAD20829.1; -.
INSEP; P18075; 1BMP.
InterPro; IPR001839; -.
InterPro; IPR0024009; -.
InterPro; IPR0024005; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               71 EASASPCCVPQDLEPLTILYY-VGRTPKVEQLSNMVVKSCKC 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29.3%; Score 186; DB 13; 39.2%; Pred. No. 3.2e-13; tive 20; Mismatches 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               115 AA
                                                                                                                                                                                                                                            GROWTH/DIFFERENTIATION FACTOR 7 (FRAGMENT).
                                                                                                                                                                                             Created)
                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. MEDLINE=99148135; Pubmed=10022976;
                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ProDom; PD000357; -; 1.
PROSITE; PS00250; TGF_BETA;
                                                                                                                                                                                                            (TrEMBLrel. 12, (TrEMBLrel. 16,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00019; TGF-beta; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS; PRO0438; GFCYSKNOT PRINTS; PRO0669; INHIBINA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 39.2% ses 40; Conservative
                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SMART; SM00204; TGFB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Glycoprotein,
                                                                                                                                                                                           01-NOV-1999
                                                                                                                                                                                                            01-NOV-1999
                                                                                                                                                                                                                             01-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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                                                                                                                              RESULT
Q9W6C0
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Q9DGE9
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5.

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Gaps

20;

34; Indels

Conservative

Local Similarity nes 40; Conserv

Matches

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9 RNLEENCCVRPLYIDFRQDLGWK-WVHEPKGYYANFCSGPCPYLRS---ADTTHSTVLGL 64

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SEQUENCE FROM N.A.

Lee K.J., Mendelsohn M., Jessell T.M.;

Neuronal patterning by BMPs: A requirement for GDF7 in the generation of a discrete class of commissural interneurons in the mouse spinal cord.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gallus gallus (Chicken).
Bukaryota: Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
Gallus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9 RNLEEN----CCVRPLYIDFRQDLGWK-WVHEPKGYYANFCSGPCPYLRSAD---TTHSTV 61
                                                                                                                                                                                                                                                                            MEDLINE-97000310; PubMed-8843395; Miya T., Morita K., Ueno N., Satoh N.; An ascidian homologue of vertebrate BMPs-5-8 is expressed in th midline of the anterior neuroectoderm and in the midline of the embryo."; Mech. Dev. 57:181-190(1996).

-1 - SIMILARITY: TO TRANSFORMING GROWTH FACTOR (TGF) BETA FAMILY. EMBL; D83183; BAA11835.1; -...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genes Dev. 0:0-0(1998).
-!- SIMILARITY: TO TRANSFORMING GROWTH FACTOR (TGF) BETA FAMILY.
EMBL; AF089086; AAC97113.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62 LGLYNTLNPEASASPCCVPQDLEPLTILYYVG-RTPKVEQLSNMVVKSCKC 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
BONE MORPHOGENIC PROTEIN A.
Halocynthia roretzi (Sea squirt).
Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea;
Stolidobranchia; Pyuridae; Halocynthia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-NAR-2001 (TrEMBLrel. 16, Last annotation update)
PUTATIVE GROWTH/DIFFERENTIATION FACTOR 6/7 (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  683 AA; 78693 MW; AOA157AE2518B686 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29.3%; Score 185.5; DB 5; 38.7%; Pred. No. 9.8e-13; iive 16; Mismatches 43;
                                                            683 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        126 AA
                                                                                                Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00019; TGF-beta; 1.
Pfam; PF00688; TGFD_propeptide; 1.
PRINTS; PR00438; GFCYSKNOT.
PRODOM; PD000357; -; 1.
PROSITE; PS00250; TGF_BETA; 1.
                                                                                                02,
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                                                            PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR001111; -. InterPro; IPR001839; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR002400; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SMART; SM00204; TGFB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 43; Conserv
                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9031;
                                                                                                                                                                                                                             NCBI_TaxID=7729;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Glycoprotein.
SEQUENCE 68
                                                                           Q94580;
01-FEB-1997
                                                          094580
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                        RESULT
094580
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                                                                                                                                                                                                                                                             7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ANTI-DORSALIZING MORPHOGENETIC PROTEIN 1.
DECB1A001349C895 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                  12 CCRQQFYIDFRL-IGWNDWIIAPAGYYGNYCEGSCPAYLAGVPGSASSFHTAVVNQYRMR 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9 RNLEEN----CCVRPLYIDFRQDLGWK-WVHEPKGYYANFCSGPCPY---LRSADTTHST 60
                                                                                                                                                                                                                                                                                             15 CCVRPLYIDFRQDLGWK-WVHEPKGYYANFCSGPCP-YLR----SADTTHSTVLGLYNT- 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE-96125170; PubMed-8575329;
MOOS M., Wang S., Krinks M.;
Manti-dorsalizing morphogenetic protein is a novel TGF-beta homolog expressed in the Spemann organizer.";
Development 121:4293-4301(1995).
-!- SIMILARITY: TO TRANSFORMING GROWTH FACTOR (TGF) BETA FAMILY.
HSSP; P18075; LBMP.
                                SECUENCE FROM N.A.
Tada T., Hirono I., Aoki T., Takashima F.;
"Clonding and sequencing of carp and medaka activin subunit genes.";
Fisheries Sci. 64:680-685(2000).
EMBL; AB009406; BAB17599.1; -.
NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11;
                                                                                                                                                                                                                                                             11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 VLGLYNTLN-PEASASPCCVPQDLEPLTILYY-VGRTPKVEQLSNMVVKSCKC 111
                                                                                                                                                                                                                       29.3%; Score 185.5; DB 13; Length 115; 37.7%; Pred. No. 1.5e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                           35; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         41; Indels
                                                                                                                                                                                                                                                                                                                                                                                          68 -LNPEASASPCCVPQDLEPLTILYYVGRTPKVEQ-LSNMVVKSCKC 111
                                                                                                                                                                12666 MW; CD38FA0DD7BD52A6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NAR-2001 (TrEMBLrel. 16, Last annotation update)
ANTI-DORSALIZING MORPHOGENETIC PROTEIN 1 PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29.3%; Score 185.5; DB 1
36.3%; Pred. No. 5.5e-13;
tive 20; Mismatches 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      390 AA
                                                                                                                                                                                                                                                           20; Mismatches
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Pfam; PF00688; TGFb_propeptide; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Probom; PD000357; ; 1. PROSITE, PS00250; TGF_BETA; SMART; SM00204; TGFB; 1. Glycoprotein; Signal.
                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR001111; -. InterPro; IPR001839; -.
                                                                                                                                               115
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NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
                                                                                                                                                                115 AA;
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                                                                                                                                                                                                                     Query Match
Best Local Similarity
NCBI_TaxID=7962;
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SEQUENCE
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Matches

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Gaps

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Length Indels

DB 5;

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65 YNTLNPEASASPCCVPQDLEPLTILYYVGRTPKV--EQLSNMVVKSCKC 111
                                                                                                                                                                                            Created)
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                                                                                                                                                 PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS: PROOG69; INHIBINA.
PRINTS: PROOF72; INHIBINBC.
PROSITE: PSO0250; TGF_BETA; 1.
SWART; SMO0204; TGFB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       39335 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00019; TGF-beta; 1.
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                                                                                                                                                 PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=10116;
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                                                                                                                                                                                                                                                      ACTIVIN BETA C.
                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-WISTAR;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           43;
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                                                                                                                                                                       09WUK5;
                                                                                                                                                 Q9WUK5
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                                                                                                        RESULT
                                                                                                                              Q9WUK5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hwang S.-P.L., Chen C.A., Chen C.-P.;
"Sea urchin TgBME2/4 gene encoding a bone morphogenetic protein
closely related to vertebrate BMP2 and BMP4 with maximal expression at
the later stages of embryonic development.";
Blochem. Blophys. Res. Commun. 258:457-463(1999).
-! SIMILARITY: TO TRANSFORMING GROWTH FACTOR (IGF) BETA FAMILY.
EMBL, AF133305; AAD30538.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                            9 RNLEENCCVRPLYIDFRQDLGW-KWVHEPKGYYANFCSGPCPY-LRS--ADTTHSTVLGL 64
                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Euechinoidea; Echinacea; Temnopleuroida; Toxopneustidae;
                                                                                                                                                                                                                                                                                                                                       .,
                                                                                                                                                                                                                                                                                          29.2%; Score 185; DB 13; Length 126; 36.1%; Pred. No. 1.9e-13; Live 23; Mismatches 40; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 204;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             65 YNTLNPEASASPCCVPQDLEPLTILYY-VGRTPKVEQLSNMVVKSCKC 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       78 MNSMDPESTPPSCCVPSKLSPISILYIDSGNNVVYKQYEDMVVETCGC 125
                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                           NON_TER 1 1
SEQUENCE 126 AA; 14265 MW; CB824D280F44A394 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CE829BDC2AA9F077 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
BONE MORPHOGENETIC PROTEIN 2/4 HOMOLOG (FRAGMENT).
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29.2%; Score 185; DB 5;
Best Local Similarity 36.7%; Pred. No. 3.2e-13;
Matches 40; Conservative 19; Mismatches 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               204 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tripneustes gratilla (Hawaian sea urchin).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. MEDLINE-99262121; PubMed=10329409;
              Interpro; IPR001839; -.
Interpro; IPR002400; -.
Interpro; IPR002405; -.
Pfam; PF00019; TGF-beta; 1.
PRINTS; PR00639; GRCYSKNOT.
PRINTS; PR00669; INHIBINA.
PROSITE; PS00505; TGF_BETA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00019; TGF-beta; 1.
PRINTS; PR00438; GFCYSKNOT.
PRINTS; PR00669; INHIBINA.
PROSITE; PS00250; TGF_BETA; 1.
SMART; SM00204; TGFB; 1.
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23697 MW;
                                                                                                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                  SMART; SM00204; TGFB; 1. Glycoprotein.
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InterPro; IPR001839; -.
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                                                                                                                                                                                                                                                                                                                Best Local Similarity
Matches 39; Conserv
P18075; 1BMP
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SEQUENCE
                                                                                                                                                                                                                                                                                            Query Match
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Q9XZ69
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TISSUE-OVARY;
Ge W., Muta T., Kobayashi H., Peter R.E., Nagahama Y.;
Ge W., Muta T., Kobayashi H., Peter R.E., Nagahama Y.;
"Cloning of cDNA for goldfish activin beta B subunit, and the expression of its messenger RNA in gonadal and non-gonadal tissues.";
J. Mol. Endocrinol. 0:0.0(0).
-I- SIMILABITY: TO TRANSFORMING GROWTH FACTOR (TGF) BETA FAMILY.
EMBL; AF004669; AAB61468-1;
                                                                                                                                                                                                                                                                                                                                                                                                                          Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RNLEENCCVRPLYIDFRQDLGW-KWVHEPKGYYANFCSGPCPYLRSAD-----TTHSTV 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
ACTIVIN BETA B SUBUNIT PRECURSOR.
Carassius auratus (Goldfish).
Eukaryota: Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Cyprininae; Carassius.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rossmanith W., Peter B., Schulte-Hermann R.;
"Rat activin beta C and beta E. sequence and expression.";
"Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: TO TRANSFORMING GROWTH FACTOR (TGF) BETA FAMILY.
EMBL; AF140031; AAD30132.1;
-INTER-PRO: IPR001318;
-INTER-PRO: IPR001318;
-INTER-PRO: IPR0018939;
-INTER-PRO: IPR001405;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LGLY--NTLNPEASASPCCVPQDLEPLTILYYVGRTPKVE-QLSNMVVKSCKCS 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LNLLKANTDAGTARRGSCCVPTSRRPLSLLYYDRDSNIVKTDIPDMVVEACGCS 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 351;
39; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6B219BF6C3E180A1 CRC64;
                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 185; DB 11;
Pred. No. 5.6e-13;
20; Mismatches 39;
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15 CCVRPLYIDFRQDLGWK-WVHEPKGYYANFCSGPCP-YLR----SADTTHSTVLGLYNT- 67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tada T., Hirono I., Aoki T., Takashima F.; "Cloning and sequencing of carp and medaka activin subunit genes."; Fisheries Sci. 64:680-685(2000).
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
101-MAR-2001 (TrEMBLrel. 16, Last annotation update)
101-MAR-2001 (TrEMGMENT).
0ryzias latipes (Medaka fish).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Neoteleostei;
Acatthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
Beloniformes; Adrianichthyidae; Oryzinae; Oryzias.
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Tada T., Hirono I., Aoki T., Takashima F.;
Tada T., Hirono I., Aoki T., Takashima F.;
"Cloning and sequencing of carp and medaka activin subunit genes.";
Fisheries Sci. 64:680-685(2000).
EMBL; AB009409; BAB17602.1; -.
NON_TER 115 115
                                                                                                                                                                                                                                                                                                                                                                                                        01-WAR-2001 (TrEMBLrel. 16, Created)
01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-WAR-2001 (TrEMBLrel. 16, Last annotation update)
INHIBIN/ACTIVIN (FRAGMENT).
Cyprinus carpio (Common carp).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Cypriniformes; Cyprinidae; Cypriniae; Cyprinia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28.9%; Score 183.5; DB 13; Length 115; 36.8%; Pred. No. 2.6e-13; Live 21; Mismatches 35; Indels 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Score 183.5; DB 13; Length; Pred. No. 2.6e-13; 21; Mismatches 35; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    68 -LNPEASASPCCVPQDLEPLTILYYVGRTPKVEQ-LSNMVVKSCKC 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CD38FBBC67BCE316 CRC64;
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                                                                                                                                                                68 -LNPEASASPCCVPQDLEPLTILYYVGRTPKVEQ-LSNMVVKSCKCS
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115 AA; 12684 MW;
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12684 MW;
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36.8%;
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NON_TER 1 1 1
NON_TER 115 115
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Best Local Similarity 36.8'
Matches 39; Conservative
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Matches 39; Conservative
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SEQUENCE
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Q9DGF1
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Q9DGE6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15 CCVRPLYIDFRQDLGWK-WVHEPKGYYANFCSGPCP-YLR----SADTTHSTVLGLYNT- 67
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01-NOV-1996 (TERMBLEEL) 16, Last annotation update)
01-MAR-2001 (TERMBLEEL) 16, Last annotation update)
ACTIVIN BETA B.
2ACTBB OR ZACTBETAB.
Brachydanio rerio (Zebrafish) (Zebra danio).
Bukaryota, Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi; Cypriniformes; Cyprinidae; Rasborinae; Danio.
NCBI_TaxID=7955;
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MEDLINE-95011555; PubMed-7926744;
Wittbrodt J., Frederic R.M.;
Wittbrodt J., Rederic R.M.;
Wittbrodt J., Rederic R.M.;
Wittbrodt J., Rederic R.M.;
Wittbrodt J., Rederic R.M.;
Wittbrodt J., CAA5336.1;
Wittbrodt J., CAA5336.1;
Wittbrodt J., Rederic R.M.;
Wittbr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 29.1%; Score 184.5; DB 13; Length Best Local Similarity 36.4%; Pred. No. 7.1e-13; Matches 39; Conservative 22; Mismatches 35; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 68 -LNPEASASPCCVPQDLEPLTILYYVGRTPKVEQ-LSNMVVKSCKCS 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ::| | : ||:| | : ||:| | 347 GISP-GSVNSCCIPTKLSTMSMLYFDDEYNIVKRDVPNMIVEECGCA 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACTIVIN BETA B SUBUNIT.
73AAA7E1C0B2450B CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL
                                                                                                                                                                    Pfam; PF00019; TGF-beta; 1.
Pfam; PF00688; TGF-beta; 1.
PRINTS; PR00671; INHIBINBB.
PRINTS; PR00672; INHIBINBC.
PROSITE: PS00250; TGF_BETA; 1.
SMART; SM00204; TGFB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Created)
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Pfam; PF00019; TGF-beta; 1.
Pfam; PF00688; TGFb_propeptide; 1.
PROMINTS; PR00438; GFCYSKNOT.
PRODOM; PD000357; -; 1.
PROSITE; PS00250; TGF_BETA; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       277 392 A
392 AA; 43853 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1996 (TrEMBLrel. 01,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 36.4 nes 39; Conservative
                                 InterPro; IPR000381; ..
InterPro; IPR001111; ..
InterPro; IPR001318; ..
InterPro; IPR001839; ..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR001111; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR001839; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                         23
392
HSSP; P18075; 1BMP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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090261 61

RESULT 090261

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Gaps

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Gaps

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Length 115;

Matches

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RESULT Q9W6T9

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10 NLEEN------CCVRPLYIDFRQDLGWK-WVHEPKGYYANFCSGPCPYLRSA---DTT 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-99146893; PubMed-10021348;
MEDLINE-99146893; PubMed-10021348;
Francis-West P.H., Abdelfattah A., Chen P., Allen C., Parish J.,
Ladher R., Allen S., MacPherson S., Luyten F.P., Archer C.W.;
"Mechanisms of GDF-5 action during skeletal development.";
"Development 126:1305-1315(1999).
-1- SIMILARIY: TO TRANSFORMING GROWTH FACTOR (TGF) BETA FAMILY.
EWBL; AF123389; AAD30451.1;
-.. InterPro; IPR001111;
-.. InterPro; IPR001839;
-.. InterPro; IPR001839;
-.. InterPro; IPR001839;
-.. InterPro; IPR0018030;
-. INTERPRO; IPR001800;
-. INTERPRO; IPR0
                                                                                                Wang S., Krinks M., Kleinwaks L., Zapalo P., Moos M. Jr.;
Submitted (NOV-1995) to the EMBL/GenBank/DDBJ databases.
I- SIMILARITY: TO TRANSFORMING GROWTH FACTOR (TGF) BETA FAMILY.
EMBL; U40034; AAD09399.1; --
HSSP; P18075; 1BMP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 58 HSTVLGLYNTLNPEASASPCCVPQDLEPLTILYYVGRTPKV-EQLSNMVVKSCKC 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |: | | :: ||: ||| | |::||: |: ||: || |::|| |: ||::| | |: || |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |:| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28.9%; Score 183; DB 13; Length 424; 33.0%; Pred. No. 1.1e-12; Live 24; Mismatches 39; Indels 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OSTEOGENIC PROTEIN-1 HOMOLOG.
C4638C7D3D0A1DE4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28.9%; Score 183; DB 13; Length 5 37.0%; Pred. No. 1.4e-12; ive 23; Mismatches 39; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        500 AA; 55952 MW; 1DE8385A3119A598 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         500 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                   InterPro; IPR001111; --
InterPro; IPR001111; --
InterPro; IPR001839; --
Pfam; PF00619; TGF-beta; 1.
ProDom; PD000357; -; 1.
PROSITE; PS00250; TGF_BETA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00019; TGF-beta; 1.
Pfam; PF00688; TGFb_propeptide;
PRINTS; PR00669; INHIBINA.
PROSITE; PS00250; TGF_BETA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           48917 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1999 (TrEMBLrel. 12, 01-NOV-1999 (TrEMBLrel. 12, 01-MAR-2001 (TrEMBLrel. 16,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 28.99
Best Local Similarity 37.09
Matches 40; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SMART; SM00204; TGFB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SMART; SM00204; TGFB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1999 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gallus gallus (Chicken)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Glycoprotein; Signal Signal SignAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           424 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
Matches 38; Conserv
                                                               SEQUENCE FROM N.A.
   \CBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9031;
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SEQUENCE 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9W6G0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rodaway A., Takeda H., Koshida S., Price B.M., Smith J.C., Patient R., Holder N.;
                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15 CCVRPLYIDFRQDLGWK-WVHEPKGYYANFCSGPCP-YLR----SADTTHSTVLGLYNT- 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29 CCROOFYIDFRL-IGWNDWIIAPAGYYGNYCEGSCPAYMAGVPGSASSFHTAVVNQYRMR 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Activin is an inducer of mesendoderm in the zebrafish germ ring.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Brachydanio rerio (2ebrafish) (Zebra danio).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Rasborinae; Danio.
                         CCVRPLYIDFRQDLGWK-WVHEPKGYYANFCSGPCP-YLR----SADTTHSTVLGLYNT-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      XOP-1H.
Renopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
-1- SIMILARITY: TO TRANSFORMING GROWTH FACTOR (TGF) BETA FAMILY.
EMBL; AJ238981; CAB43092.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                            68 -LNPEASASPCCVPQDLEPLTILYYVGRTPKVEQ-LSNMVVKSCKC 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GMSP-GSVNSCCIPTKLSTMSMLYFDDEYNIVKRDVPNMIVEEGGC 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             68 -LNPEASASPCCVPQDLEPLTILYYVGRTPKVEQ-LSNMVVKSCKC 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5BE38C763EDAC42B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
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01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
0STEOGENIC PROFEIN-1 HOMOLOG PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28.9%; Score 183.5; DB 13; 36.8%; Pred. No. 3.1e-13; ive 21; Mismatches 35;
                                                                                                                                                                                                                                                                                                                                                                                                                        138 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      424 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1999 (TrEMBLrel. 12, Created 01-NOV-1999 (TrEMBLrel. 12, Last so 01-MAR-2001 (TrEMBLrel. 16, Last an ACTIVIN BETA B PROTEIN (FRAGMENT) ACTIVIN BETA B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HSSP; P18075; 1BMP.
InterPro; IPR001839; -.
InterPro; IPR002400; -.
InterPro; IPR002405; -.
Pfam; PF00019; TGF-beta; 1.
PRINTS; PR00438; GFCYENOT.
PRINTS; PR00669; INHIBINA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PS00250; TGF_BETA; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        138 AA; 15263 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 36.89
Matches 39; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SMART; SM00204; TGFB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=7955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9W6T9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09YGH7;
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Gaps

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Length 500;

RESULT 65 Q9YGH7 Q9YGH7

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Gaps

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RESULT 67 093254

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Anguilla japonica (Japanese eel).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Anguilliformes; Anguilloidei;
Anguillidae; Anguilla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Miura T., Miura C., Eto Y., Nagahama Y.;
"Activin B gene is required for the initiation of spermatogenesis in the Japanese eel, Anguilla japonica ";
Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: TO TRANSFORMING GROWTH FACTOR (TGF) BETA FAMILY.
BENBL; AB025356; BBA83804.1; -.
HSSP; P18075; 1BMP.
                                                                                                                                                                                                               15 CCVRPLYIDFRQDLGWK-WVHEPKGYYANFCSGPCP-YLR----SADTTHSTVLGLYNT- 67
                                                                                                                                                                                                                                       15 CCVRPLYIDFRQDLGWK-WVHEPKGYYANFCSGPCP-YL----RSADTTHSTVLGLYNT-
                                                                                                                                   28.6%; Score 181.5; DB 13; Length 115; 36.8%; Pred. No. 4.3e-13; tive 20; Mismatches 36; Indels 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28.3%; Score 179.5; DB 13; Length 395; 35.5%; Pred. No. 2.6e-12; .ive 23; Mismatches 35; Indels 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      68 -LNPEASASPCCVPQDLEPLTILYYVGRTPKVEQ-LSNMVVKSCKCS 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ::| | : ||:| | :::||: | GMSP-GSMNSCCIPTRLSTMSMLYFDDEYNIVKRDVPNMIVEECGCA 395
                                                                                                                                                                                                                                                                                                               71 GMSP-GSVNSCCIPTKLSTMSMLYFDDEYNIVKRDVPNMIVEECGC 115
                                                                                                                                                                                                                                                                                           68 -LNPEASASPCCVPQDLEPLTILYYVGRTPKVEQ-LSNMVVKSCKC 111
                                                                           CD27E4BC78A3E316 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         395 AA; 43889 MW; FA56DD62D18509A3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                    395 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00019; TGF-beta; 1.
Pfam; PF00688; TGFb_propeptide; 1.
PRINTS; PR00671; INHIBINBB.
PRINTS; PR00672; INHIBINBC.
Fisheries Sci. 64:680-685(2000).
MBL; AB009405; BAB17598.1; -.
NON TER 115 115
                                                                           115 AA; 12710 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 28.3%
Best Local Similarity 35.5%
Matches 38; Conservative
                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
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InterPro; IPR001111; -.
InterPro; IPR001318; -.
InterPro; IPR001839; -.
                                                                                                                                   Query Match
Best Local Similarity
Matches 39; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. TISSUE-TESTIS;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=7937
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SEQUENCE 3
                                   NON_TER
NON_TER
SEQUENCE
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057573
ID 057573
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393 KNLKPRCSRKALHVNFK-DMGWDDWIIAPLEYEAYHCEGICEFPLRSHLEPTNHAVIQIL 451
         RNLEENCCVRPLYIDFRQDLGW-KWVHEPKGYYANFCSGPCPY-LRS--ADTTHSTVLGL 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15 CCVRPLYIDFRQDLGWK-WVHEPKGYYANFCSGPCPYLRSAD---TTHSTVLGLYNTLNP 70
                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Percoidei;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 [1]
SEQUENCE FROM N.A.
Tada T., Hirono I., Aoki T., Takashima F.;
"Cloning and sequencing of carp and medaka activin subunit genes.";
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
01-MAR-2001 (TREMBLrel. 16, Last annotation update)
1NHIBIN/ACTIVIN (FRAGMENT).
Cyprinus carpio (Common carp).
Cyprinus carpio (Common carp).
Actinopterygii, Neopterygii; Teleostei; Buteleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Cyprininae; Cyprinus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Imaoka A., Kasahara M., Inaba K.;
"Red seabream mRNA for DVR-1, partial cds.";
Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
-! SIMILARITY: TO TRANSFORMING GROWTH FACTOR (TGF) BETA FAMILY.
EMBL; ABOL6255; BAA32227.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 99;
                                                                                       65 YNTLNPEASASPCCVPQDLEPLTILYYVGRTPKV-EQLSNMVVKSCKC 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 182.5; DB 13; Length
Fred. No. 2.9e-13;
16; Mismatches 25; Indels
                                                                                                             060D880D31D3546E CRC64;
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Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                               Pagrus major (Red sea bream) (Chrysophrys major).
                                                                                                                                                                                                                               99 AA
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11359 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Interpro; IPR001839; -. Pfam; PF00019; TGF-beta; 1. SMART; SMO0204; TGFB; 1.
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Best Local Similarity 43.23
Matches 35; Conservative
                                                                                                                                                                                                                             PRELIMINARY;
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                                                                                                                                                                                                                                                               01-NOV-1998 (TrEMBLrel. 01-NOV-1998 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Sparidae; Chrysophrys.
NCBI_TaxID=8171;
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99 AA;
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NON_TER
SEQUENCE
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7;

Gaps

11;

Q9DGF0 Q9DGF0;

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09DGF0
00DGF0
AC 09DGF0
DT 01-MARDT 01-MARDT 01-MARDC COPTING
CC COPTING

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Gaps

19;

Indels

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14 NCCVRPLYIDFRQDLGW-KWVHEPKGYYANFCSGPCPY----LRSADTTHSTVLGLYNT 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kishimoto Y., Lee K.H., Zon L., Hammerschmidt M., Schulte-Merker S., "The molecular nature of zebrafish swirl: BMP2 function is essential during early dorsoventral patterning.";
Development 124:4457-4466(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Brachydanio rerio (Zebrafish) (Zebra danio).
Bukaryota: Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Buteleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Rasborinae; Danio.
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"Conservation of BMP signaling in zebrafish mesoderm patterning.";
Mech. Dev. 61:75-88(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lee K.H., Marden J.J., Thompson M.S., MacLennan H., Kishimoto Y., Pratt S.J., Schulte-Merker S., Hammerschmidt M., Johnson S.L., Postlethwaite J.H., Beier D.C., Zon L.I.;
"Cloning and Genetic Mapping of Zebrafish BMP-2.";
Dev Genet. 23:0-0(1998)
-!- SIMILARITY: TO TRANSFORMING GROWTH FACTOR (TGF) BETA FAMILY. EMBL; AF072456; AAC25595.1;
--- InterPro; IPR001111;
--- InterPro; IPR001111;
--- InterPro; IPR001189;
--- InterPro; IPR001839;
                                                                                                                                    DB 13; Length 411;
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                                                                                                                                                                                                                                                                                             68 LN---PEASASPCCVPQDLEPLTILYYVGRTPKV--EQLSNMVVKSCKC 111
                                                                            411 AA; 46894 MW; 43C86590E42A487B CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
BONE MORPHOGENETIC PROTEIN 2.
                                                                                                                                  28.3%; Score 179.5; DB 13;
38.5%; Pred. No. 2.8e-12;
Live 20; Mismatches 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                  411 AA
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01-NOV-1998 (TrEMBLrel. 08, Last sequ
01-MAR-2001 (TrEMBLrel. 16, Last anno
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Pfam; PF00688; TGFb_propeptide; 1.
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ProDom; PD000357; -; 1.
PROSITE; PS00250; TGF_BETA; 1.
SMART; SM00204; TGFB; 1.
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38.5%;
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                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
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                                                                                                                                    Query Match
Best Local Similarity
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SEQUENCE 4
                                                            Glycoprotein
                                                                                                                                                                           42;
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                                                                            SEQUENCE
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zebrafish Bmp family:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                   MEDLINE-97231284; PubMed-9076679;
Nikaido M., Tada M., Saji T., Ueno N.;
"Conservation of BMP Signaling in zebrafish mesoderm patterning.";
Mech. Dev. 61:75-88 (1997).
-1 - SIMILARITY: TO TRANSFORMING GROWTH FACTOR (TGF) BETA FAMILY.
ENEL; D40971; BRAA24406.1;
-1 - SISPSP: P18075; 1BMP.
                                                                                                            Brachydanio rerio (Zebrafish) (Zebra danio).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
Cyptiniformes; Cyptinidae; Rasborinae; Danio.
NCBI_TaxID=7955;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     049EC3BA083DEBDF CRC64;
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Last sequence update)
Last annotation update)
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Last annotation update)
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                    Created)
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Pfam; PF00688; TGFb_propeptide; 1.
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PF00688; TGFb_propeptide; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ProDom; PD000357; -; I. PROSITE; PS00250; TGE_BETA; I. SMART; SM00204; TGFB; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     411 AA; 46845 MW;
              01-JUN-1998 (TrEMBLrel. 06, 01-JUN-1998 (TrEMBLrel. 06, 01-MAR-2001 (TrEMBLrel. 16, BONE MORPHOGENETIC PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUL-1997 (TrEMBLrel. 04, 01-JUL-1997 (TrEMBLrel. 04, 01-MAR-2001 (TrEMBLrel. 16,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR001111; -. InterPro; IPR001839; -.
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                                                                                                                                                                                                                                                     TISSUE=WHOLE EMBRYO;
                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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01-MAR-2001
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                                                                                                                                                                                                                                                                                                                                   vertebrate Bmp-2/Bmp-
                                                                                                                                                                                                                                                                                                        MEDLINE-98090067; PubMed-9362472;
Miya T., Morita K., Suzuki A., Ueno N., Satoh N.;
"Functional analysis of an ascidian homologue of vertebrate Bmp-2/Bmp-4 suggests its role in the inhibition of neural fate specification.";
Development 124:5149-5159(1997).
-! SIMILARITY: TO TRANSFORMING GROWTH FACTOR (TGF) BETA FAMILY.
                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
   Gaps
                        14 NCCVRPLYIDFRQDLGW-KWVHEPKGYYANFCSGPCPY----LRSADTTHSTVLGLYNT 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13 ENCCVRPLYIDFRQDLGW-KWVHEPKGYYANFCSGPCP----YLRSADTTHSTVLGLYN 66
   19;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 443;
                                                                                  367 VNSNIPKA----CCIPTELSPISLL-YLDEYEKVILKNYQDMVVEGGGC 410
                                                                     LN---PEASASPCCVPQDLEPLTILYYVGRTPKV--EQLSNMVVKSCKC 111
  28; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              36; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SYDPSLTPKPCCVPTELSPIAML-YVDECELVVLKTYQQMAVEGGGC 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                67 TLNPEASASPCCVPQDLEPLTILYYVGRTPKV--EQLSNMVVKSCKC 111
                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea;
Stolidobranchia; Pyuridae; Halocynthia.
NCBI_TaxID=7729;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DCABOC606D8D95FC CRC64;
                                                                                                                                                                           01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
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Last annotation update)
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Pred. No. 3.4e-12;
                                                                                                                                                         443 AA
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20; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
                                                                                                                                                      PRT;
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Pfam; PF00688; TGFb_propeptide; 1.
                                                                                                                                                                                                                                      Halocynthia roretzi (Sea squirt).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28.2%; Scc
35.5%; Pre
tive 21;
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PROSITE; PS00250; TGF_BETA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  443 AA; 51677 MW;
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                                                                                                                                                                                                               HOMOLOG OF DPP SUBCLASS BMP.
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nes 38; Conservative
 Conservative
                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SMART; SM00204; TGFB; 1.
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                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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42;
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                                                                                                                                                                  076851;
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P87373
AC P87373
AD P87373
DT 01-MAX
DT 01-MAX
DE BMP5.
OC GAllus
OC Archosiy
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Matches
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. Takashima F.; Tada T., Hirono I., Aoki T., Takashima F.; "Cloning and sequencing of carp and medaka activin subunit genes."; Fisheries Sci. 64:680-685(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INHIBIN/ACTIVIN (FRAGMENT).
Oryzias latipes (Medaka fish).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15 CCVRPLYIDFRQDLGW-KWVHEPKGYYANFCSGPCP----YLRSADTTHSTVLGLYNTL
                                                                     developing vestibular and auditory sensory organs.";
J. Neurosci. 16:6465-6475(1996).
-i - SINILARITY: TO TRANSFORMING GROWTH FACTOR (TGF) BETA FAMILY.
EMBL; S81278; AAB49514.1; -.
HSSP; P180775; 1BMP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 453;
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Beloniformes; Adrianichthyidae; Oryzinae; Oryzias.
MEDLINE=97000882; PubMed=8815925;
Oh S.H., Johnson R., Wu D.K.;
"Differential expression of bone morphogenetic proteins in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     68 INPEASASPCCVPQDLEPLTILYYVGRTPKV-EQLSNMVVKSCKC 111
                                                                                                                                                                                                                                                                                                                                                                                                                                             AB946FE878BF32B2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13037 MW; E745FD3D91875E78 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (TrEMBLrel. 16, Created)
(TrEMBLrel. 16, Last sequence update)
(TrEMBLrel. 16, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             40;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28.2%; Score 179; DB 13; 35.2%; Pred. No. 3.5e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28.1%; Score 178; DB 13; 34.9%; Pred. No. 1.1e-12; ive 21; Mismatches 38;
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2; Mismatches
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                                                                                                                                                                                                                                                               Pfam; PF00019; TGF-beta; 1.
Pfam; PF00689; TGFD_propeptide;
PRINTS; PR00438; GFCYSKNOT.
PRODOM; PD000357; 1.
PROSITE; PS00250; TGF_BETA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                          453 AA; 51628 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             37; Conservative
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                                                                                                                                                                                          InterPro; IPR001111; -.
InterPro; IPR001839; -.
InterPro; IPR002400; -.
                                                                                                                                                                                                                                                                                                                                                                                      SMART; SM00204; TGFB; 1.
Glycoprotein.
SEQUENCE 453 AA; 5162
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nes 37; Conserv
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Gaps

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Length 364;

**09XX07** 

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SEQUENCE FROM N.A.
MEDLINE-98036031; PubMed-9370264;
MEDLINE-98036031; PubMed-9370264;
Martinez-Barbera J.P., Toresson H., DaRocha S., Krauss S.;
Martinez-Barbera J.P., Toresson of three members of the zebrafish Bmp family:
Bmp2a, Bmp2b and Bmp4.";
Gene 198:53-59(1997).
--- SIMILARITY: TO TRANSFORMING GROWTH FACTOR (TGF) BETA FAMILY.
EMBL: U82233; AACGO287.1; ---
HSSP; P18075; IBMP.
                                                                                                                                                                                                                                                                                                                                            9 RNLE--ENCCVRPLYIDFRQDLGWK-WVHEPKGYYANFCSGPCPYLRSAD---TTHSTVL 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14 NCCVRPLYIDFRQDLGWK-WVHEPKGYYANFCSGPCPY----LRSADTTHSTVLGLYNT 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Brachydanio rerio (Zebrafish) (Zebra danio).
Eukaryota: Metazoa; Chordata: Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Rasborinae; Danio.
NCBI_TaxID=7955;
                                                                                                                                                                                                                                                                                                                                                                                                63 GLYNTLN-PEASASPCCVPQDLEPLTILYY-VGRTPKVEQLSNMVVKSCKC 111
                                                                                                                                                                                                                                                                                                                                                                                                                      342 VNSNIPRA----CCVPTDLSPVSLL-YLDEYERVILKNYQDMVVEGGGG 385
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; Pred. No. 4.4e-12;
18; Mismatches 29; Indels
                                                                                                                                                                                     76565716FBEB78D8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   386 AA; 43374 MW; EA0954E7D3FBA1D7 CRC64;
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Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                             DB 13;
                                                                                                                                                                                                                                        28.0%; Score 177.5; DB 13; 36.0%; Pred. No. 4.1e-12; ive 20; Mismatches 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  386 AA
                     InterPro; involution; InterPro; IPR002405; -...
Pfam, PF00019; TGF-beta; 1.
PFfam; PF0068; TGF-bropeptide; 1.
PRINTS; PR00669; INHIBINA.
PRODOM; PD000357; -; 1.
PROSITE; PS00250; TGF-BETA; 1.
SMART; SM00204; TGFB; 1.
Glycoprotein.
SEQUENCE 364 AA; 40071 MW: 765657
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Pfam; PF00688; TGFb_propeptide;
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PROSITE; PS00250; TGF_BETA; 1.
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39.4%;
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04,
16,
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                   IPR001839;
InterPro; IPR001111;
                                                                                                                                                                                                                                                             Local Similarity
nes 40; Conserv
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Best Local Similarity
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SEQUENCE 3
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01-JUL-1997
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Best Local S
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Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDILNE-99418628; Pubmed-10490096;
Joubin K., Stern C.D.;
Cell Movements of Gastrulation.";
EMBL: AF082178; AAD52011.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                             Lytechinus variegatus (Sea urchin).
Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Euechinoidea; Echinacea; Temnopleuroida; Toxopneustidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9 RNLEENCCVRPLYIDFRQDLGWK-WVHEPKGYYANFCSGPCPYLRSA---DTTHSTVLGL 64
                                                                                                                                                                                                                                                       Angerer L.M., Oleksyn D.W., Logan C.Y., McClay D.R., Dale L.,
Angerer R.C.;
Angerer R.C.;
Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
I- SIMILARITY: TO TRANSFORMING GROWTH FACTOR (TGF) BETA FAMILY.
BENBL, AF119712; AAD28038.1; --
HSSP; P18075; 1BMP.
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60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         417 AA; 47727 MW; 5EB93E3022BFC50F CRC64;
                                                                     Last sequence update)
Last annotation update)
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Last annotation update)
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               417 AA
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                                                    Created)
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               PRT;
                                                                                                  BONE MORPHOGENETIC PROTEIN BMP2/4.
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InterPro; IPR001839; ...
InterPro; IPR002405; ...
Pfam; PF00019; TGF-beta; 1.
Pfam; PF00689; TGFb_propeptide; 1.
PRINTS; PR00669; INHIBINA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Probom; PD000357; -; 1.
PROSITE; PS00250; TGF_BETA; 1.
                                              1-NOV-1999 (TrEMBLrel. 12,
1-NOV-1999 (TrEMBLrel. 12,
1-MAR-2001 (TrEMBLrel. 16,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 28.19
Best Local Similarity 35.89
Matches 39; Conservative
               PRELIMINARY;
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09PVK1; Q9PVK1

RESULT 77 Q9PVK1

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Q26468
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                                                                                                                                                                                                                                                                                             Strongylocentrotus purpuratus (Purple sea urchin).
Bukaryota, Metazoa; Echinodermata; Eleutherozoa; Echinoidea; Euchinoidea; Euchinoidea; Ethinoidea; Strongylocentrotidae; Strongylocentrotus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Angerer L.M., Oleksyn D.W., Logan C.Y., McClay D.R., Dale L., Angerer R.C.; "A BMP pathway regulates cell fate allocation along the sea urchin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
TISSUE=WHOLE EMBRYO;
MEDLINE=97231284; PubMed=9076679;
Nikaido M., Tada M., Saji T., Ueno N.;
"Conservation of BMP signaling in zebrafish mesoderm patterning.";
Mech. Dev. 61:75-88(1997).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    animal-vegetal embryonic axis.";
Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
-! SIMILARITY: TO TRANSFORMING GROWTH FACTOR (TGF) BETA FAMILY.
HSSP: P18075; 1BMP.
InterPro: IPR002480; -.
InterPro: IPR002440; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      239 VNSVNPALVPRACCVPTELSAISML-YLDEYEKVVLKNYQDMVVEGGGC 286
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                                                                                                                                  01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NAR-2001 (TrEMBLrel. 16, Last annotation update)
BONE MORPHOGENETIC PROTEIN BMP2/4 (FRAGMENT).
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PRINTS; PR00438; GFCYSKNOT.
PRINTS; PR00669; INHIBINA.
PROSITE; PS00250; TGF_BETA; 1.
SMART; SM00204; TGFB; 1.
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Best Local Similarity 35.8'
Matches 39; Conservative
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[2]
SEQUENCE FROM N.A.
MEDLINE=97447702; PubMed=9303442;
MEDLINE=P7447702; Lin Y.C., Liu C.H.;
"The zebrafish BMP4 gene: sequence analysis and expression pattern
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MEDLINE-89072730; PubMed=3201241;
Wozney J.M., Rosen V., Celoste A.J., Mitsock L.M., Whitters M.J.,
Kriz R.W., Hewick R.M., Wang E.A.;
"Novel regulators of bone formation: molecular clones and
activities.";
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MEDLINE-95395871; PubMed=7666445;
Newfeld S.J., Gelbart W.M.;
"Identification of two Drosophila TGF-beta family members in the
                                                                                                                                                                                                                                SEQUENCE FROM N.A. Hwang S.P., Tavou M.F., Lin Y.C., Liu C.H.; Brang S.P., Tavou M.F., Lin Y.C., Liu C.H.; Submitted (MAR-1998) to the EMBL/Genbank/DDBJ databases.
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1996 (TrEMBLrel. 16, Last annotation update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
TRANSFORMIG GROWTH FACTOR-BETA (FREMENT).
Schistocerca americana (American grasshopper).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Meoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha; Acridoidea; Acrididae; Schistocerca.
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MEDILINE=87090408; PubMed=3467201;
Padgett R.W., Johnston R.D., Gelbart W.M.;
Tanscript from a Drosphila pattern gene predicts a prothomologous to the transforming growth factor-beta family.";
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J. Mol. Evol. 41:155-160(1995).
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Pfam; PF00688; TGF-propeptide; 1.
ProDom; PD000357; -; 1.
PROSITE; PS00250; TGF-BETA; 1.
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                                                                                                                                                 during embryonic development.";
DNA Cell Biol. 16:1003-1011(1997).
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EMBL; AF056336; AAC13302.1;
HSSP; P18075; 1BMP.
InterPro; IPR001111; --
InterPro; IPR001839; --
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Best Local Similarity 37.7%
Matches 43; Conservative
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SEQUENCE 4
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346 AIIQLLVHGLKDLSIPKPCCVPYHLHPETLLYLNNEGDALLREFKDMSVSSCSC 399
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Pfam; PF00688; TGFb_propeptide;
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HSSP; P18075; 1BMP.
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                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN-GI; TISSUE-WHOLE ANIMAL;
Oril H., Karb K., Agata K., Watanabe K.;
"Molecular cloning of bone morphogenetic protein (BMP) gene from the planarian Dugesia japonica.";
Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.
-: SIMILARITY: TO TRANSFORMING GROWTH FACTOR (TGF) BETA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 DTNYCFRNLEENCCVRPLYIDFRQDLGW-KWVHEPKGYYANFCSGPCPYLRSAD---TTH 58
                                                                                                                                                                                                                  RNLEENCCVRPLYIDFRQDLGW-KWVHEPKGYYANFCSGPCPYLRSA---DTTHSTVLGL 64
                                                                                                                                                                                                                                                                                                                                                                                                                 Dugesia japonica (Planarian).
Eukaryota; Metazoa; Platyhelminthes; Rhabditophora; Turbellaria;
Tricladida; Paludicola; Dugesiidae; Dugesia.
NCBI_TaxID=6161;
Science 242:1528-1534(1988).
-!- SIMILARITY: TO TRANSFORMING GROWTH FACTOR (TGF) BETA FAMILY.
EMBL; U23785; AAA81169.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .
9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              59 STVLGLYNTLNPEASASPCCVPQDLEPLTILYYVGR-TPKVEQLSNMVVKSCKC 111
                                                                                                                                                                                             9
                                                                                                                                                                      Length 191;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27.3%; Score 173; DB 5; Length 400; 35.1%; Pred. No. 1.5e-11;
                                                                                                                                                                                                                                                             65 YNTLNPEASASPCCVPQDLEPLTILYYVGRTPKV-EQLSNMVVKSCKC 111
                                                                                                                                                                                                                                                                                   143 MNSMNPGLVPKACCIPTQLTSISMLYLDEESKVVLKNYHEMAVVGCGC 190
                                                                                                                                                                                            48; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BONE MORPHOGENETIC PROTEIN. 34220CB5140CB5A4 CRC64;
                                                                                                                                     FA73DF060878F4C0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20;
                                        InterPro; IPR00169; ...
InterPro; IPR001839; ...
Pfam; PF00019; TGF-beta; 1.
PROSITE; PS00250; TGF_BETA; 1.
PROSITE; PS00639; THIOL_PROTEASE_HIS; UNKNOWN_1.
                                                                                                                                                                      27.3%; Score 173; DB 5; 34.3%; Pred. No. 6.7e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18; Mismatches
                                                                                                                                                                                                                                                                                                                                           400 AA.
                                                                                                                                                                                            17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                     01-MAR-2001 (TrEMBLrel. 16, Last annot BONE MORPHOGENETIC PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last seq
                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AB010966; BAA32087.1; -. HSSP; P18075; 1BMP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     47031 MW:
                                                                                                                                     21879 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS00250; TGF_BETA; 1.
SMART; SM00204; TGFB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00019; TGF-beta; 1.
                                                                                                                                                                                           37; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            40; Conservative
                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                   SMART; SM00204; TGFB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR001839; -. InterPro; IPR002405; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           400
                                                                                                                                    191 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   400 AA;
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Best Local Similarity
                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                               Glycoprotein.
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                                  P18075
                                                                                                                          NON_TER
SEQUENCE
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SEQUENCE
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076147;
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RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Galle R.F.,
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M. Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Adams M.D., Call Blazel R.G., Change M., Miklos G.L.G.,
RA Ballew R.M., Basu A., Baxendall J., Bayraktaroglu L., Beasley E.M.,
Ballew R.M., Basu A., Baxendall J., Bayraktaroglu L., Beasley E.M.,
Ballew R.M., Basu A., Baxendall J., Bayraktaroglu L., Beasley E.M.,
Besson K.Y., Bences P.V., Berman B.P., Bhandari D., Bolshakov S.,
Burtis R.C., Busam D.A., Dahlke C., Davenport L.B., Davies P.,
RA Burtis R.C., Busam D.A., Dahlke C., Davenport L.B., Davies P.,
RA Burtis R.C., Busam D.A., Dahlke C., Davenport L.B., Davies P.,
RA Burtis R.C., Busam D.A., Butler H., Cadieu E., Center A., Chadra I.,
RA Godon K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Bocken R., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Glodek A., Gong F. Gorrell J.H., Gu Z., Genbart W.M., Glasser K.,
A Hostin D., Houston K.A., Howland T.J., Hernandez J.R., Harris M.L.
A Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibeyam C.,
Jasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
Liu X., Mattel B., Marford G.H., Ke Z., Kennison J.A., Ketchum K.A.,
Anoth S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
Merkilov G., Milshina N.V., Mobarry C., Moris J., Woshrefi A.,
Ralazolo M., Pittumo G.S., Pan S., Pollard J., Puri V., Reese M.G.,
Rabiert K., Remington K.A., Nixon K., Nusskern D.R., Parl W., Smith H.O.,
Spier E., Spradling A.C., Stapleton M., Strong R., San E.,
Spier E., Spradling A.C., Stapleton M., Strong R., San R.,
Spier E., Spradling A.C., Stapleton M., Strong R., San R.,
Spier E., Spradling A.C., Stapleton M., Strong R., San R.,
Spier E., Spradling A.C., Stapleton M., Strong R., Shan W.,
Wang Z.-Y., Wassarman D.A., Wolder J.C.,
Ralinger M., Wolder S., Wolde
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- SIMILARITY: TO TRANSFORMING GROWTH FACTOR (TGF) BETA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                   Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                  Drosophila melanogaster (Fruit fly).
Eukaryota, Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
                                                                                                                             Last sequence update)
Last annotation update)
¥
                                                                                    Created)
PRT;
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MEDLINE-20196006; PubMed-10731132;
                                                                            01-MAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
01-MAR-2001 (TrEMBLrel. 16,
PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                             CG16987 PROTEIN.
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NCBI_TaxID=7227;
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
TRANSFORMING GROWTH FACTOR-B HOMOLOG.
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Interpro; IPR001839; -.
Interpro; IPR002400; -.
Pfam; PF00619; TGF_beta; 1.
Pfam; PF00688; TGF_beropeptide; 1.
PRNINTS; PR00438; GFCYSKNOT.
Probom; PD000357; -; 1.
PROSITE; PS00250; TGF_BETA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
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InterPro; IPR001111; -.
InterPro; IPR001839; -.
InterPro; IPR002409; -.
Pfam; PF00019; TGF-beta; 1.
Pfam; PF00688; TGFD_propeptide; 1.
ProDom; PD000357; -; 1.
PROSITE; PS00250; TGF_BETA; 1.
                                                                                                                                                                                                                                                                                                                                                                                             428 AA; 49959 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                              SMART; SM00204; TGFB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          428 AA;
                                                                                                                                                                                                                       HSSP; P18075; 1BMP
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
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                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Glycoprotein.
SEQUENCE 42
                                                                                                                                                                                                                                                                                                                                                                              Glycoprotein
SEQUENCE 4:
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                                                  BP-TGH-1
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                                                                                                                                      7 CFRNLEENCCVRPLYIDFRQDLGW-KWVHEPKGYYANFCSGPCPYLRS---ADTTHSTVL 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9 RNLEENCCVRPLYIDFRQDLGWK-WVHEPKGYYANFCSGPC--PYLRSAD-TTHSTVLGL 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lelong C. Mathleu M., Favrel P.;

Lelong C. Mathleu M., Favrel P.;

"Structure and expression of mGDF, a new member of the TGF-beta
T superfamily in Crassostrea gigas (Mollusca Bivalvia).";

Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.

--- SIMILARITY: TO TRANSPORMING GROWTH FACTOR (TGF) BETA FAMILY.

R HSSP; P18075; 1BMP.

R InterPro; IPR001839; -.

R InterPro; IPR001839; -.

R InterPro; IPR001839; -.

R Pfam; PF00019; TGF-beta; 1.

Pfam; PF00068; TGFD_Dropetide; 1.

R PRINTS; PR00666; INHIBINA.

R PROSITE: PS00250; TGF_BETA; 1.

SMART; SM00204; TGFB: 1.

W Glycoprotein; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                   Crassostrea gigas (Pacific oyster).
Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorphia; Ostreoida;
Ostreoidea; Ostreidae; Crassostrea.
NCBI_TaxID=29159;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10;
                                                                                                                                                                                                                      63 GLYNT--LNPEASASPCCVPQDLEPLTILYY-VGRTPKVEQLSNMVVKSCKC 111
                                                                             DB 5; Length 586;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 27.1%; Score 172; DB 5; Length 301; Best Local Similarity 36.4%; Pred. No. 1.4e-11; Matches 40; Conservative 19; Mismatches 41; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  65 YNTLNPEASASPCCVPQDLEPLTILY --- YVGRTPKVEQLSNMVVKSCKC 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  253 VNSIDPRAAPKPCCVPTELSSLSLLYTDEHGAVVLKVYQ--DMVVEGCGC 300
                                                                                                           Indels
              Glycoprotein; Hydrolase; Metalloprotease; Zinc.
SEQUENCE 586 AA; 67184 MW; 582582D7F370D549 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MGDF PRECURSOR.
5217AD88239C9009 CRC64;
                                                                                                                                                                                                                                                                                                                                          Created)
Last sequence update)
Last annotation update)
                                                                         1. 27.2%; Score 172.5; DB 5; Similarity 36.6%; Pred. No. 2.5e-11; 11; Conservative 17; Mismatches 45;
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                                                                                                                                                                                                                                                                                                               301 AA
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                                                                                                                                                                                                                                                                                                               PRT;
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SMART; SM00204; TGFB; 1.
                                                                                                                                                                                                                                                                                                               PRELIMINARY;
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                                                                                                        41;
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Best Local
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RESULT 85 016123 ID 016123 AC 016123 DT 01-JAN

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14; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Brugia malayi.
Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
Onchocercidae; Brugia.
NCBI_TaxID=6279;
Brugia pahangi.
Rakaryota: Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
Onchocrcidae; Brugia.
NCBL_TaxID-6280;
                                                                                                                                                                                                Gomez-Escobar N., Maizels R.M.;
Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: TO TRANSFORMING GROWTH FACTOR (TGF) BETA FAMILY.
EMBL; AF010495; AAB65415.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gomez-Escobar N., Maizels R.M.;
Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARIY: TO TRANSFORMING GROWTH FACTOR (TGF) BETA FAMILY.
EMBL; AF012878; AAB71839.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             59 STVLGLYNTLNPEASASPCCVPQDLEPLTILYY-VGRTPKVEQLSNMVVKSCKC 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  374 AIVQGLINSVDPNLVPAPCCVPTEMESLAILYIDVEGKIVIKNYPDMEVLSCGC 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27.1%; Score 172; DB 5; Length 428; 36.0%; Pred. No. 2e-11; live 16; Mismatches 43; Indels
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
TRANSFORMING GROWTH FACTOR-BETA HOMOLOG.
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SEQUENCE
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Best Local S:
Matches 34,
                                                                                                                                                              SECUENCE
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RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Worthan J.R., Yandell M.D., Zhang Q., Chen L.X.,
Radadon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Abril J.E., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
Radilaw R.M., Basu A., Baxendale J., Bayraktaroly L., Beasley E.M.,
Besson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
Burtis Y.M., Cawley S., Dallike C., Davenport L.B., Davies P.,
RA Burtis S.D. Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Cherry J.M., Cawley S., Dallike C., Davenport L.B., Davies P.,
RA Burtis S.D., Davies M., Dugan-Rocha S., Dunkov B.C., Dun P.
Cherry J.M., Cawley S., Dallike C., Davenport L.B., Davies P.,
RA Booson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dun P.
RA Borlos B., Delcher A., Davies M., Dugan-Rocha S., Dunkov B.C.,
RA Hortin N.J., Brangelista C.C., Ferraz C., Ferriara S., Fleischman M.,
RA Glodek A., Gong F. Gorrell J.H., Gu Z., Gelbart W.M., Glasser K.,
A Jalai M., Kalush F., Kapten G. H., Ke Z., Kannison J.A., Ketchun K.A.,
Jalai M., Kalush F., Rapen G. H., Ke Z., Kannison J.A., Ketchun K.A.,
Almel B.E., Kodira C.D., Kraft C., Kravitz S., Moshrefi A.,
A Mandel B.E., Kodira C.D., Kraft C., Kravitz S., Moshrefi A.,
A Munt S.M., Moy M., Murphy B., Murphy L., Murany D.M., Nelson D.L.,
A Bazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Rese M.G.,
Radon R., Woy M., Murphy B., Murphy L., Murany D.M., Nelson D.K.,
A Banzzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Rees M.,
Spier E., Sofarat M., Stappson M., Stupski M.P., Sainth T.,
Radon D.K., Wassarman D.A., Weinster E., Wang A.H., Wang A.K.,
A Hang Z.-Y., Wassarman D.A., Weinster D., Wang S., Yao Q. A.,
R. The genome sequence of Drosophila melanogaster "."
                                            ŝ
                                                                                                                                                                                                                                                                                                                                                    Drosophila melanogaster (Fruit fly).

Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Pterygota; Meoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.
                                                                                                323 DKNYCRRT-----QLLVDF-NELNWQDWILAPSSYSAYQCQGECPNPLTSHFNTTNH 373
                                              14; Gaps
                                                                         3 DINYCFRNLEENCCVRPLYIDFRQDLGWK-WVHEPKGYYANFCSGPCPYLRSA---DTTH 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Science 287:2165-2195(2000).
-!- SIMILARITY: TO TRANSFORMING GROWTH FACTOR (TGF) BETA FAMILY.
                                                                                                                                           59 STVLGLYNTLNPEASASPCCVPQDLEPLTILYY-VGRTPKVEQLSNMVVKSCKC 111
                                                                                                                                                              374 AIVQGLINSVDPNLVPAPCCVPTEMESLAILYIDVEGKIVIKNYPDMEVLSCGC 427
          Query Match 27.1%; Score 172; DB 5; Length 428; Best Local Similarity 36.0%; Pred. No. 2e-11; Matches 41; Conservative 16; Mismatches 43; Indels
                                                                                                                                                                                                                                                                                         01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
                                                                                                                                                                                                                                                              588 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=BERKELEY;
MEDLINE=20196006; Pubmed=10731132;
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                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                               DPP PROTEIN
                                                                                                                                                                                                                                                                            Q9VQC6;
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Q9VQC6
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481 KNHDDTCRRHSLYVDF-SDVGWDDWIVAPLGYDAYYCHGKCPF-PLADHFNSTNHAVVQT 538
                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                             9 RNLEENCCVRPLYIDFRQDLGW-KWVHEPKGYYANFCSGPCPYLRSAD----TTHSTVLG 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15 CCVRPLYIDFRQDLGWK-WVHEPKGYYANFCSGPCP----YLRSADTTHSTVLGLYNT- 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Carassius auratus (Goldfish).
Weltzera Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Actinopterygii; Neopterygii; Teleostei; Buteleostei; Ostariophysi; Cypriniformes; Cyprinidae; Cypriniae; Carassius.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-9329066; PubMed-8512569; MEDLINE-93290666; PubMed-8512569; Ge W., Gallin W.J., Strobeck.C., Peter R.E.; "Cloning and sequencing of goldfish activin subunit genes: strong structural conservation during vertebrate evolution."; Biochem. Biophys. Res. Commun. 193:711-717(1993).

-: SIMILARITY: TO TRANSFORMING GROWTH FACTOR (TGF) BETA FAMILY. HSSP; P18075; IBMP.
                                                                                                                                                                                                                                                                                                                                                                             8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6
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                                                                                                                                                                                                                                                                                                                            Length 588;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            64 LYNTLNPEASASPCCVPQDLEPLTILYYVGR-TPKVEQLSNMVVKSCKC 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                  588 AA; 65867 MW; 2C8166C1BD2F666B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OF5E17FA198F94D9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2001 (TEMBLrel. 16, Last annotation update)
ACTIVIN BETA-A SUBUNIT (FRAGMENT).
                                                                                                                                                                                                                                                                                                                       27.1%; Score 172; DB 5; Le
35.8%; Pred. No. 2.8e-11;
ive 16; Mismatches 46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27.1%; Score 171.5; DB 13;
40.0%; Pred. No. 5.2e-12;
tive 14; Mismatches 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  102 AA
FlyBase; FBgn0000490; dpp.
InterPro; IPR00111; -.
InterPro; IPR0018405; -.
Pfam; PF00019; TGF-beta; 1.
Pfam; PF00689; TGF-bropeptide; 1.
PRNTTS; PR00669; INHIBINA.
PROSITE; PS00220; TGF_BETA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR001839; -. Pfam; PF00019; TGF-beta; 1. PROSITE; PS00250; TGF-BETA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          102 102
102 AA; 11849 MW;
                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 35.84
Matches 39; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SMART; SM00204; TGFB; 1.
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tgfb3p.rspt

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SMART; SM00204; TGFB; 1
                Glycoprotein.
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NON_TER
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                                       NON_TER
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Activin is an inducer of mesendoderm in the zebrafish germ ring."; Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
-! SIMILARITY: TO TRANSFORMING GROWTH FACTOR (TGF) BETA FAMILY.
EMBL; AJ238980; CAB43091.1; -..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
Rodaway A., Takeda H., Koshida S., Price B.M., Smith J.C., Patient
Holder N.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Brachydanio rerio (Zebrafish) (Zebra danio).
Eukaryota: Metazoa: Chordata; Craniata: Vortebrata; Euteleostomi;
Eukaryota: Metazoa: Chordata; Craniata: Vortebrata; Euteleostomi;
Cypriniformes; Cyprinidae; Rasborinae; Danio.
                                                                                                                                                                                 Johanson J.A., Breen M., Lepine A., Murphy K.E.;
"Identification and chromosomal localization of the gene encoding canine bone morphogenetic protein 4 (bmpl.",
Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
-! SIMILARITY: TO TRANSFORMING GROWTH FACTOR (TGF) BETA FAMILY.
EMBL; AF136233, AAF82188.1;
                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Carnivora, Fissipedia, Canidae, Canis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 288 TLVNSVNSSIPKA----CCVPTELSAISML-YLDEYDKVVLKNYQEMVVEGGGC 336
                                                                                                                                                                                                                                                                                                                                                                                                              19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63 GLYNTLN---PEASASPCCVPQDLEPLTILYYVGRTPKV--EQLSNMVVKSCKC 111
                                                                                                                                                                                                                                                                                                                                                                                   26.9%; Score 170.5; DB 6; Length 337; 37.7%; Pred. No. 2.3e-11; ive 17; Mismatches 35; Indels 19;
                                                                                                                                                                                                                                                                                                                                                 BC91231431FDCA27 CRC64;
                                             01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
BONE MORPHOGENETIC PROTEIN 4 (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
                         337 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         120 AA
                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                  Pfam; PF00019; TGF-beta; 1.
Pfam; PF00688; TGFb_propeptide; 1.
PROSITE; PS00250; TGF_BETA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACTIVIN BETA A PROTEIN (FRAGMENT). ACTIVIN BETA A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HSSP; P18075; 1BMP.
InterPro; PR0001839; -.
InterPro; PR0002405; -.
Pfam; PF00019; TGF-beta; 1.
PRINTS; PR00669; INHIBINA.
ProDom; PD000359; -; 1.
PROSITE; PS00250; TGF_BETA; 1.
                                                                                                                                                                                                                                                                                                                                   NON_TER 1 1
SEQUENCE 337 AA; 38792 MW;
                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 37.78 Matches 43; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                         PRELIMINARY;
                                                                                                                                                                                                                                                            InterPro; IPR001111; -. InterPro; IPR001839; -.
                                                                                                           Canis familiaris (Dog).
                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                               NCBI_TaxID=9615;
                                                                                                                                                                                                                                                                                                                          Glycoprotein.
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                                    09MZV5;
                        Q9MZV5
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RESULT 89
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MEDLINE=97398455; PubMed=9256353;
Bruneau S., Mourrain P., Rosa F.M.;
"Expression of Contact, a new zebrafish DVR member, marks mesenchymal
cell.lineages in the developing pectoral fins and head and is
regulated by retinoic acid.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15 CCVRPLYIDFRQDLGWK-WVHEPKGYYANFCSGPCPYLRSADTTH-----STVLGLYNT- 67
                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9 RNLEENCCVRPLYIDFRQDLGW-KWVHEPKGYYANFCSGPCPY-LRS--ADTTHSTVLGL 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Brachydanio rerio (Zebrafish) (Zebra danio).
Rukaryota: Metazoa: Chordata: Craniata: Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Rasborinae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mech. Dev. 65:163-173(1997).
-!- SIMILARITY: TO TRANSFORMING GROWTH FACTOR (TGF) BETA FAMILY EMBL; Y12005; CAA72733.1; -. HSSP; P18075; 1BMP.
                                                                                                                                                  12;
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                                                                                                   Length 120;
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                                                                                                                                                  Indels
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                                                                                                                                                                                                                                                                                             68 -LNPEASASPCCVPQDLEPLTILYYVGRTPKV--EQLSNMVVKSC 109
                                                                                                                                                                                                                                                                                                                        :| : |||| | :::||| | ::||| 70 GYSPFTNIKSCCVPTRLRAMSMLYY-NEEQKIVKKDIQNMIVEEC 113
120
13583 MW; D6B395EB4B40D705 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL.
6D64F0542F948849 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (TrEMBLrel. 05, Last sequence update) (TrEMBLrel. 16, Last annotation update)
                                                                                              Query Match 26.7%; Score 169; DB 13; Best Local Similarity 34.3%; Pred. No. 1.2e-11; Matches 36; Conservative 21; Mismatches 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26.7%; Score 169; DB 13; 34.3%; Pred. No. 2.6e-11; tive 25; Mismatches 40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   257 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
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InterPro; IPR001839; -.
InterPro; IPR002400; -.
Pfam; PF00019; TGF-beta; 1.
PRINTS; PR00438; GFCXSKNOT.
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257 PO
: 29787 MW;
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SMART; SM00204; TGFB; 1.
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05,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
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120 1
120 AA;
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Matches 37; Conserv
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SEQUENCE FROM N.A.
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Query Match
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                                                                                                                                                                                                                                                                                                                                                                        15 CCVRPLYIDFRQDLGWK-WVHEPKGYYANFCSGPCP-YLR----SADTTHSTVLGLYNT- 67
                                                                                                                                                                                                                                                                                                                                                                                    Cynops pyrrhogaster (Japanese common newt).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Caudata; Salamandroidea; Salamandridae; Cynops.
                                                                                                                                                Yamamoto T., Nakayama Y., Abe S.; "Expression of activin beta subunit genes in Sertoli cells of newt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Brachydanio rerio (Zebrafish) (Zebra danio).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Rasborinae; Danio.
                                                                                                                                                                             Biochem. Biophys. Res. Commun. 224:451-456(1996).
-i- SIMILARITY: TO TRANSFORMING GROWTH FACTOR (TGF) BETA FAMILY.
EMBL; D84517; BAA12694.1; -.
HSSP; P18075; IBMP.
                                                                                                                                                                                                                                                                                                                                                    11;
                                                                                                                                                                                                                                                                                                                               Query Match 26.6%; Score 168.5; DB 13; Length 104; Best Local Similarity 37.6%; Pred. No. 1.2e-11; Matches 38; Conservative 19; Mismatches 33; Indels 11;
                                                                                                                                                                                                                                                                                     104
11676 MW; A0087EB4A4E517FC CRC64;
                 01-FEB-1997 (TrEMBLrel. 02, Created)
01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUL-1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                  68 -LNPEASASPCCVPQDLEPLTILYYVGRTPKVEQ-LSNMVV 106
                                                                                                                                                                                                                                                                                                                                                                                                                               ||| ::||:| |::||:|
65 GLNP-GTVNSCCIPTKLSTMSMLYFDDEYNIVKRDVPNMIV 104
 104 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           400 AA.
 PRT;
                                                  ACTIVIN BETA-B SUBUNIT (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR001111; -.
InterPro; IPR001111; -.
InterPro; IPR001839; -.
Pfam; PF00019; TGF_beta; 1.
Probom; PF00688; TGFb_propeptide; 1.
Probom; P0000357; -; 1.
                                                                                                                          TISSUE=TESTIS;
MEDLINE=96295508; PubMed=8702409;
                                                                                                                                                                                                                              Pfam; PF00019; TGF-beta; 1.
PROSITE; PS00250; TGF-BETA; 1.
SMART; SM00204; TGFB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                        IPR001839; -.
                                                                                                                                                                                                                                                                                               104 AA;
                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                            NCBI_TaxID=8330;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=7955;
                                                                                                                                                                                                                                                                   Glycoprotein.
                                                                                                                                                                                                                                                                           NON_TER
NON_TER
SEQUENCE
                                                                                                                                                                                                                       nterPro;
                                                                                                                                                                      testes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      013107;
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013107
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                                                                                                                                                                                                                                                                                       294 RKRNRNCRRHALYVDF-SDVGWNDWIVAPPGYQAYYCHGECPFPLADHLNS--TNHAIVQ 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               313 RNAKGNYCKKIPLYIDFK-ELGWDSWIIAPPGYEAYECRGVCNYPLAEHLIPTKHAIIQA 371
                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                          9 RNLEENCCVRPLYIDFRQDLGWK-WVHEPKGYYANFCSGPCPY----LRSADTTHSTVL 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Celeste A.; "Mouse Bone Morphogenetic Protein 10 (BMP-10) Genomic Sequence, Full Coding Region of Exon 2."; Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases. -: SIMILARITY: TO TRANSFORMING GROWTH FACTOR (TGF) BETA FAMILY. EBBLS, ARC77461.1; -: EMBL, AF101440; AAC77461.1; -JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9 RNLEENCCVR-PLYIDFRQDLGW-KWVHEPKGYYANFCSGPCPYLRS---ADTTHSTVLG 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                             13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7;
                                                                                                                                                          Length 400;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 421;
                                                                                                                                                                                                                                                                                                                                                               63 GLYNTLNPEASASPCCVPQDLEPLTILYYVGRTPKV--EQLSNMVVKSCKC 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  64 LYNTLNPEASASPCCVPQDLEPLTILYY - VGRTPKVEQLSNMVVKSCKC 111
                                                                                                                                                                                                                                                                                                                                                                                               26.6%; Score 168.5; DB 11; Length 35.8%; Pred. No. 5e-11; Live 17; Mismatches 46; Indels
                                                                             400 AA; 45757 MW; 427D1DB8FE12D025 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            421 AA; 47917 MW; 703422876A64A18F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-WAY-1999 (TrEMBLrel. 10, Created)
01-WAY-1999 (TrEMBLrel. 10, Last sequence update)
01-WAR-2001 (TrEMBLrel. 16, Last annotation update)
BONE MORPHOGENETIC PROTEIN 10.
                                                                                                                                                       DB 13;
                                                                                                                                                     26.6%; Score 168.5; DB 13; 36.9%; Pred. No. 4.7e-11; ive 16; Mismatches 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               421 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    102 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00019; TGF-beta; 1.
Pfam; PF00688; TGFD_propeptide; 1.
PRINTS; PR00669; INHIBINA.
PROSIDE; PS00250; TGF_BETA; 1.
SMART; SM00204; TGF_BETA; 1.
Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9DET1;
01-MAR-2001 (TrEMBLrel. 16, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
PROSITE; PS00250; TGF_BETA; 1.
SMART; SM00204; TGFB; 1.
Glycoprotein.
SEQUENCE 400 AA; 45757 MW;
                                                                                                                                                                               Best Local Similarity 36.99
Matches 41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 35.88
Matches 39; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HSSP; P18075; 1BMP.
InterPro; IPR001111; -.
InterPro; IPR001839; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR002405;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=10090;
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8;

Gaps

19;

Indels

32;

Mismatches

18;

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Conservative
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                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HSSK; FICTOR INTERPROPERTY -. InterPro; IPR001839; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SMART; SM00204; TGFB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Xenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
Matches 42; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Glycoprotein
SEQUENCE 40
                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1996
01-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAR-2001
              42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROTEIN 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                            091703;
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                                                                  Φ
                 Matches
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Q91703
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
RAINBOW TROUT DNA FOR MATURE PEPTIDE. EXON2, PARTIAL CDS (FRAGMENT).
Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostel; Euteleostel;
NCBI_TaxID=8022;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15 CCVRPLYIDFRQDLGWK-WVHEPKGYYANFCSGPCP----YLRSADTTHSTVLGLYNTL 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.

Kim J., Chen H.-D., Roh D.-H., Ault K.T., Xu R.-H., Park M.-J.,

Kung H.-F.;

Submitted (MAX-1998) to the EMBL/GenBank/DDBJ databases.

-I- SIMILARITY: TO TRANSFORMING GROWTH FACTOR (TGF) BETA FAMILY.

EMBL; AF058764; AAC61694.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Takashi T., Hirono I., Aoki T., Takashima F.; "Structure and expression of activin genes in rainbow trout."; Mol. Mar. Biol. Biotechnol. 7:72-77(1988).

EMBL; D88464; BAB16973.1; --
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 26.4%; Score 167.5; DB 13; Length Best Local Similarity 38.8%; Pred. No. 1.5e-11; Matches 33; Conservative 14; Mismatches 29; Indels
                                                                                                                                                                                                                                                                                                                                             Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                102 102
102 AA; 11562 MW; DB2745E872C93D48 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A3147E4FACB4553F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (TrEMBLrel. 07, Last sequence update)
(TrEMBLrel. 16, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 165.5; DB 13;
Pred. No. 1e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             400 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-AUG-1998 (TrEMBLrel. 07, Created)
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Pfam; PF00688; TGFb_propeptide; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64 GYAPFONIKSCCVPNALRAMSMLYY 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             69 N--PEASASPCCVPQDLEPLTILYY 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ProDom; PD000357; -; 1. PROSITE; PS00250; TGE_BETA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       400 AA; 45810 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BONE MORPHOGENETIC PROTEIN 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26.1%;
36.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HSSP; P18075; IBMP.
InterPro; IPR001111; -.
InterPro; IPR001839; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SMART; SM00204; TGFB; 1. Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Xenopodinae; Xenopus.
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Best Local Similarity
                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=8355
                                                                                                                                                                                                                                                                                         TISSUE-BLOOD;
                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE-BLOOD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-AUG-1998
01-MAR-2001
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NON_TER
SEQUENCE
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                                                                                                                                                                                                                                                                                                                      Aoki T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96
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294 RKKNKHCRRHSLYVDF-SDVGWNDMIVAPPGYQAFYCHGDCPFPLADHLNS--TNHAIVQ 350
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"Bone morphogenetic protein 4: a ventralizing factor in early Xenopus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  294 RKKNKHCRRASLYVDF-SDVGWNDWIVAPPGYQAFYCHGDCPFPLADHLNS--TNHAIVQ 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9 RNLEENCCVRPLYIDFRQDLGWK-WVHEPKGYYANFCSGPCPY----LRSADTTHSTVL 62
RNLEENCCVRPLYIDFRQDLGWK-WVHEPKGYYANFCSGPCPY----LRSADTTHSTVL 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.

Metz A., Knoechel S., Buechler P., Koester M., Knoechel W.;
Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.

-i- SIMILARITY: TO TRANSFORMING GROWTH FACTOR (TGF) BETA FAMILY.
EMBL; X64538; CAA45836.1; -.
EMBL; AJ005076; CAA06333.1; -.
HSSP; P18075; 1BMP.
                                                                                                                             63 GLYNTLN-*-PEASASPCCVPQDLEPLTILYYVGRTPKV--EQLSNMVVKSCKC 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        63 GLYNTLN---PEASASPCCVPQDLEPLTILYYVGRTPKV--EQLSNMVVKSCKC 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 400;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Smith J.C.; Submitted (FEB-1992) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     B81472F9BCB4506E CRC64;
                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26.1%; Score 165.5; DB 13;
illarity 36.8%; Pred. No. 1e-10;
Conservative 18; Mismatches 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ź
                                                                                                                                                                                                                                                                                400 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Xenopus laevis (African clawed frog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9YHW9;
01-MAY-1999 (TrEMBLrel. 10, Created)
                                                                                                                                                                                                                                                                                                                                     Created)
                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR001839; -. Pfam; PF00019; TGF-beta; 1. Pfam; PF00688; TGFb_propeptide; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 1-20 FROM N.A. MEDLINE-93048819; Pubmed-1425340;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     400 AA; 45778 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                development.";
Development 115:573-585(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Probom; PD000357; -; 1.
PROSITE; PS00250; TGF_BETA; 1.
                                                                                                                                                                                                                                                                                                                                (TrEMBLrel. 01, (TrEMBLrel. 01, (TrEMBLrel. 16,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E S E
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TGF\_BETA; 1.

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P79707:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5,
                                                  Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                  TISSUE-LEG BUD;
MEDLINE=99119368; PubMed=9918693;
MEDLINE=99119368; PubMed=9918693;
Merino R., Mactas D., Ganan Y., Economides A.N., Wang X., Wu Q.,
Merino R., Mactas D., Ganan P., Hurle J.M.;
Stahl N., Sampath K.T., Varona P., Hurle J.M.;
"Expression and function of Gdf-5 during digit skeletogenesis in the embryonic chick leg bud.";
Dev. Biol. 206:33-45(1999).
-!- SIMILARITY: TO TRANSFORMING GROWTH FACTOR (TGF) BETA FAMILY.
HSSP; P18075; 1BMP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9 RNLEENCCVRPLYIDFRQDLGW-KWVHEPKGYYANFCSGPCPY-LRS--ADTTHSTVLGL 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1996 (TrEMBLrel. 16, Last annotation update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
ACTIVIN BETA-B-1 SUBUNIT (FRAGMENT).
Carassius auratus (Goldfish).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Cyprininae; Carassius.
NUBL_TAXID=7957;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=93290666; PubMed=8512569; MEDLINE=93290666; PubMed=8512569; Ge W., Gallin W.J., Strobeck C., Peter R.E.; Ge W. Gallin W.J., Strobeck C., Peter R.E.; Cloning and sequencing of goldfish activin subunit genes: strong structural conservation during vertebrate evolution."; Biochem. Biophys. Res. Commun. 193:711-717(1993).

EMBL; L15340; AAA49160.1; -- HSSP; P18075; LBMP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 324;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0B8A7CB111375007 CRC64;
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
GROWTH DIFFERENTIATION FACTOR 5 PRECURSOR (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        285 MISMDPESTPPTCCVPTRLSPISILF-----IDSANNVYK 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      65 YNTLNPEASASPCCVPQDLEPLTILYYVGRTPKVEQLSNMVVK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match 26.0%; Score 165; DB 13; Best Local Similarity 34.0%; Pred. No. 9.4e-11; Matches 35; Conservative 24; Mismatches 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         102 AA
                                                                                                                                                                                                                                                                                                                                                                                    Pfam, PF00019; TCF.beta; 1.
Pfam, PF00068; TGFb_propeptide; 1.
PRINTS; PR00669; INHIBINA.
PROSITE; PS00250; TGF_BETA; 1.
SMART; SM00204; TGFB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  37206 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                         InterPro; IPR001111; -.
InterPro; IPR001839; -.
InterPro; IPR002405; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                324 AA;
                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                       NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Glycoprotein.
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Caudata; Salamandroidea; Salamandridae; Cynops.
                                                                                                                                                                                                                                            15 CCVRPLYIDFRQDLGWK-WVHEPKGYYANFCSGPCP-YLR----SADTTHSTVLGLYNT-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=EMBRYO;
Suzuki A.S., Tabata T., Sakaguchi K., Takabatake T., Takeshima K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29 GWK-WVHEPKGYYANFCSGPCPYLRSA---DTTHSTVLGLYNTLNPEASASPCCVPQDLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Serial expression of the genes in a mesodermalizing ectoderms of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   early Cynops gastrula.";
Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: TO TRANSFORMING GROWTH FACTOR (TGF) BETA FAMILY.
                                                                                                                                                                                                        10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4
                                                                                                                                                                Length 102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 83;
                                                                                                                                                                                                        26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21; Indels
                                                                                                    222222E54A828A7C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            83
9530 MW; 1538F56763FC4A67 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAY-1997 (TrEMBLrel. 03, Created)
01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
11-MAR-2001 (TrEMBLrel. 16, Last annotation update)
VG-1 (FRACMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Score 162; DB 13;
; Pred. No. 5e-11;
13; Mismatches 21;
                                                                                                                                                              25.9%; Score 164; DB 13; 38.8%; Pred. No. 3.7e-11; Live 16; Mismatches 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         83 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cynops pyrrhogaster (Japanese common newt).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                  65 GISP-GSVNSCCIPTKLSTMSMLYF 88
                                                                                                                                                                                                                                                                                                                           68 -LNPEASASPCCVPQDLEPLTILYY 91
                                                                               102
11358 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR001839; -.
Pfam; PF00019; TGF-beta; 1.
PROSITE; PS00250; TGF_BETA; 1.
SMART; SM00204; TGFB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; D89444; BAA13959.1; -. HSSP; P18075; 1BMP.
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                                                                                                                                                                                                        Conservative
PROSITE; PS00250; TGF_BE
SMART; SM00204; TGFB; 1.
Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                               102 1
102 AA;
                                                                                                                                                                                   Similarity
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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83 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=8330;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Glycoprotein.
                                                                                                                                                              Query Match
Best Local Simi
Matches 33;
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